

72448

4-13

220601

STIC-Biotech/ChemLib

From:

Sent:

To:

Subject:

Duffy, Patricia

Saturday, March 31, 2007 11:32 AM

STIC-Biotech/ChemLib

SPDI search

IN RE:10/063,546

SPDI search SEQ ID NO:38 commercial and interference.

Thanks.

AA 720

Patricia A. Duffy, Ph.D.

Primary Patent Examiner

571-272-0855,

Remsen 3B05,

Mailbox: 3C18

1645

ME

ABSS

Searcher: AA

Searcher Phone: _____

Date Searcher Picked up: 4-4Date completed: 4-9-07

Searcher Prep Time: _____

Online Time: _____

PMP 15

Q 15

Type of Search

NA# _____ AA# _____

S/L: _____ Oligomer: _____

Encode/Transl: _____

Structure #: _____ Text: _____

Inventor: _____ Litigation: _____

Vendors and cost where applicable

STN: _____

DIALOG: _____

QUESTEL/ORBIT: _____

LEXIS/NEXIS: _____

SEQUENCE SYSTEM: _____

WWW/Internet: _____

Other (Specify): _____

THIS PAGE BLANK (USPTO)

GenCore version 6.2
Copyright (c) 1993 - 2007 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: April 4, 2007, 21:57:24 ; Search time 347 Seconds

(without alignments)
2224.581 Million cell updates/sec

Title: US-10-063-546-38

Perfect score: 3945

Sequence: 1 MELGCGWTGQLGFLQLLLIS.....LSAPFKVLPEKDWIERNNK 720

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 3281787 seqs, 1072124677 residues

Total number of hits satisfying chosen parameters: 3281787

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database :

1: uniprot_8.4.*

2: uniprot_sprot.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3945	100.0	720	2	Q6UXH9_HUMAN
2	3941	99.9	720	2	Q5JPI4_HUMAN
3	3936	99.8	720	2	Q6N062_HUMAN
4	3926.5	99.5	737	2	Q5EBJ7_HUMAN
5	3921.5	99.4	737	2	Q96WJ2_HUMAN
6	3898	98.8	720	2	Q5RDI1_PONPY
7	3616	91.7	720	2	Q5E9P5_BOVIN
8	3612	91.6	720	2	Q8BU25_MOUSE
9	3612	91.6	720	2	Q8K2B8_MOUSE
10	2823	71.6	722	2	Q6DIV5_XENTR
11	2059	52.2	417	2	Q71RE9_HUMAN
12	1566	39.7	1009	2	Q4SAF4_TETNG
13	1122.5	28.5	488	2	Q4SHD4_TETNG
14	949	24.1	181	2	Q9Y432_HUMAN
15	678	17.2	1019	2	Q8Y9S1_TACTR
16	672	17.0	1019	1	LFC_TACTR
17	665	16.9	1019	1	LFC_CARRO
18	665	16.9	1083	2	Q26423_CARRO
19	608.5	15.4	680	2	Q268H7_BRABE
20	604	15.3	680	2	Q868H5_BRABE
21	597	15.1	688	2	Q868H6_BRABE
22	576.5	14.6	688	2	Q868H4_BRABE
23	507.5	12.9	698	2	Q6GPF9_XENLA
24	490.5	12.4	730	2	Q6Q108_CHICK
25	489.5	12.4	698	2	Q9PU71_XENLA
26	483	12.2	701	2	Q9JUS9_RAT
27	482.5	12.2	703	2	Q8CHN8_RAT
28	482	12.2	717	2	Q8AXR1_XENLA
29	478	12.1	699	1	MASPI_HUMAN
30	475	12.0	704	1	MASPI_MOUSE
31	468	11.9	728	2	Q9GRS4_HUMAN

32	467	11.8	697	2	Q8CG43_RAT	Q8CG43_rattus norv
33	466	11.8	717	2	Q8AXR0_XENLA	Q8AXR0_xenopus lae
34	459	11.6	733	2	Q8CD27_MOUSE	Q8CD27_mus musc
35	457	11.6	719	2	Q9PY22_TRISC	Q9PY22_titiaki scy
36	452	11.5	733	2	Q920S0_MOUSE	Q920S0_mus muscu
37	450.5	11.4	687	2	Q5XHB9_XENTR	Q5XHB9_xenopus tro
38	448	11.4	745	2	Q9PYV3_CYPCA	Q9PYV3_cyprius ca
39	447	11.3	686	2	Q6Q109_CHICK	Q6Q109_gallus gall
40	436.5	11.1	681	2	Q7ZT70_LAMJA	Q7ZT70_lampecta ja
41	432.5	11.0	705	2	Q4SB49_TETNG	Q4SB49_tetraodon n
42	428	10.8	707	2	C1RA_MOUSE	Q8CG16_mus muscu
43	428	10.8	707	2	Q56616_MOUSE	Q56616_mus muscu
44	423	10.7	685	1	MASP2_RAT	Q9J168_r_mannan-bi
45	422.5	10.7	713	2	Q5DVT1_EPRBU	Q5DVT1_epitretus
46	421.5	10.7	688	2	Q9PYV4_XENLA	Q9PYV4_xenopus lae
47	417	10.6	685	1	MASP2_MOUSE	Q91WY0_m_mannan-bi
48	416.5	10.6	706	1	C1RB_MOUSE	Q8CF9_mus muscu
49	414	10.5	708	2	Q2VFN1_XENLA	Q2VFN1_xenopus lae
50	404.5	10.3	705	2	Q5JHT9_HUMAN	Q5JHT9_homo sapien
51	403.5	10.2	705	1	C1R_HUMAN	P00736_homo sapien
52	403.5	10.2	705	2	Q6BD77_HUMAN	Q6BD77_homo sapien
53	401.5	10.2	496	2	Q8CHP7_CAVPO	Q8CHP7_cavia porce
54	401.5	10.2	746	2	Q81AD8_HAIRO	Q81AD8_halocynthia
55	400.5	10.2	686	1	MASP2_HUMAN	Q00187_h_mannan-bi
56	400.5	10.2	746	2	Q01654_HAIRO	Q01654_halocynthia
57	398.5	10.1	686	2	Q9DGC2_CYPCA	Q9DGC2_cyprius ca
58	395.5	10.0	705	2	Q5JH09_HUMAN	Q5JH09_homo sapien
59	395	10.0	721	2	Q7ZT69_LAMJA	Q7ZT69_lampecta ja
60	394.5	10.0	705	1	C1R_PANTR	Q51W3_pan troglod
61	394.5	10.0	705	1	C1R_PONPY	Q5154_pongo pygma
62	390.5	9.9	702	2	Q4SNE6_TETNG	Q4SNE6_tetraodon n
63	390.5	9.9	705	2	Q4R577_MACPA	Q4R577_macaca fasc
64	384	9.7	688	1	CS1B_MOUSE	Q8CF98_mus muscu
65	382.5	9.7	752	2	Q01655_HAIRO	Q01655_halocynthia
66	382	9.7	722	2	Q8AW90_LAMJA	Q8AW90_lampecta ja
67	381	9.7	722	2	Q9PEZ5_LAMJA	Q9PEZ5_lampecta ja
68	380.5	9.6	687	1	C1S_PIG	Q694K8_sus scrofa
69	378.5	9.6	695	1	CABE_MESAU	P15156_mesocricetu
70	378	9.6	676	2	Q4SBS1_TETNG	Q4SBS1_tetraodon n
71	373.5	9.5	688	2	Q4SNE7_TETNG	Q4SNE7_tetraodon n
72	372.5	9.4	752	2	Q81AD7_HAIRO	Q81AD7_halocynthia
73	368	9.3	685	2	Q9DGC1_CYPCA	Q9DGC1_cyprius ca
74	366	9.3	685	2	Q9DGC0_CYPCA	Q9DGC0_cyprius ca
75	364	9.2	688	1	CS1A_MOUSE	Q8CG14_mus muscu
76	359	9.1	685	1	Q3V5Q0_CYPCA	Q3V5Q0_cyprius ca
77	357	9.0	676	2	Q6DUJ6_CYPCA	Q6DUJ6_cyprius ca
78	354	9.0	1524	2	Q91674_XENLA	Q91674_xenopus lae
79	346	8.8	690	2	Q5EFN3_CHICK	Q5EFN3_gallus gall
80	345	8.7	638	2	Q17H79_ABDAB	Q17H79_aedes aegyp
81	340.5	8.6	688	1	C1S_RAT	Q6P6T1_rattus norv
82	340	8.6	688	2	Q3T9K7_MOUSE	Q3T9K7_mus muscu
83	339.5	8.6	707	2	Q70W31_ONCGR	Q70W31_oncorynchu
84	337.5	8.6	479	2	Q5HYM1_HUMAN	Q5HYM1_homo sapien
85	337.5	8.6	608	2	Q7PY92_ANOGA	Q7PY92_anopheles g
86	335	8.5	666	2	Q69BL0_MANSE	Q69BL0_manduca sex
87	334	8.5	503	2	Q8AYE4_BRABE	Q8AYE4_brachydantio
88	334	8.5	688	1	C1S_HUMAN	Q90871_homo sapien
89	333	8.4	730	2	Q4RHT0_TETNG	Q4RHT0_tetraodon n
90	331.5	8.4	1019	2	Q4RHT0_TETNG	P98070_homo sapien
91	331.5	8.4	1019	2	Q2NKL7_HUMAN	Q2NKL7_homo sapien
92	330.5	8.4	1034	1	ENTK_PIG	P98074_sus scrofa
93	329.5	8.4	1034	1	CSMD1_HUMAN	Q96927_homo sapien
94	329	8.3	3564	1	CSMD1_MOUSE	Q92213_mus muscu
95	328.5	8.3	2966	2	Q59FF8_HUMAN	Q59FF8_homo sapien
96	328	8.3	855	1	ST14_HUMAN	Q9Y5V6_h suppresso
97	325	8.2	483	1	PA10_TROCA	Q4GT9_tropidochis
98	324	8.2	3564	2	Q4SNC2_RAT	Q4SNC2_rattus norv
99	319.5	8.1	455	1	PA10V_TROCA	P81428_tropidochis
100	319.5	8.1	455	2	Q11657_TROCA	Q11657_tropidochis
101	318.5	8.1	455	2	Q4F879_PSAUR	Q4F879_notechis sc
102	318	8.1	483	2	Q11659_PSEUR	Q11659_pseudonaja
103	318	8.1	827	2	Q1R1P8_BRABE	Q1R1P8_brachydantio
104	318	8.1	3467	1	CSMD2_HUMAN	Q72408_homo sapien

105	318	8.1	3631	2	Q53TY4_HUMAN	Q53TY4_homo sapien	178	281.5	7.1	476	2	O6GLK4_XENLA	O6GLK4_xenopus lae
106	317.5	8.0	455	2	O58L92_HOPST	O58L92_hoplostethus	179	281.5	7.1	558	1	HABP2_MOUSE	O8K0D1_r hyaluron
107	317.5	8.0	1035	2	ENTK_BOVIN	P880072 bos taurus	180	281.5	7.1	558	1	HABP2_RAT	O61121 m musculus
108	316.5	8.0	460	1	PROC_MOUSE	P33587 m vitamin k	181	281	7.1	481	1	FA10_MOUSE	O88947 mus musculus
109	315	8.0	444	1	FA7_RABIT	P98139 oryctolagus	182	281	7.1	481	2	Q4F0S7_MOUSE	Q4F0S7_mus musculus
110	314.5	8.0	454	2	Q58L93_PSEPO	P58193 pseudocallis	183	281	7.1	481	2	Q3TRR2_MOUSE	Q3TRR2_m nod-deriv
111	314.5	8.0	475	1	FA10_CHICK	P25155 gallus galli	184	281	7.1	483	2	Q3MHW2_BOVIN	Q3MHW2_bos taurus
112	314	8.0	855	1	ST14_MOUSE	P56677 mus musculus	185	281	7.1	492	1	FA10_BOVIN	P00743 bos taurus
113	314	8.0	855	2	Q543E3_MOUSE	O543E3_m 0 day neo	186	281	7.1	492	2	Q3TD9_MOUSE	Q3TD9_bos taurus
114	313	7.9	855	2	Q9J177_RAT	O9J177_rattus norv	187	281	7.1	493	2	Q3UJY1_MOUSE	Q3UJY1_mus musculus
115	312.5	7.9	685	2	Q32N65_XENLA	Q32N65_xenopus lae	188	280.5	7.1	264	1	CTRL_HUMAN	P40313 homo sapien
116	312	7.9	467	2	Q58L95_OXYMI	Q58L95_oxyuratus m	189	280.5	7.1	259	2	O8LIW0_HUMAN	O8LIW0_homo sapien
117	311	7.9	446	1	FA7_RAT	Q7C366 brachydantio	190	280	7.1	562	1	TPA_HUMAN	P00750 homo sapien
118	310.5	7.9	444	2	Q7T3B6_BRARE	Q7T3B6_brachydantio	191	278.5	7.1	466	1	FA7_HUMAN	P08709 homo sapien
119	310.5	7.9	453	2	Q58L94_9SAUR	O58L94_notechia sc	192	278.5	7.1	824	2	O6TCC2_HUMAN	O6TCC2_homo sapien
120	310.5	7.9	461	1	PROC_HUMAN	P24070 h vitamin k	193	278	7.0	408	2	Q9VW19_DROME	Q9VW19_drosophila
121	310.5	7.9	461	2	Q53E74_HUMAN	Q53E74_homo sapien	194	278	7.0	433	2	Q804X5_CHICK	O804X5_gallus galli
122	309.5	7.8	689	2	Q4VA78_XENTR	Q4VA78_xenopus tro	195	278	7.0	488	1	FA10_HUMAN	P00742 homo sapien
123	309.5	7.8	799	1	TMPS6_MOUSE	Q4DB10 mus musculus	196	278	7.0	488	2	Q5JVE7_HUMAN	O5JVE7_homo sapien
124	309.5	7.8	811	2	Q3KN88_MOUSE	Q3KN88_mus musculus	197	278	7.0	562	2	Q503B0_HUMAN	O503B0_homo sapien
125	305	7.7	456	1	PROC_CANFA	Q28278 c vitamin k	198	278	7.0	113	1	CORIN_MOUSE	Q92319 mus musculus
126	304	7.7	1069	1	ENTK_MOUSE	P97435 mus musculus	199	277	7.0	559	1	TPA_RAT	P19637 rattus norv
127	302.5	7.7	445	2	Q19A27_PIG	Q19A27_bos scrofa	200	277	7.0	562	2	Q5R8U0_PONPY	O5R8U0_pongo pygma
128	302.5	7.7	446	1	FA7_MOUSE	P70375 mus musculus	201	276.5	7.0	24	2	Q53FV9_HUMAN	O53FV9_homo sapien
129	302.5	7.7	446	2	Q542C2_MOUSE	Q542C2_m b6-derivate	202	276.5	7.0	625	2	Q3MER7_BOVIN	Q3MER7_bos taurus
130	301.5	7.6	433	2	O8JHD0_BRARE	O8JHD0_brachydantio	203	276.5	7.0	655	1	HGFA_HUMAN	O44756 homo sapien
131	300.5	7.6	463	2	O6IT10_PSETE	O6IT10_pseudonaja	204	276.5	7.0	655	2	O51X47_HUMAN	O51X47_homo sapien
132	299.5	7.6	433	2	O504H3_BRARE	O504H3_brachydantio	205	276.5	7.0	679	2	Q9EPQ8_HUMAN	Q9EPQ8_homo sapien
133	299.5	7.6	467	2	O6IT09_PSETE	O6IT09_pseudonaja	206	276	7.0	559	2	Q6P7U0_MOUSE	Q6P7U0_homo sapien
134	299	7.6	1111	2	O80VNA_RAT	O80VNA_rattus norv	207	275.5	7.0	444	2	Q5JVF1_MOUSE	O5JVF1_m plasmod
135	298.5	7.6	433	2	Q90YK1_XENLA	Q90YK1_brachydantio	208	275.5	7.0	498	2	Q4RP66_TETNG	Q4RP66_tetradon n
136	298.5	7.6	553	2	O6P719_XENLA	O6P719_xenopus lae	209	275.5	7.0	655	2	Q2M1V7_HUMAN	Q2M1V7_homo sapien
137	298	7.6	449	2	O5CAN9_PSETE	O5CAN9_pseudonaja	210	275.5	7.0	1134	2	Q7RRY7_HUMAN	Q7RRY7_homo sapien
138	297.5	7.5	777	2	O8CAN9_MOUSE	O8CAN9_mus musculus	211	275.5	7.0	3247	2	Q4RC1_TETNG	Q4RC1_tetradon n
139	297.5	7.5	3239	2	Q4S0Y8_TETNG	Q4S0Y8_tetradon n	212	275	7.0	497	2	Q4SVF9_TETNG	Q4SVF9_tetradon n
140	297	7.5	456	2	Q5FV22_XENTR	Q5FV22_xenopus tro	213	275	7.0	1047	2	Q566K6_MOUSE	Q566K6_mus musculus
141	297	7.5	459	1	PROC_PIG	O5G1P2 c vitamin k	214	274.5	7.0	445	2	Q504J5_BRARE	Q504J5_brachydantio
142	296	7.5	463	2	O1L658_PSETE	O1L658_pseudonaja	215	274.5	7.0	547	2	O5BKN3_XENTR	O5BKN3_xenopus tro
143	296	7.5	458	1	PROC_RABIT	Q28661 o vitamin k	216	274.5	7.0	566	2	Q2KJG9_BOVIN	Q2KJG9_bos taurus
144	296	7.5	485	2	Q4VA71_XENTR	Q4VA71_xenopus tro	217	274.5	7.0	625	1	THRB_BOVIN	P00735 bos taurus
145	295.5	7.5	336	2	O8C1R9_MOUSE	O8C1R9_mus musculus	218	274.5	7.0	654	1	HGFA_CANFA	Q6QNT4_canis fami1
146	295.5	7.5	441	2	O804X2_FUGRU	O804X2_fugu rubrip	219	274.5	7.0	1235	2	Q6S9T9_CIOIN	O6S9T9_ciona intes
147	295.5	7.5	505	2	Q4SB52_TETNG	Q4SB52_tetradon n	220	274.5	7.0	3670	1	CSDM3_HUMAN	O7Z407_homo sapien
148	295	7.5	425	2	O804X7_CHICK	O804X7_gallus galli	221	273.5	6.9	443	2	O8JHC9_BRARE	O8JHC9_brachydantio
149	294	7.5	461	2	O68FY8_RAT	O68FY8_rattus norv	222	273.5	6.9	466	1	FA7_PANTR	Q2F992_pan troglod
150	293.5	7.4	364	2	Q4G030_RAT	Q4G030_rattus norv	223	273.5	6.9	517	2	Q3V1U8_MOUSE	Q3V1U8_mus musculus
151	293.5	7.4	446	2	Q38U75_CANFA	Q38U75_canis fami1	224	273.5	6.9	566	1	TPA_BOVIN	O28198_bos taurus
152	293.5	7.4	447	1	FA7_BOVIN	P22457 bos taurus	225	273	6.9	394	2	Q5S1X0_IXOSC	O5S1X0_ixodes scap
153	293.5	7.4	1331	2	Q4S572_TETNG	Q4S572_tetradon n	226	273	6.9	507	2	Q1RLV2_BRARE	O1RLV2_brachydantio
154	293	7.4	430	2	O804X0_FUGRU	O804X0_fugu rubrip	227	273	6.9	560	1	HABP2_HUMAN	O14530_h hyaluron
155	292	7.4	461	1	PROC_RAT	P31394 r vitamin k	228	273	6.9	2796	1	CSDM3_MOUSE	O80C79_mus musculus
156	291.5	7.4	390	2	O69D13_PIG	O69D13_bos scrofa	229	273	6.9	2972	2	Q4S1Z1_TETNG	Q4S1Z1_tetradon n
157	291	7.4	475	2	O804W9_FUGRU	O804W9_fugu rubrip	230	272.5	6.9	321	2	Q6MWL2_HUMAN	Q6MWL2_homo sapien
158	290.5	7.4	479	2	O19A26_PIG	O19A26_bos scrofa	231	272.5	6.9	466	1	FA7_PANPA	Q2F994_pan paniscu
159	290	7.3	464	2	O5FW21_XENTR	O5FW21_xenopus tro	232	271.5	6.9	244	1	KLKE_HUMAN	O92876_homo sapien
160	289.5	7.3	466	1	FA9_FELCA	O6EA95_felis silve	233	271.5	6.9	244	2	O6H3J1_HUMAN	O6H3J1_homo sapien
161	287.5	7.3	802	1	TMPS6_HUMAN	O6IUB0_homo sapien	234	271.5	6.9	461	2	O6TBE4_RAT	O6TBE4_rattus norv
162	287.5	7.3	980	2	O6ETN7_BUFRAR	O6ETN7_bufo arenar	235	271	6.9	433	2	O8M1L0_RABIT	O8M1L0_oryctolagus
163	287	7.3	467	2	Q58L96_SSAUR	Q58L96_oxyuratus s	236	271	6.9	433	2	O8MHY7_RABIT	O8MHY7_oryctolagus
164	287	7.3	452	1	Q4V971_BRARE	Q4V971_brachydantio	237	271	6.9	375	2	TPA_MOUSE	O5WIK5_nilavu
165	285.5	7.2	504	2	FA9_CANFA	P19540 canis fami1	238	270.5	6.9	375	2	O5WIK5_NILLU	O5WIK5_nilaparvata
166	285	7.2	504	2	O6PGW7_BRARE	O6PGW7_brachydantio	239	270.5	6.9	1032	2	Q4T9V1_TETNG	Q4T9V1_tetradon n
167	284	7.2	432	2	O6GNA2_XENLA	O6GNA2_xenopus lae	240	270	6.8	477	1	UR1_DBSRO	P98119_desmodus ro
168	284	7.2	974	2	Q90W88_BURFA	Q90W88_bufo japoni	241	270	6.8	490	1	FA10_RABIT	O19045_oryctolagus
169	283.5	7.2	482	1	FA10_RAT	O63207_rattus norv	242	269	6.8	261	2	Q6DHD9_BRARE	O6DHD9_brachydantio
170	283.5	7.2	589	2	O6PJU5_HUMAN	O6PJU5_homo sapien	243	269	6.8	265	2	Q56IU4_BRARE	O56IU4_brachydantio
171	283	7.2	376	1	FA10_HOPST	P83370 hoplostcephal	244	269	6.8	643	2	O97506_PIG	O97506_bos scrofa
172	282.5	7.2	320	2	O8C1R7_RAT	O8C1R7_rattus norv	245	269	6.8	833	2	O96442_STRPU	O96442_strongylo
173	282.5	7.2	666	2	O2KJG3_BOVIN	O2KJG3_bos taurus	246	268.5	6.8	290	2	O58B07_XENLA	O58B07_xenopus lae
174	282	7.1	456	1	PROC_BOVIN	P00745 b vitamin k	247	268	6.8	558	1	HABP2_BOVIN	O5E922_b hyaluron
175	282	7.1	469	2	Q9GMD9_ORNAN	Q9GMD9_ornithorhyn	248	268	6.8	740	2	Q3MHR6_BOVIN	O3MHR6_bos taurus
176	282	7.1	1466	2	Q7ZZ41_BRARE	Q7ZZ41_brachydantio	249	268	6.8	740	2	Q4TB33_TETNG	Q4TB33_tetradon n
177	282	7.1	3417	2	Q1L898_BRARE	Q1L898_brachydantio	250	267.5	6.8	268	2	O6GQ89_XENLA	O6GQ89_xenopus lae

251	267	6.8	455	2	Q7SY86_XENLA	Q78Y86 xenopus lae	324	255.5	6.5	359	2	Q28XR0_DROPS	Q28XR0 drosophila
252	267	6.8	463	2	Q5M8Y0_XENTR	Q5M8Y0 xenopus tro	325	255.5	6.5	587	2	Q17FW1_AEDAE	Q17FW1 aedes aegypt
253	267	6.8	868	2	Q9Y1V3_POLMI	Q9Y1V3 polyanthrocra	326	255.5	6.5	763	2	Q31430_LAMJA	Q31430 lampecta ja
254	266.5	6.8	441	2	Q4SU02_TETNG	Q4SU02 tetraodon n	327	255	6.5	325	2	Q15944_SARPE	Q15944 sarcoptahaga
255	266	6.7	352	2	Q7KVM3_DROME	Q7KVM3 drosophila	328	255	6.5	845	2	Q6GR54_XENLA	Q6GR54 xenopus lae
256	266	6.7	359	2	Q17FW0_AEDAE	Q17FW0 aedes aegypt	329	254.5	6.5	250	2	Q28YV4_DROPS	Q28YV4 drosophila
257	266	6.7	359	2	Q4SU09_TETNG	Q4SU09 tetraodon n	330	254.5	6.5	315	2	Q7TT44_MOUSE	Q7TT44 mus musculus
258	266	6.7	889	2	Q5GCC1_CARRO	Q5GCC1 carciuncoscor	331	254.5	6.5	461	2	Q95NDC_PANTR	Q95NDC pan troglod
259	265.5	6.7	250	2	Q9Y514_DROME	Q9Y514 drosophila	332	254.5	6.5	314	2	Q9VR15_DROME	Q9VR15 drosophila
260	265.5	6.7	264	2	Q5SEW3_TETNG	Q5SEW3 tetraodon n	333	254	6.4	617	1	THR8_RAT	THR8 rat
261	265	6.7	311	2	Q502L4_BRARE	Q502L4 brachydantio	334	254	6.4	998	2	Q5H875_CIOIN	Q5H875 ciona intes
262	265	6.7	381	2	Q29DF3_DROPS	Q29DF3 drosophila	335	253.5	6.4	471	2	Q3UES1_MOUSE	Q3UES1 mus musculus
263	265	6.7	381	2	Q4SU07_TETNG	Q4SU07 tetraodon n	336	253.5	6.4	487	2	Q9NZP8_HUMAN	Q9NZP8 homo sapien
264	264.5	6.7	431	1	URTB_DESRO	P98121 desmodus ro	337	253.5	6.4	615	2	Q6GNK4_XENLA	Q6GNK4 xenopus lae
265	264.5	6.7	618	1	THRB_MOUSE	P19221 mus musculus	338	253.5	6.4	628	2	Q9VER6_DROME	Q9VER6 drosophila
266	264.5	6.7	618	1	Q3J094_MOUSE	Q3J094 mus musculus	339	253	6.4	263	2	Q4SEW1_TETNG	Q4SEW1 tetraodon n
267	264	6.7	653	1	HGFA_MOUSE	Q9J098 mus musculus	340	253	6.4	471	1	FAJ2_CHICK	FAJ2 gallus gall
268	264	6.7	653	2	Q545J3_MOUSE	Q545J3 m 10 day ol	341	253	6.4	616	1	FAJ2_PIG	FAJ2 aplysia cal
269	264	6.7	653	2	Q5EBA7_RAT	Q5EBA7 rattus norv	342	253	6.4	1070	2	P91972_APICA	P91972 sparus aura
270	264	6.7	910	2	Q4RBD7_TETNG	Q4RBD7 tetraodon n	343	252.5	6.4	241	2	Q4QY79_SPRAU	Q4QY79 sparus aura
271	263.5	6.7	253	2	Q7SX97_BRARE	Q7SX97 brachydantio	344	252.5	6.4	487	2	Q5JGX9_HUMAN	Q5JGX9 homo sapien
272	263.5	6.7	444	2	Q2E9N5_PONPY	Q2E9N5 pongo pygma	345	252	6.4	260	2	Q6E2V9_XENTR	Q6E2V9 xenopus tro
273	263.5	6.7	444	2	Q2E9N4_PONPY	Q2E9N4 pongo pygma	346	252	6.4	261	2	Q66HW9_BRARE	Q66HW9 brachydantio
274	263	6.7	431	2	Q5SWM9_HUMAN	Q5SWM9 homo sapien	347	252	6.4	600	2	Q5R976_PONPY	Q5R976 pongo pygma
275	263	6.7	431	2	Q5JXS3_HUMAN	Q5JXS3 homo sapien	348	252	6.4	607	2	Q6DRJ5_XENLA	Q6DRJ5 xenopus lae
276	263	6.7	653	2	Q8VCS4_MOUSE	Q8VCS4 mus musculus	349	251.5	6.4	267	2	Q7R694_ANOGA	Q7R694 anopheles g
277	263	6.7	3239	2	Q4SIT9_TETNG	Q4SIT9 tetraodon n	350	251.5	6.4	389	2	Q177F1_AEDAE	Q177F1 aedes aegypt
278	262.5	6.7	300	2	Q819P4_AURAU	Q819P4 aurelia aur	351	251	6.4	263	2	Q51029_XENTR	Q51029 xenopus tro
279	262.5	6.7	461	1	FA9_HUMAN	P00740 homo sapien	352	251	6.4	295	2	Q8CIP7_RAT	Q8CIP7 rattus norv
280	262.5	6.7	461	1	FA9_PANTR	Q95ND7 pan troglod	353	251	6.4	343	2	Q504K1_BRARE	Q504K1 brachydantio
281	262.5	6.7	461	2	Q5JYJ8_HUMAN	Q5JYJ8 homo sapien	354	251	6.4	407	2	Q7OKL1_ANOGA	Q7OKL1 anopheles g
282	262.5	6.7	1042	2	CORTN_HUMAN	Q9Y5G5 homo sapien	355	251	6.4	537	2	Q804W8_FUGRU	Q804W8 fugu rubrip
283	262.5	6.7	1042	2	Q2TBDZ_HUMAN	Q2TBDZ homo sapien	356	251	6.4	969	2	Q2ABP0_BRARE	Q2ABP0 brachydantio
284	262	6.6	314	2	Q29LAI_DROPS	Q29LAI drosophila	357	251	6.4	1215	2	Q4H2P2_CIOIN	Q4H2P2 ciona intes
285	262	6.6	477	1	UR12_DESRO	P15638 desmodus ro	358	251	6.4	1378	2	Q48YJ3_DROPS	Q48YJ3 drosophila
286	262	6.6	653	2	Q3TDB8_XENLA	Q3TDB8 mus musculus	359	250.5	6.3	347	1	HPT_RABIT	HPT oryctolagus
287	261.5	6.6	284	2	Q8AXO8_MOUSE	Q8AXO8 xenopus lae	360	250.5	6.3	548	2	Q502D2_BRARE	Q502D2 brachydantio
288	261.5	6.6	442	1	UROK_PIG	P04185 sus scrofa	361	250.5	6.3	875	1	NERR_PANTR	NERR pan troglod
289	261	6.6	431	1	UROK_HUMAN	P00749 h urokinase	362	250	6.3	263	2	Q1UPZ1_BRARE	Q1UPZ1 brachydantio
290	261	6.6	433	1	UROK_BOVIN	P00559 bos taurus	363	250	6.3	306	1	BSSP4_MOUSE	BSSP4 mus musculus
291	261	6.6	969	2	Q5KOU1_MACPA	Q5KOU1 macaca fasc	364	250	6.3	562	2	Q8S023_PIG	Q8S023 sus scrofa
292	260.5	6.6	264	2	Q9EQZ8_RAT	Q9EQZ8 rattus norv	365	250	6.3	845	2	Q63Z06_XENLA	Q63Z06 xenopus lae
293	260.5	6.6	456	2	Q7T443_MOUSE	Q7T443 mus musculus	366	250	6.3	1379	2	Q9VAN6_DROME	Q9VAN6 drosophila
294	260.5	6.6	462	2	Q6PAG2_XENLA	Q6PAG2 xenopus lae	367	250	6.3	1397	2	Q7KQO9_DROME	Q7KQO9 drosophila
295	260.5	6.6	482	2	Q3U709_MOUSE	Q3U709 mus musculus	368	249.5	6.3	303	2	Q16NA7_AEDAE	Q16NA7 aedes aegypt
296	260.5	6.6	482	2	Q3V019_MOUSE	Q3V019 mus musculus	369	249.5	6.3	400	2	Q27081_TACTR	Q27081 tachypleus
297	260.5	6.6	1042	2	Q5KOU3_MACPA	Q5KOU3 macaca fasc	370	249.5	6.3	430	2	Q1RLR1_BRARE	Q1RLR1 brachydantio
298	260	6.6	431	2	Q5R929_PONPY	Q5R929 pongo pygma	371	249.5	6.3	435	2	Q4TBY8_TETNG	Q4TBY8 tetraodon n
299	259	6.6	245	1	CTRB_GADMO	P80646 gadus morhu	372	249.5	6.3	552	2	Q1J029_BRARE	Q1J029 brachydantio
300	259	6.6	416	1	PA9_BOVIN	P00741 bos taurus	373	249.5	6.3	875	1	NERR_HUMAN	NERR homo sapien
301	259	6.6	474	2	Q8UHC8_BRARE	Q8UHC8 brachydantio	374	249	6.3	263	2	Q6GPI1_HUMAN	Q6GPI1 homo sapien
302	259	6.6	581	2	Q9XZM7_STRPU	Q9XZM7 stryngyloce	375	249	6.3	263	2	Q9CR35_MOUSE	Q9CR35 mus musculus
303	259	6.6	1005	2	Q5KOU2_MACPA	Q5KOU2 macaca fasc	376	249	6.3	328	2	Q3UEP7_MOUSE	Q3UEP7 mus musculus
304	258.5	6.6	255	2	Q7QCS5_ANOGA	Q7QCS5 anopheles g	377	249	6.3	409	1	FA9_PIG	FA9 pig
305	258.5	6.6	411	2	Q5PY49_HUMAN	Q5PY49 homo sapien	378	248.5	6.3	548	2	Q5MBR5_MANSE	Q5MBR5 manduca sex
306	258.5	6.6	787	1	STUB_DROME	Q95J19 drosophila	379	248.5	6.3	241	2	Q4QRT3_SPRAU	Q4QRT3 sparus aura
307	258	6.5	253	2	Q9PWQ6_GADMO	Q9PWQ6 gadus morhu	380	248.5	6.3	401	2	Q4R8B3_TETNG	Q4R8B3 tetraodon n
308	258	6.5	432	2	Q17PV2_AEDAE	Q17PV2 aedes aegypt	381	248.5	6.3	459	1	FA9_MOUSE	FA9 mouse
309	258	6.5	343	1	UROK_PAPCY	P16227 p urokinase	382	248.5	6.3	623	2	Q19AZ8_PIG	Q19AZ8 sus scrofa
310	258	6.5	444	2	Q5MPB9_MANSE	Q5MPB9 manduca sex	383	248.5	6.3	744	2	Q7OJ17_ANOGA	Q7OJ17 anopheles g
311	258	6.5	612	2	Q804W7_FUGRU	Q804W7 fugu rubrip	384	248.5	6.3	876	1	NERR_GORGO	NERR gorilla gor
312	257.5	6.5	580	2	Q50IG7_ORYLA	Q50IG7 oryzae lat	385	248	6.3	259	2	Q6AZC2_BRARE	Q6AZC2 brachydantio
313	257.5	6.5	607	2	Q4OR53_XENLA	Q4OR53 xenopus lae	386	248	6.3	261	2	Q9W7Q4_PAROL	Q9W7Q4 paralicthy
314	257.5	6.5	680	2	Q294V2_DROPS	Q294V2 drosophila	387	248	6.3	263	1	CTRB1_HUMAN	CTRB1 homo sapien
315	257.5	6.5	1004	2	P79953_XENLA	P79953 xenopus lae	388	248	6.3	540	2	Q800Y7_MEGA	Q800Y7 meleagris g
316	257	6.5	273	2	Q708L2_ANOGA	Q708L2 anopheles g	389	248	6.3	638	1	KIKX1_HUMAN	KIKX1 homo sapien
317	257	6.5	607	2	Q5FW11_XENTR	Q5FW11 xenopus tro	390	248	6.3	638	1	Q4HSC3_HUMAN	Q4HSC3 homo sapien
318	257	6.5	999	2	Q5H876_CIOIN	Q5H876 ciona intes	391	248	6.3	638	2	Q17RE9_HUMAN	Q17RE9 homo sapien
319	256.5	6.5	264	2	Q9D7P8_MOUSE	Q9D7P8 mus musculus	392	248	6.3	638	2	Q17RE8_HUMAN	Q17RE8 homo sapien
320	256.5	6.5	264	2	Q9ER05_MOUSE	Q9ER05 mus musculus	393	248	6.3	764	1	CFAB_PANTR	CFAB pan troglod
321	256.5	6.5	453	2	Q4SUA1_TETNG	Q4SUA1 tetraodon n	394	248	6.3	775	2	Q6P550_MOUSE	Q6P550 mus musculus
322	256	6.5	243	2	Q7PWE3_ANOGA	Q7PWE3 anopheles g	395	248	6.3	991	2	Q6NZM2_MOUSE	Q6NZM2 mus musculus
323	255.5	6.5	268	2	Q64288_XENTR	Q64288 xenopus tro	396	248	6.3				

397	248	6.3	1469	2	Q29BZ7_DROPS	Q29BZ7_drosophila	470	242	6.1	725	2	Q4SGT4_TETNG	Q4SGT4_tetradon n
398	247.5	6.3	307	2	Q7TMC0_MOUSE	Q7TMC0_mus musculus	471	241.5	6.1	269	2	Q4S850_TETNG	Q4S850_tetradon n
399	247.5	6.3	311	2	Q9WLC2_DROME	Q9WLC2_drosophila	472	241.5	6.1	279	2	Q9WSM4_MOUSE	Q9WSM4_mus musculus
400	247.5	6.3	991	1	BMPL_MOUSE	P88063_mus musculus	473	241.5	6.1	279	2	Q3M154_MOUSE	Q3M154_mus musculus
401	247	6.3	235	2	Q287J1_RABIT	P15944_canis fam1	474	241.5	6.1	416	2	Q86T26_HUMAN	Q86T26_homo sapien
402	247	6.3	275	1	TRYT_CANFA	Q19174_drosophila	475	241.5	6.1	623	1	THRB_PONPY	Q51537_pongo pygma
403	247	6.3	364	2	Q917V4_DROME	Q81924_bombyx mori	476	241.5	6.1	875	1	NETR_SAGLB	Q5G265_sagulinus la
404	247	6.3	386	2	Q81924_BOMMO	P00751_homo sapien	477	241.5	6.1	1	NETR_TRAPH	Q5G265_tachypthe	
405	247	6.3	764	1	CPAB_HUMAN	Q5JPE7_homo sapien	478	241	6.1	296	2	Q5FVY7_XENTR	Q5FVY7_xenopus tro
406	247	6.3	764	2	Q5JPE7_HUMAN	Q5JPE7_homo sapien	479	241	6.1	346	1	HPT_MESAU	Q35086_mesocricetu
407	247	6.3	764	2	Q5JPE9_HUMAN	Q5JPE9_homo sapien	480	241	6.1	818	1	Q6PBA6_BRARE	Q6PBA6_brachydantio
408	247	6.3	764	1	Q5T5S0_HUMAN	Q5T5S0_homo sapien	481	241	6.1	1452	2	Q7Q058_ANOCA	Q7Q058_anopheles g
409	247	6.3	986	1	BMPI_HUMAN	P13497_homo sapien	482	241	6.1	2	Q8MJ16_BOVIN	Q8MJ16_bos taurus	
410	246.5	6.2	235	2	Q90387_CYNPY	Q90387_cynops pyr	483	240.5	6.1	1238	2	Q9W706_PAROL	Q9W706_parallelitche
411	246.5	6.2	264	2	Q9D960_MOUSE	Q9D960_mus musculus	484	240.5	6.1	266	2	Q4QY80_SPAU	Q4QY80_sparus aura
412	246.5	6.2	297	2	Q88781_RATRT	Q88781_rattus ratc	485	240.5	6.1	366	2	Q279Y2_BOVIN	Q279Y2_bos taurus
413	246.5	6.2	335	2	Q4T7B2_TETNG	Q4T7B2_tetradon n	486	240.5	6.1	442	2	Q8WVC1_HUMAN	Q8WVC1_homo sapien
414	246.5	6.2	347	1	HPT_ATEGE	P50417_ateles geof	487	240.5	6.1	3548	2	Q5VTE4_HUMAN	Q5VTE4_homo sapien
415	246.5	6.2	418	2	Q4R6T2_MACFA	Q4R6T2_macaca fasc	488	240	6.1	242	2	Q92099_PARGG	Q92099_parmotche
416	246.5	6.2	486	2	Q5PRA6_BRARE	Q5PRA6_brachydantio	489	240	6.1	1059	1	TMPS9_HUMAN	Q72410_homo sapien
417	246.5	6.2	622	1	THRB_HUMAN	P00734_homo sapien	490	239.5	6.1	240	2	Q8BTHQ_YTELE	Q8BTHQ_entele
418	246.5	6.2	622	1	Q4QZ50_HUMAN	Q4QZ50_homo sapien	491	239.5	6.1	371	2	Q5MPC6_MANSE	Q5MPC6_manduca sex
419	246.5	6.2	622	2	Q53H06_HUMAN	Q53H06_homo sapien	492	239.5	6.1	406	1	HPT_HUMAN	P00738_homo sapien
420	246.5	6.2	622	2	Q53H04_HUMAN	Q53H04_homo sapien	493	239.5	6.1	1015	1	Q2M1H1_HUMAN	Q2M1H1_homo sapien
421	246.5	6.2	622	2	Q727P3_HUMAN	Q727P3_homo sapien	494	239.5	6.1	1015	2	Q2M1H1_HUMAN	Q2M1H1_homo sapien
422	246	6.2	249	2	Q5TNA8_ANOCA	Q5TNA8_anopheles g	495	239.5	6.1	3567	1	Q9ES77_MOUSE	Q9ES77_mus musculus
423	246	6.2	263	2	Q9D8X8_MOUSE	Q9D8X8_mus musculus	496	239	6.1	245	1	CTRA_BOVIN	P00766_bos taurus
424	246	6.2	267	2	Q5BK00_XENTR	Q5BK00_xenopus tro	497	239	6.1	264	2	Q4QY78_SPAU	Q4QY78_sparus aura
425	246	6.2	764	1	CPAB_GORGO	Q66469_gorilla gor	498	239	6.1	268	2	Q7PZ03_ANOCA	Q7PZ03_anopheles g
426	246	6.2	812	1	PLMN_BOVIN	Q80461_bos taurus	499	239	6.1	335	2	Q2AAD0_PHACA	Q2AAD0_phalaecrocor
427	245.5	6.2	265	2	Q804G1_BRARE	Q804G1_brachydantio	500	239	6.1	435	2	Q7OC30_ANOCA	Q7OC30_anopheles g
428	245.5	6.2	467	2	Q967X8_PANAR	Q967X8_pannulirus a	501	239	6.1	436	1	HEPS_MOUSE	Q35433_mus musculus
429	245	6.2	263	2	Q6GNF7_XENLA	Q6GNF7_xenopus lae	502	239	6.1	638	2	Q5FV52_RAT	Q5FV52_rattus norv
430	245	6.2	277	2	Q7PKE8_ANOCA	Q7PKE8_anopheles g	503	239	6.1	977	2	Q91925_XENLA	Q91925_xenopus lae
431	245	6.2	369	2	Q2VGB6_BOMMO	Q2VGB6_bombyx mori	504	238.5	6.0	268	2	Q46151_PACIE	Q46151_pactiaecacu
432	245	6.2	638	2	Q8R0P5_MOUSE	Q8R0P5_mus musculus	505	238.5	6.0	578	2	Q6Q017_BOVIN	Q6Q017_bos taurus
433	245	6.2	639	1	BMPI_STRPU	P88063_strongyloce	506	238.5	6.0	625	1	FALI_BOVIN	Q5NCT3_bos taurus
434	245	6.2	1167	2	Q5T6B6_HUMAN	Q5T6B6_homo sapien	507	238.5	6.0	928	2	Q7QAH1_ANOCA	Q7QAH1_anopheles g
435	244.5	6.2	223	2	Q4QY74_SPAU	Q4QY74_sparus aura	508	238	6.0	237	1	TRYP_ASTEL	P00765_aetacus flu
436	244.5	6.2	242	2	Q7Q9W3_ANOCA	Q7Q9W3_anopheles g	509	238	6.0	242	2	Q1AMP9_DISMA	Q1AMP9_dissotichu
437	244.5	6.2	511	2	Q570Z4_MOUSE	Q570Z4_mus musculus	510	238	6.0	263	1	Q1AMP9_DISMA	Q1AMP9_dissotichu
438	244.5	6.2	608	2	Q9PTW7_STRCA	Q9PTW7_struthio ca	511	238	6.0	275	1	TRYT_PIG	P04813_canis fam1
439	244.5	6.2	1061	1	TMPS9_RAT	P65922_rattus norv	512	238	6.0	283	2	Q7PY20_ANOCA	Q7PY20_anopheles g
440	244	6.2	263	2	Q9DC86_MOUSE	Q9DC86_mus musculus	513	238	6.0	347	1	HPT_PONPY	Q51566_pongo pygma
441	244	6.2	311	2	Q11V42_BRARE	Q11V42_brachydantio	514	238	6.0	375	1	PCE_TACTR	P21992_tachypleus
442	244	6.2	322	2	Q920S2_MOUSE	Q920S2_mus musculus	515	238	6.0	435	2	Q9NFT2_ANOCA	Q9NFT2_anopheles g
443	244	6.2	445	2	Q3U0U6_MOUSE	Q3U0U6_mus musculus	516	238	6.0	767	2	Q9DGR2_XENLA	Q9DGR2_xenopus lae
444	244	6.2	638	1	KLKB1_MOUSE	P26162_mus musculus	517	237.5	6.0	251	2	Q171W0_AEDAE	Q171W0_aedes aegy
445	244	6.2	986	2	Q2ABP1_BRARE	Q2ABP1_brachydantio	518	237.5	6.0	267	2	Q4QRF8_BRARE	Q4QRF8_brachydantio
446	244	6.2	1806	2	Q571B7_MOUSE	Q571B7_mus musculus	519	237.5	6.0	371	2	Q177E4_AEDAE	Q177E4_aedes aegy
447	243.5	6.2	285	2	Q8CG42_RAT	Q8CG42_rattus norv	520	237.5	6.0	449	2	Q7PY21_ANOCA	Q7PY21_anopheles g
448	243.5	6.2	435	2	SNAK_DROME	P05045_drosophila	521	237.5	6.0	475	2	Q31Z06_MOUSE	Q31Z06_mus musculus
449	243.5	6.2	435	2	Q29QF0_DROME	Q29QF0_drosophila	522	237.5	6.0	607	2	Q297J7_DROPS	Q297J7_drosophila
450	243.5	6.2	555	2	Q5FVX1_XENTR	Q5FVX1_xenopus tro	523	237.5	6.0	735	2	Q57381_XENLA	Q57381_xenopus lae
451	243.5	6.2	764	1	CPAB_PONPY	Q5G269_pongo pygma	524	237.5	6.0	735	2	Q66K13_XENLA	Q66K13_xenopus lae
452	243.5	6.2	877	1	NETR_PONPY	Q5A787_tetradon n	525	237.5	6.0	810	1	PLMN_ERIEU	Q29445_erinaeus e
453	243	6.2	261	2	Q4RHR8_TETNG	Q4RHR8_tetradon n	526	237	6.0	237	2	Q91515_FUGRU	Q91515_fugu rubrip
454	243	6.2	273	1	TRYT_SHEEP	Q9XSM2_ovis aries	527	237	6.0	263	1	CTRB1_RAT	P07338_rattus norv
455	243	6.2	331	2	Q16G06_AEDAE	Q16G06_aedes aegy	528	237	6.0	263	2	Q6PGS4_XENLA	Q6PGS4_xenopus lae
456	243	6.2	442	2	Q804X1_FUGRU	Q804X1_fugu rubrip	529	237	6.0	963	3	Q5H874_CIOIN	Q5H874_ciona lntes
457	242.5	6.1	233	2	Q4RV18_TETNG	Q4RV18_tetradon n	530	236.5	6.0	227	2	Q7QDT9_ANOCA	Q7QDT9_anopheles g
458	242.5	6.1	279	2	Q3JUN5_MOUSE	Q3JUN5_mus musculus	531	236.5	6.0	248	2	Q28X04_DROPS	Q28X04_drosophila
459	242.5	6.1	564	2	Q8MKR1_RABIT	Q8MKR1_cytocolagus	532	236.5	6.0	251	2	Q7Q9W2_ANOCA	Q7Q9W2_anopheles g
460	242.5	6.1	564	2	Q5R502_PONPY	Q5R502_pongo pygma	533	236.5	6.0	274	1	MCPT6_RAT	P50342_rattus norv
461	242.5	6.1	574	2	Q86RL8_JCAEN	Q86RL8_ilyanassa o	534	236.5	6.0	707	1	Q29BPS_DROPS	Q29BPS_drosophila
462	242.5	6.1	578	2	Q17GV5_AEDAE	Q17GV5_aedes aegy	535	236.5	6.0	761	2	Q99JG8_RAT	Q99JG8_rattus lae
463	242.5	6.1	891	2	Q57658_CHICK	Q57658_gallus galli	536	236.5	6.0	1013	1	Q99JG8_RAT	Q99JG8_rattus lae
464	242.5	6.1	893	2	Q59F71_HUMAN	Q59F71_homo sapien	537	236.5	6.0	267	2	Q7QAK5_ANOCA	Q7QAK5_anopheles g
465	242.5	6.1	875	1	NETR_HYLLE	Q5G268_hyllobates l	538	236	6.0	328	2	Q5BL24_BRARE	Q5BL24_brachydantio
466	242.5	6.1	875	1	NETR_MACMU	Q5G267_macaca mul	539	236	6.0	328	2	Q5MG68_LONON	Q5MG68_lononia obi
467	242.5	6.1	1019	1	TLI2_XENLA	Q57382_xenopus lae	540	236	6.0	519	2	PLMN_MOUSE	P20918_mus musculus
468	242.5	6.1	1065	1	TMPS9_MOUSE	P65925_mus musculus	541	236	6.0	812	1	PLMN_MOUSE	P20918_mus musculus
469	242.5	6.1	3574	2	Q4LDES_HUMAN	Q4LDES_homo sapien	542	236	6.0	1550	2	Q4T392_TETNG	Q4T392_tetradon n

543	235.5	6.0	259	2	Q50BF4_9DIPT	050b4 culicoides	616	230	5.8	372	2	Q9Y1K6_ANOGA	Q9Y1K6 anopheles g
544	235.5	6.0	260	2	Q9W7Q3_PAROL	Q9w7q3 paratichthy	617	230	5.8	607	2	Q91001_CHICK	Q91001 gallus gall
545	235.5	6.0	359	2	Q6AXZ6_RAT	Q6axz6 rattus norv	618	229.5	5.8	235	2	Q19WT4_BUBBU	Q19wt4 bubalus bub
546	235.5	6.0	433	2	Q812A6_MOUSE	Q812a6 mus musculu	619	229.5	5.8	329	1	HPT_CANFA	P19006 canis famli
547	235.5	6.0	734	2	Q28C16_XENTR	Q28c16 xenopus tiro	620	229.5	5.8	374	2	Q9VTG2_DROME	Q9vtg2 drosoephila
548	235	6.0	261	2	Q4QY77_SPAUV	Q4qy77 sparus aura	621	229.5	5.8	514	2	Q16N50_AEADAE	Q16n50 aedes aegyp
549	235	6.0	270	1	TRYT_MERUN	P50342 meriones un	622	229.5	5.8	624	1	FALL_MOUSE	Q91447 mus musculu
550	235	6.0	322	2	Q16V45_AEADAE	Q16v45 aedes aegyp	623	229	5.8	267	2	Q9BK47_9ECHI	Q9bk47 luidia foli
551	235	6.0	336	2	Q7RTY5_HUMAN	Q7rty5 homo sapien	624	229	5.8	274	2	Q3UN30_MOUSE	Q3un30 mus musculu
552	235	6.0	345	2	Q28800_PANTR	Q28800 pan troglod	625	229	5.8	274	2	Q924N9_MOUSE	Q924n9 mus musculu
553	235	6.0	524	2	Q7SXH8_BRARE	Q7sxh8 brachydantio	626	229	5.8	490	2	Q3UKES3_MOUSE	Q3uk3 mus musculu
554	235	6.0	622	2	Q5NKF9_ONCMY	Q5nkf9 oncorhynch	627	229	5.8	722	2	Q6NWF5_XENTLA	Q6nwf5 xenopus lae
555	235	6.0	812	1	PLMN_RAT	Q01177 rattus norv	628	229	5.8	733	2	Q9VXT9_DROME	Q9vxt9 drosoephila
556	235	6.0	812	1	Q5BK66_RAT	Q5bk66 rattus norv	629	229	5.8	845	2	Q9DGR1_XENTLA	Q9dgr1 xenopus lae
557	235	6.0	1420	1	APQA_MACMU	P14417 macaca mula	630	228.5	5.8	347	2	Q63927_9MURI	Q63927 mus sp. hap
558	234.5	5.9	259	2	Q4S849_TETNG	Q4s849 tetradon n	631	228.5	5.8	352	2	Q6UWB4_HUMAN	Q6uwb4 homo sapien
559	234.5	5.9	267	2	Q561U9_BRARE	Q561u9 brachydantio	632	228.5	5.8	446	2	Q2TUC1_9DIPT	Q2tuc1 phlebotomus
560	234.5	5.9	271	2	Q5R1Z2_BRARE	Q5r1z2 brachydantio	633	228.5	5.8	573	2	Q7PV58_ANOGA	Q7pv58 anopheles g
561	234.5	5.9	291	2	Q175R9_AEADAE	Q175r9 aedes aegyp	634	228.5	5.8	600	2	Q17490_ANOGA	Q17490 anopheles g
562	234.5	5.9	300	2	Q175S0_AEADAE	Q175s0 aedes aegyp	635	228.5	5.8	761	2	Q2KTU6_BOVIN	Q2ktu6 bos taurus
563	234.5	5.9	326	2	Q32PT2_BRARE	Q32pt2 brachydantio	636	228.5	5.8	1084	2	Q9BP40_HAURO	Q9bp40 halocynthia
564	234.5	5.9	375	2	Q2M165_DROPS	Q2m165 anopheles g	637	228.5	5.8	2516	2	Q7TQ52_MOUSE	Q7tq52 mus musculu
565	234.5	5.9	382	2	Q7Q432_ANOGA	Q7q432 anopheles g	638	228.5	5.8	2526	2	Q7TQ51_MOUSE	Q7tq51 mus musculu
566	234.5	5.9	395	2	Q9BZM1_HUMAN	Q9bzm1 homo sapien	639	228.5	5.8	2531	1	NOTCL_MOUSE	Q01705 mus musculu
567	234.5	5.9	418	2	Q6NPO2_DROME	Q6np02 drosoephila	640	228.5	5.8	2531	2	Q8K428_MOUSE	Q8k428 mus musculu
568	234.5	5.9	433	1	TMPS3_MOUSE	Q8k10 mus musculu	641	228.5	5.8	2531	2	Q7TQ50_MOUSE	Q7tq50 mus musculu
569	234.5	5.9	433	1	Q2M1G4_MOUSE	Q2m1g4 mus musculu	642	228	5.8	263	2	Q5H2D0_XENTR	Q5h2d0 xenopus tiro
570	234.5	5.9	624	2	Q9DAT3_MOUSE	Q9dat3 mus musculu	643	228	5.8	3687	2	Q9W332_DROME	Q9w332 drosoephila
571	234	5.9	417	1	DESCA_RAT	Q5qsk8 rattus norv	644	227.5	5.8	235	2	Q91004_GECKO	Q91004 gecko gecko
572	234	5.9	575	2	Q8IRB8_DROME	Q8irb8 drosoephila	645	227.5	5.8	242	1	TRV1_SALSA	P35031 salmo salar
573	234	5.9	3623	1	CUNN_MOUSE	Q9j1l4 mus musculu	646	227.5	5.8	251	1	KLKI4_HUMAN	Q9pg3 homo sapien
574	233.5	5.9	263	1	CTRA_GADMO	P47796 gadus morhu	647	227.5	5.8	251	1	Q6B089_HUMAN	Q6b089 homo sapien
575	233.5	5.9	267	2	Q7S2S1_BRARE	P27521 brachydantio	648	227.5	5.8	251	2	Q1RMZ2_HUMAN	Q1rmz2 homo sapien
576	233.5	5.9	420	2	Q90504_EPTST	Q90504 eptatretus	649	227.5	5.8	349	2	Q28802_PANTR	Q28802 pan troglod
577	233.5	5.9	553	2	Q16FV2_AEADAE	Q16fv2 aedes aegyp	650	227.5	5.8	418	2	Q6R15 RAT	Q6r15 rattus norv
578	233.5	5.9	779	2	Q4SC10_TETNG	Q4sc10 tetradon n	651	227	5.8	249	2	Q6RT79_9LABR	Q6rt79 taeniolabr
579	233	5.9	260	2	Q70845_ANOGA	Q70845 anopheles g	652	227	5.8	242	2	Q7PKR4_ANOGA	Q7pkr4 anopheles g
580	233	5.9	273	2	Q9XSM1_SHEEP	Q9xsm1 ovis aries	653	227	5.8	263	2	Q7ST54_XENTLA	Q7st54 xenopus lae
581	233	5.9	334	2	Q5MPC9_MANSE	Q5mpc9 manduca sex	654	227	5.8	275	2	Q7YS62_HORSE	Q7ys62 equus cabal
582	233	5.9	336	2	Q2L2S9_DROPS	Q2l2s9 drosoephila	655	227	5.8	324	1	TESTR_MOUSE	Q9j1f7 mus musculu
583	233	5.9	445	2	Q8CJ17_RAT	Q8cj17 rattus norv	656	227	5.8	324	2	Q54AE4_MOUSE	Q54ae4 mus musculu
584	233	5.9	541	2	Q1ED24_BRARE	Q1ed24 brachydantio	657	227	5.8	336	2	Q80YD8_MOUSE	Q80yd8 mus musculu
585	232.5	5.9	334	2	Q5VAN3_PAPHA	Q5van3 papio hamad	658	227	5.8	372	2	Q7QKL2_ANOGA	Q7qkl2 anopheles g
586	232.5	5.9	485	2	Q29K17_DROPS	Q29k17 drosoephila	659	227	5.8	417	1	DESCA_MOUSE	Q8b510 mus musculu
587	232.5	5.9	936	2	Q81FX2_CRAGI	Q81fx2 crasostrea	660	227	5.8	484	2	Q31IU4_MACMU	Q31iu4 macaca mula
588	232.5	5.9	1013	1	Q43897_homo sapien	Q43897 homo sapien	661	227	5.8	1468	2	Q9TYH4_SCHMA	Q9tyh4 schistosoma
589	232	5.9	387	2	Q17FW2_AEADAE	Q17fw2 aedes aegyp	662	227	5.8	1464	2	Q23995_DROME	Q23995 drosoephila
590	232	5.9	397	2	Q1HP06_BOMMO	Q1hp06 bombyx mori	663	227	5.8	1464	2	Q24132_DROME	Q24132 drosoephila
591	232	5.9	416	1	HEPS_RAT	Q05511 rattus norv	664	227	5.8	1464	2	Q9VC47_DROME	Q9vc47 drosoephila
592	232	5.9	638	1	KLKBI_RAT	P14272 rattus norv	665	226.5	5.7	238	1	TRV3_SALSA	P35033 salmo salar
593	232	5.9	812	2	Q3V1T9_MOUSE	Q3v1t9 mus musculu	666	226.5	5.7	280	2	Q177F3_AEADAE	Q177f3 aedes aegyp
594	231.5	5.9	269	1	ELAZA_BOVIN	Q29461 bos taurus	667	226.5	5.7	371	2	Q8MS52_DROME	Q8ms52 drosoephila
595	231.5	5.9	270	2	Q91039_GADMO	Q91039 gadus morhu	668	226.5	5.7	761	1	NERR_MOUSE	Q08762 mus musculu
596	231.5	5.9	371	2	Q8CJ16_RAT	Q8cj16 rattus norv	669	226.5	5.7	1272	2	Q3W1T3_HUMAN	Q3w1t3 homo sapien
597	231.5	5.9	395	2	Q5SMW8_HUMAN	Q5smw8 homo sapien	670	226.5	5.7	1429	2	ATRN_HUMAN	Q75882 homo sapien
598	231.5	5.9	483	2	Q81BX4_DROME	Q81bx4 drosoephila	671	226	5.7	274	2	Q7PQO0_ANOGA	Q7pqo0 anopheles g
599	231.5	5.9	493	2	Q9VK10_DROME	Q9vk10 drosoephila	672	226	5.7	394	1	URTG_DESRO	P49150 desmoudes ro
600	231.5	5.9	603	2	Q4V8T5_BRARE	Q4v8t5 brachydantio	673	226	5.7	416	2	Q4T4R1_TETNG	Q4t4r1 tetradon n
601	231.5	5.9	531	2	Q5M879_RAT	Q5m879 rattus norv	674	226	5.7	437	1	TMPS4_HUMAN	Q9nrs4 homo sapien
602	231.5	5.9	624	2	Q25ME7_RABIT	Q25me7 corycolagus	675	226	5.7	488	2	Q4RY82_TETNG	Q4ry82 tetradon n
603	231.5	5.9	664	2	Q2MON7_DROPS	Q2mon7 drosoephila	676	226	5.7	490	2	Q6PYD7_RAT	Q6pyd7 rattus norv
604	231.5	5.9	666	2	Q6VP08_DROVI	Q6vp08 drosoephila	677	226	5.7	625	1	FALL_HUMAN	P03351 homo sapien
605	231.5	5.9	1157	2	Q17KWS_AEADAE	Q17kws aedes aegyp	678	226	5.7	217	2	Q4M5C2_HUMAN	Q4m5c2 homo sapien
606	231	5.9	242	2	Q93266_PSEAM	Q93266 pseudopleur	679	225.5	5.7	429	2	Q5THX3_ANOGA	Q5thx3 anopheles g
607	231	5.9	310	2	Q2YDQ2_BRARE	Q2ydg2 brachydantio	680	225.5	5.7	312	2	Q7WT55_MOUSE	Q7wt55 mus musculu
608	231	5.9	328	2	Q16G08_AEADAE	Q16g08 aedes aegyp	681	225.5	5.7	347	1	HPT_PIG	Q8ps7 sus scrofa
609	231	5.9	1008	1	TLLI_CHICK	Q4der7 gallus gall	682	225.5	5.7	363	2	Q16XC4_AEADAE	Q16xc4 aedes aegyp
610	231	5.9	1012	1	TLL2_MOUSE	Q9wvme mus musculu	683	225.5	5.7	410	2	Q7Q956_ANOGA	Q7q956 anopheles g
611	230.5	5.8	259	2	Q69E27_HUMAN	Q69e27 homo sapien	684	225.5	5.7	418	2	Q7VAB7_DROME	Q7vab7 drosoephila
612	230.5	5.8	295	2	Q69E28_HUMAN	Q69e28 homo sapien	685	225.5	5.7	418	2	Q8SZK2_DROME	Q8szk2 drosoephila
613	230	5.8	244	2	Q8QGW3_ANGJA	Q8qgw3 anguilla ja	686	225.5	5.7	429	2	Q8AYB0_BRARE	Q8ayb0 brachydantio
614	230	5.8	265	2	Q9VVT3_DROME	Q9vvt3 drosoephila	687	225.5	5.7	457	1	TMPS5_HUMAN	Q9nbs3 homo sapien
615	230	5.8	318	2	Q7RTY9_HUMAN	Q7rty9 homo sapien	688	225.5	5.7	1404	2	Q160R6_AEADAE	Q16ir6 aedes aegyp

689	225	5.7	234	2	Q4RH74_TETNG	Q4rh74 tetradon n	762	221.5	5.6	247	2	Q547S4_BOVIN	Q547s4 bos taurus
690	225	5.7	237	2	Q7Q0S56_ANOGA	Q7q0s56 anophelies g	763	221.5	5.6	271	2	Q803J24_BRAE	Q803j24 brachydanio
691	225	5.7	328	2	Q80Z40_RAT	Q80z40 rattus norv	764	221.5	5.6	648	2	Q17MAJ3_AEDAE	Q17maj3 aedes aegypt
692	225	5.7	347	1	HPT_PAPHA	Q5vnt1 papio hamad	765	221.5	5.6	2531	1	NORC1_RAT	Q07008 rattus norv
693	225	5.7	387	2	Q9XT57_CTEFE	Q9xv57 ctenocephal	766	221.5	5.6	3620	1	CUEN_CANPA	Q9cui3 canis famill
694	225	5.7	393	2	Q6RX66_PDIPT	Q6rx66 armigeres s	767	221	5.6	231	1	TRY2_SALSA	Q35032 salmo salar
695	225	5.7	455	2	Q8CDR0_MOUSE	Q8cdr0 mus musculu	768	221	5.6	258	2	Q97J39_PHASE	Q97j39 phaedon coc
696	225	5.7	490	2	Q7TNO4_MOUSE	Q7tno4 mus musculu	769	221	5.6	264	2	Q2MOD7_DROPS	Q2mod7 drosoophila
697	225	5.7	490	2	Q920K3_RAT	Q920k3 rattus norv	770	221	5.6	268	1	CLCR_RAT	P55091 rattus norv
698	225	5.7	615	1	PA12_HUMAN	P00748 homo sapien	771	221	5.6	273	1	TRYB1_RAT	P27453 rattus norv
699	224.5	5.7	246	2	Q88J301_MOUSE	Q88j301 mus musculu	772	221	5.6	273	2	Q6P6W8_RAT	Q6p6w8 rattus norv
700	224.5	5.7	251	2	Q548S4_RAT	Q548s4 rattus norv	773	221	5.6	314	2	Q6RUT2_MOUSE	Q6rut2 mus musculu
701	224.5	5.7	253	2	Q91V82_MOUSE	Q91v82 mus musculu	774	221	5.6	445	2	Q4SCU6_TETNG	Q4scu6 tetradon n
702	224.5	5.7	271	1	ELA2A_RAT	P00774 rattus norv	775	221	5.6	810	2	Q5R8X6_PONPY	Q5r8x6 pongo pygma
703	224.5	5.7	347	1	HPT_MOUSE	Q6i646 mus musculu	776	221	5.6	974	2	P916S8_DROME	P916s8 drosoophila
704	224.5	5.7	347	2	Q3UES3_MOUSE	Q3ub3 m bore mar	777	221	5.6	1198	2	Q5VYW3_HUMAN	Q5vyw3 homo sapien
705	224.5	5.7	580	2	Q29DB1_DROPS	Q29db1 drosoophila	778	221	5.6	1299	2	Q7PIQ7_ANOGA	Q7piq7 anophelies g
706	224.5	5.7	1022	1	TLL1_BRAE	Q57460 brachydanio	779	221	5.6	1347	2	Q7PNR7_ANOGA	Q7pnr7 anophelies g
707	224.5	5.7	1427	2	Q8AV11_ONCKE	Q8av11 mesocricetu	780	220.5	5.6	250	2	Q8CGR5_MOUSE	Q8cgr5 mus musculu
708	224	5.7	222	2	Q8VIB7_MESAU	Q8vib7 mesocricetu	781	220.5	5.6	277	2	Q8OMW7_MOUSE	Q8omw7 mus musculu
709	224	5.7	242	2	Q7TIR8_9TELE	Q7tir8 pangasinu h	782	220.5	5.6	288	2	Q7Q9W5_ANOGA	Q7q9w5 anophelies g
710	224	5.7	245	1	CTRB_BOVIN	P00767 bos taurus	783	220.5	5.6	360	2	Q17489_ANOGA	Q17489 anophelies g
711	224	5.7	248	2	O161Z6_9ASCI	O161z6 boletenia vi	784	220.5	5.6	360	2	Q7E9V7_ANOGA	Q7e9v7 anophelies g
712	224	5.7	261	1	KLK2_HORSE	Q6h321 equus caball	785	220.5	5.6	468	2	Q9U0G3_PACIE	Q9u0g3 pacifastacu
713	224	5.7	343	2	Q5R812_PONPY	Q5rb12 pongo pygma	786	220.5	5.6	808	2	Q7YUJ36_DROME	Q7yu36 drosoophila
714	224	5.7	484	2	Q31I08_HYLSY	Q31i08 hylobates s	787	220.5	5.6	814	2	Q5DVP8_ONCMY	Q5dvp8 oncorhynch
715	224	5.7	490	1	TMPS2_MOUSE	Q9j1g8 mus musculu	788	220.5	5.6	1004	2	Q4SRX0_TETNG	Q4srx0 tetradon n
716	224	5.7	1174	2	Q9VVR4_DROME	Q9vvr4 drosoophila	789	220	5.6	1067	2	TLD_DROME	P25723 drosoophila
717	224	5.7	2602	2	Q7PSV8_ANOGA	Q7pav8 anophelies g	790	220	5.6	1237	2	Q52V24_PONLE	Q52v24 pontastacus
718	223.5	5.7	234	2	Q90Z44_ACTIR	Q90z44 acipenser t	791	220	5.6	260	2	Q9W7P9_PAROL	Q9w7p9 paratichthy
719	223.5	5.7	266	2	Q9W7Q0_PAROL	Q9w7q0 paratichthy	792	220	5.6	261	2	Q96ZG7_CULPI	Q96zg7 culx pipie
720	223.5	5.7	348	1	HPTR_HUMAN	P00739 homo sapien	793	220	5.6	275	1	TRYB1_HUMAN	O16561 homo sapien
721	223.5	5.7	417	2	Q5R5E8_PONPY	Q5r5e8 pongo pygma	794	220	5.6	275	2	Q6B0S1_HUMAN	O6b0s1 homo sapien
722	223.5	5.7	427	2	Q299R1_DROPS	Q299r1 drosoophila	795	220	5.6	331	2	Q8RIAG_MOUSE	O8rix6 mus musculu
723	223.5	5.7	809	2	Q19A29_PIG	Q19a29 sus scrofa	796	220	5.6	331	2	Q8OX17_MOUSE	Q8ox17 mus musculu
724	223.5	5.7	1242	1	JAG1A_BRAE	Q90y57 brachydanio	797	220	5.6	527	2	Q17B77_AEDAE	P70059 xenopus lae
725	223.5	5.7	1629	2	Q9V513_DROME	Q9v513 drosoophila	798	219.5	5.6	244	1	TRY2_XENIA	Q961y0 xenopus lae
726	223.5	5.7	1674	2	Q8SV35_DROME	Q8sv35 drosoophila	799	219.5	5.6	248	2	Q7SZT1_XENIA	Q7szt1 xenopus lae
727	223	5.7	201	2	Q5XUG4_DREAU	Q5xug4 oreochromis	800	219.5	5.6	255	2	Q961Y0_GALME	O961y0 galleria me
728	223	5.7	238	2	O16PK7_AEDAE	O16pk7 aedes aegypt	801	219.5	5.6	255	2	Q6GND2_XENIA	O6gnd2 xenopus lae
729	223	5.7	242	2	Q9W707_PAROL	Q9w7q0 paratichthy	802	219.5	5.6	255	2	Q4OR60_XENIA	Q4ore0 xenopus lae
730	223	5.7	261	2	Q56GM3_CULPI	Q56gm3 culx pipie	803	219.5	5.6	259	2	Q3ZB43_MOUSE	Q3zb43 mus musculu
731	223	5.7	264	2	Q28Z63_DROPS	Q28z63 drosoophila	804	219.5	5.6	271	1	ELA2A_MOUSE	P05204 mus musculu
732	223	5.7	274	2	Q7Q299_ANOGA	Q7q299 anophelies g	805	219.5	5.6	347	1	HPT_MUSCR	O60574 mus caroli
733	223	5.7	454	1	TMPS3_HUMAN	P57727 homo sapien	806	219.5	5.6	353	2	Q28F41_DROPS	Q28fx1 drosoophila
734	223	5.7	538	2	Q5USC7_HUMAN	Q5usc7 homo sapien	807	219.5	5.6	482	2	Q16116_AEDAE	Q16116 aedes aegypt
735	222.5	5.6	411	2	Q9VUF0_DROME	Q9vuf0 drosoophila	808	219.5	5.6	570	2	Q16H41_AEDAE	P04186 mus musculu
736	222.5	5.6	417	1	HEPS_HUMAN	P05981 homo sapien	809	219.5	5.6	761	1	CFAB_MOUSE	Q3ueg8 mus musculu
737	222.5	5.6	434	1	UROK_CHICK	P15120 gallus galli	810	219.5	5.6	761	2	Q3UEG8_MOUSE	Q3ubh0 mus musculu
738	222.5	5.6	455	1	TMPS5_MOUSE	Q9er04 mus musculu	811	219.5	5.6	1378	2	Q3UHB0_MOUSE	Q3ubh2 mus musculu
739	222.5	5.6	514	2	Q2PKD2_XENIA	Q2pkd2 xenopus lae	812	219.5	5.6	1378	2	Q68HV2_MOUSE	O68hv2 mus musculu
740	222.5	5.6	757	2	Q2Y2P1_GINCI	Q2y2p1 ginglymosto	813	219.5	5.6	1444	2	Q6A0S1_MOUSE	O6a0s1 mus musculu
741	222.5	5.6	790	1	PLMN_PIG	P06867 sus scrofa	814	219	5.6	249	2	Q7QAM5_ANOGA	Q7qam5 anophelies g
742	222.5	5.6	954	2	Q7SUD6_ACHTE	Q7sud6 achaeatarnea	815	219	5.6	287	2	Q171W2_AEDAE	Q171w2 aedes aegypt
743	222	5.6	203	2	Q5XUG5_ORENI	Q5xug5 oreochromis	816	219	5.6	306	2	Q16RR3_AEDAE	Q16rr3 aedes aegypt
744	222	5.6	267	2	Q9V942_DROME	Q9v942 drosoophila	817	219	5.6	318	2	Q80UR4_MOUSE	Q80ur4 mus musculu
745	222	5.6	269	1	ELA2A_PIG	P08414 sus scrofa	818	219	5.6	343	1	PRSS8_HUMAN	O16651 homo sapien
746	222	5.6	273	2	Q921N4_MOUSE	Q921n4 mus musculu	819	219	5.6	365	2	Q97J66_HOLDI	Q97j66 holotrichia
747	222	5.6	275	1	TRYA1_HUMAN	P15157 homo sapien	820	218.5	5.5	355	2	Q16EL5_AEDAE	Q16el5 aedes aegypt
748	222	5.6	275	1	TRYB2_HUMAN	P20231 homo sapien	821	218.5	5.5	374	2	Q81862_DERVA	Q81862 dermacentor
749	222	5.6	275	2	Q86T38_HUMAN	Q86tm8 homo sapien	822	218.5	5.5	375	2	Q817W8_DERVA	Q817w8 dermacentor
750	222	5.6	275	2	Q6B0S2_HUMAN	Q6b0s2 homo sapien	823	218.5	5.5	435	1	TMPS4_MOUSE	O8vcs5 mus musculu
751	222	5.6	275	2	Q7Q6S1_ANOGA	Q7q6s1 anophelies g	824	218.5	5.5	495	2	Q16VA5_AEDAE	O16vas aedes aegypt
752	222	5.6	276	2	Q86UAS_HUMAN	Q86uas homo sapien	825	218.5	5.5	787	2	Q6S1G0_NAUTA	Q6s1g0 naja kaouth
753	222	5.6	282	2	Q6NZY1_HUMAN	Q6nzy1 homo sapien	826	218.5	5.5	1007	1	TLL1_XENIA	O61236 homo sapien
754	222	5.6	345	2	Q16G07_AEDAE	Q16g07 aedes aegypt	827	218.5	5.5	1379	2	Q7SKX0_BRAE	O7skx0 brachydanio
755	222	5.6	363	2	Q7PXP3_ANOGA	Q7pxp3 anophelies g	828	218	5.5	242	2	Q5M908_XENIR	O5m908 xenopus tro
756	222	5.6	419	2	Q4M5P3_HUMAN	Q4m5p3 homo sapien	829	218	5.5	252	2	Q7Q064_ANOGA	Q7q064 anophelies g
757	222	5.6	423	1	TM11E_HUMAN	Q4v152 homo sapien	830	218	5.5	260	2	Q54213_STROR	Q54213 streptomycy
758	222	5.6	569	2	Q4RLS7_AEDAE	Q4rls7 aedes aegypt	831	218	5.5	271	2	Q17B76_AEDAE	Q17b76 aedes aegypt
759	222	5.6	658	2	Q4RLS7_TETNG	Q4rls7 tetradon n	832	217.5	5.5	243	2	Q7MA13_MECP	O7ma13 megabombus
760	222	5.6	696	2	Q17IR1_AEDAE	Q17ir1 aedes aegypt	833	217.5	5.5	269	2	Q6ISU5_HUMAN	O6isus5 homo sapien
761	222	5.6	761	2	Q4ORB3_BRAE	Q4qres brachydanio	834	217.5	5.5				

835	217.5	5.5	376	2	Q17EY0_AEDAE	Q17EY0 aedes aegypti	908	214.5	5.4	1322	2	Q9NATO_ANOGA	Q9NATO anopheles g
836	217.5	5.5	431	2	Q1URP2_MOUSE	Q1URP2 mus musculus	909	214.5	5.4	1428	1	ATRN_MOUSE	Q9u60 mus musculus
837	217.5	5.5	3570	2	Q7OJ37_ANOGA	Q7OJ37 anopheles g	910	214	5.4	252	2	Q5QBG0_9D1PT	Q5QBG0 culicoides
838	217	5.5	229	1	KLR2_CAVPO	P12333 cavia porce	911	214	5.4	262	2	Q5G3K5_PYGNE	Q5G3K5 pygathrix n
839	217	5.5	268	1	CLCR_HUMAN	Q99895 homo sapien	912	214	5.4	262	2	Q5G3K6_TTRAFF	Q5G3K6 tetrachypte
840	217	5.5	233	1	TRYBI_MOUSE	Q02844 mus musculus	913	214	5.4	262	2	Q5G3K7_PYGBI	Q5G3K7 pygathrix b
841	217	5.5	275	2	Q9GRZ6_HUMAN	Q9GRZ6 homo sapien	914	214	5.4	275	2	Q6FHB8_HUMAN	Q6FHB8 homo sapien
842	217	5.5	280	2	Q6GLK1_XENLA	Q6GLK1 xenopus lae	915	214	5.4	342	1	PRSS8_RAT	Q9e887 rattus norv
843	217	5.5	597	2	Q35727_MOUSE	Q35727 mus musculus	916	214	5.4	342	1	Q6GSY8_RAT	Q6GSY8 rattus norv
844	217	5.5	603	1	FA12_CAVPO	Q04962 cavia porce	917	214	5.4	578	2	Q1DGQ5_AEDAE	Q1DGQ5 aedes aegypti
845	217	5.5	2703	1	NOTCH_DROME	P07207 drosophila	918	214	5.4	697	2	Q1EWJ0_AEDAE	Q1EWJ0 aedes aegypti
846	216.5	5.5	235	2	Q6BAR4_BOVIN	Q6BAR4 bos taurus	919	214	5.4	881	2	Q1ELI9_AEDAE	Q1ELI9 aedes aegypti
847	216.5	5.5	277	2	Q96899_9MYRI	Q96899 scolopendra	920	214	5.4	1290	2	Q1CSA2_AEDAE	Q1CSA2 aedes aegypti
848	216.5	5.5	288	1	Q16GG3_AEDAE	Q16GG3 aedes aegypti	921	213.5	5.4	241	2	Q98TG5_PYTLE	Q98TG5 pygathrix j
849	216.5	5.5	365	1	HPRR_PAVIR	Q28801 pan troglod	922	213.5	5.4	248	2	Q9VQ98_DROME	Q9VQ98 drosophila
850	216.5	5.5	365	2	Q7PWE1_ANOGA	Q7PWE1 anopheles g	923	213.5	5.4	249	2	Q7QKSO_ANOGA	Q7QKSO anopheles g
851	216.5	5.5	1048	2	Q4SJ96_TETNG	Q4SJ96 tetractodon n	924	213.5	5.4	251	2	Q4V675_DROME	Q4V675 drosophila
852	216.5	5.5	2528	2	Q8AXP0_CYNPY	Q8AXP0 cynops pyrr	925	213.5	5.4	270	2	Q5JCG5_BRARE	Q5JCG5 brachydanto
853	216.5	5.5	2616	1	NUDEL_DROME	P98159 drosophila	926	213.5	5.4	314	2	Q175S1_AEDAE	Q175S1 aedes aegypti
854	216	5.5	255	2	Q7TNI0_MOUSE	Q7TNI0 mus musculus	927	213.5	5.4	381	2	Q7PN97_ANOGA	Q7PN97 anopheles g
855	216	5.5	259	2	Q4KIC6_XENLA	Q4KIC6 xenopus lae	928	213.5	5.4	442	1	TM1LE_MOUSE	Q5e248 mus musculus
856	216	5.5	259	2	Q3STP2_MOUSE	Q3STP2 mus musculus	929	213.5	5.4	543	1	TMPSD_MOUSE	Q5u405 mus musculus
857	216	5.5	269	2	Q9D7T9_MOUSE	Q9D7T9 mus musculus	930	213.5	5.4	704	2	Q28ZD1_DROPS	Q28ZD1 drosophila
858	216	5.5	269	2	Q9CQ52_MOUSE	Q9CQ52 m adult mal	931	213.5	5.4	2352	2	Q61240_HALRO	Q61240 halocynthia
859	216	5.5	355	2	Q7PEM0_ANOGA	Q7PEM0 anopheles g	932	213	5.4	211	2	Q4SBS0_TETNG	Q4SBS0 tetractodon n
860	216	5.5	376	2	Q5TU09_ANOGA	Q5TU09 anopheles g	933	213	5.4	355	2	Q9NFT1_ANOGA	Q9NFT1 anopheles g
861	216	5.5	1218	1	JAG1_MOUSE	Q9qxx0 mus musculus	934	213	5.4	394	2	Q9NFT1_ANOGA	Q9NFT1 tachypneus
862	216	5.5	1218	2	Q3UVN4_MOUSE	Q3UVN4 mus musculus	935	213	5.4	541	2	Q4SM14_TACTR	Q4SM14 tetractodon n
863	215.5	5.5	243	2	Q9TXD8_AGEAP	Q9TXD8 agelenopsis	936	213	5.4	615	2	Q81Z25_HUMAN	Q81Z25 homo sapien
864	215.5	5.5	247	1	TRY2_CANFA	P06872 canis famli	937	213	5.4	1243	2	Q1K13_AEDAE	Q1K13 aedes aegypti
865	215.5	5.5	247	2	Q5H728_MACMU	Q5H728 macaca mula	938	213	5.4	1477	2	Q4H3A4_CIOIN	Q4H3A4 ciona intes
866	215.5	5.5	248	1	TRY3_CHICK	Q90629 gallus galli	939	212.5	5.4	242	2	Q7PQB3_ANOGA	Q7PQB3 anopheles g
867	215.5	5.5	252	2	Q3B898_XENLA	Q3B898 xenopus lae	940	212.5	5.4	247	2	Q3SY19_HUMAN	Q3SY19 homo sapien
868	215.5	5.5	253	2	Q3B856_MOUSE	Q3B856 mus musculus	941	212.5	5.4	260	2	Q7RTY3_HUMAN	Q7RTY3 homo sapien
869	215.5	5.5	254	2	Q8CGR4_MOUSE	Q8CGR4 mus musculus	942	212.5	5.4	265	2	Q4VB04_XENLA	Q4VB04 xenopus lae
870	215.5	5.5	259	2	Q6GN82_XENLA	Q6GN82 xenopus lae	943	212.5	5.4	282	1	KLK11_HUMAN	Q9uix7 homo sapien
871	215.5	5.5	317	1	BSSP4_HUMAN	Q9gzr4 homo sapien	944	212.5	5.4	339	2	Q9G144_MOUSE	Q9G144 mus musculus
872	215.5	5.5	321	2	Q8OY38_MOUSE	Q8OY38 mus musculus	945	212.5	5.4	397	2	Q7PZ85_ANOGA	Q7PZ85 anopheles g
873	215.5	5.5	326	2	Q9D9M0_MOUSE	Q9D9M0 mus musculus	946	212.5	5.4	420	2	Q6IE14_RAT	Q6IE14 rattus norv
874	215.5	5.5	415	2	Q17HP3_AEDAE	Q17HP3 aedes aegypti	947	212.5	5.4	501	2	Q28YV6_DROPS	Q28YV6 drosophila
875	215.5	5.5	429	2	Q16PR4_AEDAE	Q16PR4 aedes aegypti	948	212.5	5.4	693	2	Q2SHS3_HARHC	Q2SHS3 habella che
876	215.5	5.5	562	2	Q675X7_OIKDI	Q675X7 oikopleura	949	212.5	5.4	778	2	Q9VS19_DROME	Q9VS19 drosophila
877	215.5	5.5	740	2	Q5RE78_PONPY	Q5RE78 pongo pygma	950	212.5	5.4	849	1	POLS2_MOUSE	Q5KX28 mus musculus
878	215.5	5.5	751	2	Q6MG74_RAT	Q6MG74 rattus norv	951	212	5.4	260	1	NREN_MOUSE	Q61955 mus musculus
879	215	5.4	211	1	TRYX_GADMO	Q91041 gadus morhu	952	212	5.4	274	2	Q6GNFO_XENLA	Q6GNFO xenopus lae
880	215	5.4	256	2	Q2S081_HYPLI	Q2S081 hypodermia 1	953	212	5.4	340	2	Q8BJV6_MOUSE	Q8BJV6 mus musculus
881	215	5.4	260	2	Q7O5K4_ANOGA	Q7O5K4 anopheles g	954	212	5.4	875	2	Q5DPT1_MOUSE	Q5DPT1 mus musculus
882	215	5.4	270	2	Q7PKX5_ANOGA	Q7PKX5 anopheles g	955	212	5.4	1322	2	Q9NJS5_ANOGA	Q9NJS5 anopheles g
883	215	5.4	388	2	Q4RRR7_TETNG	Q4RRR7 tetractodon n	956	212	5.4	2031	2	Q2SGH8_DROPS	Q2SGH8 drosophila
884	215	5.4	389	2	Q9PVX7_XENLA	Q9PVX7 xenopus lae	957	211.5	5.4	257	2	Q16CM9_AEDAE	Q16CM9 aedes aegypti
885	215	5.4	422	2	Q4RG82_TETNG	Q4RG82 tetractodon n	958	211.5	5.4	272	2	Q7PWE5_ANOGA	Q7PWE5 anopheles g
886	215	5.4	597	2	Q6PER0_MOUSE	Q6PER0 mus musculus	959	211.5	5.4	401	2	Q2TBU0_BOVIN	Q2TBU0 bos taurus
887	215	5.4	609	2	Q8OYCS_MOUSE	Q8OYCS mus musculus	960	211.5	5.4	413	2	Q5M8E7_XENTR	Q5M8E7 xenopus tro
888	215	5.4	749	2	Q9YGB8_ONCMY	Q9YGB8 oncorhynch	961	211.5	5.4	418	1	TM1LD_HUMAN	Q6o235 homo sapien
889	215	5.4	760	2	Q8JG08_TETNG	Q8JG08 tetractodon n	962	211.5	5.4	484	2	Q7QCVO_ANOGA	Q7QCVO anopheles g
890	215	5.4	762	2	Q4SFT0_TETNG	Q4SFT0 tetractodon n	963	211.5	5.4	629	2	Q6AZS7_XENLA	Q6AZS7 xenopus lae
891	215	5.4	810	1	PLMN_HUMAN	P00747 homo sapien	964	211.5	5.4	719	2	Q6DJ90_XENTR	Q6DJ90 xenopus tro
892	215	5.4	810	2	Q5TER4_HUMAN	Q5TER4 homo sapien	965	211	5.3	237	1	Q29464_BOVIN	Q29464 bos taurus
893	215	5.4	1116	2	Q7TP05_RAT	Q7TP05 rattus norv	966	211	5.3	276	1	MCPT6_MOUSE	P21845 mus musculus
894	215	5.4	1497	2	Q5T938_HUMAN	Q5T938 homo sapien	967	211	5.3	313	2	Q7PX33_ANOGA	Q7PX33 anopheles g
895	214.5	5.4	195	2	Q819P3_AURAU	Q819P3 aedes aegypti	968	211	5.3	444	2	Q170T8_AEDAE	Q170T8 aedes aegypti
896	214.5	5.4	244	2	Q5BEB2_XENTR	Q5BEB2 xenopus tro	969	211	5.3	510	2	Q7Q554_ANOGA	Q7Q554 anopheles g
897	214.5	5.4	247	1	TRY2_BOVIN	Q29463 bos taurus	970	211	5.3	650	2	Q17MA7_AEDAE	Q17MA7 aedes aegypti
898	214.5	5.4	249	2	Q6D1W2_XENTR	Q6D1W2 xenopus tro	971	211	5.3	1218	2	JAG1_HUMAN	P78504 homo sapien
899	214.5	5.4	274	1	TRY1_ANOGA	P35035 bombyx mori	972	211	5.3	1218	2	Q4KCR2_HUMAN	Q4KCR2 homo sapien
900	214.5	5.4	303	2	Q45RG0_BOMMO	Q45RG0 bombyx mori	973	211	5.3	2447	2	Q11149_FUGRU	Q11149 fuigu rubrip
901	214.5	5.4	366	2	Q7O170_MOUSE	Q7O170 mus musculus	974	210.5	5.3	247	1	TRYP_STMYI	P35048 simulium vl
902	214.5	5.4	505	2	Q966V4_HALRO	Q966V4 halocynthia	975	210.5	5.3	275	1	TRY3_ANOGA	P35037 anopheles g
903	214.5	5.4	570	2	Q172N8_AEDAE	Q172N8 aedes aegypti	976	210.5	5.3	280	2	Q8N171_HUMAN	Q8N171 homo sapien
904	214.5	5.4	593	1	FA12_BOVIN	P8140 bos taurus	977	210.5	5.3	300	2	Q5W8S2_MOUSE	Q5W8S2 mus musculus
905	214.5	5.4	1019	2	Q16XC0_AEDAE	Q16XC0 aedes aegypti	978	210.5	5.3	342	1	PRSS8_MOUSE	Q9e82 mus musculus
906	214.5	5.4	1130	2	Q7QINT7_ANOGA	Q7QINT7 anopheles g	979	210.5	5.3	360	2	Q9W1X6_DROME	Q9W1X6 drosophila
907	214.5	5.4	1309	2	Q16TDT7_AEDAE	Q16TDT7 aedes aegypti	980	210.5	5.3	470	2	Q173L6_AEDAE	Q173L6 aedes aegypti

981	210.5	5.3	572	1	TMPS7_HUMAN	Q7ITY8	homo sapien	1054	206.5	5.2	321	1	TRYG1_HUMAN	Q9AIR2	homo sapien
982	210.5	5.3	572	2	Q17RH4_HUMAN	Q17RH4	homo sapien	1055	206.5	5.2	359	2	Q705Z6_ANOGA	Q705Z6	anopheles g
983	210.5	5.3	754	2	Q28290_CANPA	Q28290	CANPA	1056	206.5	5.2	467	2	Q86WX2_HUMAN	Q86WX2	homo sapien
984	210.5	5.3	855	1	POL52_HUMAN	Q5K463	homo sapien	1057	206.5	5.2	476	2	Q5T5Y9_HUMAN	Q5T5Y9	homo sapien
985	210.5	5.3	1219	1	JAG1_RAT	Q53722	rattus norv	1058	206.5	5.2	573	2	Q9V516_DROME	Q9V516	drosophila
986	210	5.3	262	2	Q5G3K8_BUNHO	Q5G3K8	bumphithicu	1059	206.5	5.2	728	2	Q70BP4_ANOGA	Q70BP4	anopheles g
987	210	5.3	750	1	CO2_BOVIN	Q38Y42	bos taurus	1060	206.5	5.2	741	2	Q4SIU3_TETNG	Q4SIU3	tetradon n
988	210	5.3	2437	1	NOTC1_BRARE	P65310	brachydanio	1061	206.5	5.2	837	2	Q1MSE7_RHIL3	Q1MSE7	rhithobium l
989	209.5	5.3	260	2	Q3KO12_XENLA	Q3KO12	xenopus lae	1062	206.5	5.2	1065	2	Q810H2_MOUSE	Q810H2	mus muscucu
990	209.5	5.3	280	1	TRYM_CANPA	P19236	canis famli	1063	206.5	5.2	1403	2	Q70E20_MOUSE	Q70E20	mus muscucu
991	209.5	5.3	313	2	Q8IN51_DROME	Q8IN51	drosophila	1064	206	5.2	238	2	Q7QKH8_ANOGA	Q7QKH8	anopheles g
992	209.5	5.3	347	1	HPT_MUSSA	Q62558	mus saxicol	1065	206	5.2	263	2	Q9NB92_AGRIP	Q9NB92	agrotis ips
993	209.5	5.3	423	2	Q5FBE1_HUMAN	Q5FBE1	homo sapien	1066	206	5.2	264	2	Q4R278_TETNG	Q4R278	tetradon n
994	209.5	5.3	441	2	Q17079_AEDAE	Q17079	aedes aegypt	1067	206	5.2	269	2	Q6AZF9_XENLA	Q6AZF9	xenopus lae
995	209.5	5.3	516	2	Q17BG4_AEDAE	Q17BG4	aedes aegypt	1068	206	5.2	374	2	Q49QW1_SPUT	Q49QW1	spodoptera
996	209.5	5.3	562	2	Q1RMR8_HUMAN	Q1RMR8	homo sapien	1069	206	5.2	389	2	Q3UD41_MOUSE	Q3UD41	mus muscucu
997	209.5	5.3	875	1	POL52_RAT	Q1RME6	homo sapien	1070	206	5.2	395	2	Q6R559_OSTRU	Q6R559	ostrinia nu
998	209.5	5.3	1441	2	Q723G3_HUMAN	Q723G3	rattus norv	1071	206	5.2	429	2	Q17319_AEDAE	Q17319	aedes aegypt
999	209.5	5.3	1492	2	Q29F55_DROPS	Q29F55	drosophila	1072	206	5.2	492	2	Q72155_9EUC4	Q72155	chironomantes
1000	209	5.3	263	1	AMI_XENLA	Q63ZK0	xenopus lae	1073	206	5.2	826	2	Q16QB1_AEDAE	Q16QB1	aedes aegypt
1001	209	5.3	279	2	Q4RGF3_TETNG	Q4RGF3	glossina mo	1074	206	5.2	1161	2	Q16WL3_AEDAE	Q16WL3	aedes aegypt
1002	209	5.3	340	2	Q216Z4_GLOMR	Q216Z4	glossina mo	1075	206	5.2	2040	2	Q5VMD7_HUMAN	Q5VMD7	homo sapien
1003	209	5.3	384	2	Q9W630_CYPCA	Q9W630	cypripus ca	1076	206	5.2	2040	2	Q1HP67_HUMAN	Q1HP67	homo sapien
1004	209	5.3	401	2	Q7QXD2_ANOGA	Q7QXD2	anopheles g	1077	206	5.2	4548	1	APOA_HUMAN	APOA	homo sapien
1005	209	5.3	433	1	UROK_MOUSE	P66869	m urokinase	1078	205.5	5.2	245	2	Q7PQR9_ANOGA	Q7PQR9	anopheles g
1006	209	5.3	893	2	Q9TYH3_CAEBR	Q9TYH3	caenorhabdi	1079	205.5	5.2	257	2	Q5OBL5_9DIPT	Q5OBL5	9dipt
1007	208.5	5.3	236	2	Q9TYH3_SCHEM	Q9TYH3	schistosoma	1080	205.5	5.2	269	2	Q6ISM5_HUMAN	Q6ISM5	homo sapien
1008	208.5	5.3	258	2	Q28803_PANTR	Q28803	pan troglod	1081	205.5	5.2	269	2	Q6ISP9_HUMAN	Q6ISP9	homo sapien
1009	208.5	5.3	311	2	Q80XZ3_RAT	Q80XZ3	rattus norv	1082	205.5	5.2	284	2	Q16Y22_AEDAE	Q16Y22	aedes aegypt
1010	208.5	5.3	322	2	Q16FK7_AEDAE	Q16FK7	aedes aegypt	1083	205.5	5.2	347	1	HPT_RAT	HPT	rattus norv
1011	208.5	5.3	371	2	Q1FW3_AEDAE	Q1FW3	aedes aegypt	1084	205.5	5.2	357	2	Q5MPC8_MANSE	Q5MPC8	manuca sex
1012	208.5	5.3	417	1	TM1LD_MOUSE	Q8VHK6	m cranssemb	1085	205.5	5.2	363	2	Q2VPE0_XENLA	Q2VPE0	xenopus lae
1013	208.5	5.3	444	2	Q9V4W6_DROME	Q9V4W6	haemaphysal	1086	205.5	5.2	374	2	Q80YD3_MOUSE	Q80YD3	mus muscucu
1014	208.5	5.3	464	2	Q6L725_HAELO	Q6L725	haemaphysal	1087	205.5	5.2	416	2	Q8BZ30_MOUSE	Q8BZ30	mus muscucu
1015	208.5	5.3	581	1	TMPSD_HUMAN	Q9Y82	homo sapien	1088	205.5	5.2	416	2	Q5CZL0_XENTR	Q5CZL0	xenopus tro
1016	208	5.3	256	2	Q25082_HYPLI	Q25082	hypoderma 1	1089	205.5	5.2	470	2	TMPS2_HUMAN	TMPS2	homo sapien
1017	208	5.3	271	2	Q8HYJ2_BOVIN	Q8HYJ2	bos taurus	1090	205.5	5.2	492	1	Q6GRK7_HUMAN	Q6GRK7	homo sapien
1018	208	5.3	275	2	Q8IXD7_HUMAN	Q8IXD7	homo sapien	1091	205.5	5.2	492	2	Q5RBP4_PONNY	Q5RBP4	pomo pygma
1019	208	5.3	295	2	Q706S2_ANOGA	Q706S2	anopheles g	1092	205.5	5.2	752	2	Q2KRC3_RHIEC	Q2KRC3	rhithobium e
1020	208	5.3	326	2	Q7RTY6_HUMAN	Q7RTY6	homo sapien	1093	205.5	5.2	848	2	Q2KRC3_RHIEC	Q2KRC3	rhithobium e
1021	208	5.3	352	2	Q16H66_AEDAE	Q16H66	aedes aegypt	1094	205	5.2	220	2	Q4LL4_9NEOP	Q4LL4	9neopia non
1022	208	5.3	357	2	Q4KLE1_XENLA	Q4KLE1	xenopus lae	1095	205	5.2	256	1	HYPB_HYPLI	HYPB	hypoderma 1
1023	208	5.3	525	2	Q17G15_AEDAE	Q17G15	aedes aegypt	1096	205	5.2	264	2	Q02569_CULPO	Q02569	culex quinq
1024	208	5.3	534	2	Q176U7_AEDAE	Q176U7	aedes aegypt	1097	205	5.2	273	2	Q16KM4_AEDAE	Q16KM4	aedes aegypt
1025	207.5	5.3	195	2	Q8J006_HUMAN	Q8J006	homo sapien	1098	205	5.2	396	2	Q4SY35_TETNG	Q4SY35	tetradon n
1026	207.5	5.3	239	2	Q91218_ONCMY	Q91218	oncothyranhu	1099	205	5.2	445	2	Q16UV5_AEDAE	Q16UV5	aedes aegypt
1027	207.5	5.3	247	2	Q7L729_AEDAE	Q7L729	aedes aegypt	1100	205	5.2	492	2	Q96T73_HUMAN	Q96T73	homo sapien
1028	207.5	5.3	256	1	TRYB_MANSE	P35074	manduca sex	1101	205	5.2	870	2	Q81QG6_DROME	Q81QG6	drosophila
1029	207.5	5.3	266	2	Q92077_GADMO	Q92077	gadus morhu	1102	205	5.2	4181	2	Q291E2_DROPS	Q291E2	drosophila
1030	207.5	5.3	269	1	ELASNB_HUMAN	P08217	homo sapien	1103	204.5	5.2	246	1	TRY2_RAT	TRY2	rattus norv
1031	207.5	5.3	269	2	Q6ISNB_HUMAN	Q6ISNB	homo sapien	1104	204.5	5.2	247	2	Q9CPN9_MOUSE	Q9CPN9	mus muscucu
1032	207.5	5.3	298	2	Q9NH06_HELZE	Q9NH06	heliothis z	1105	204.5	5.2	247	2	Q9D7Y7_MOUSE	Q9D7Y7	mus muscucu
1033	207.5	5.3	778	2	Q28DA4_XENTR	Q28DA4	xenopus tro	1106	204.5	5.2	256	1	TRYC_MANSE	TRYC	manuca sex
1034	207.5	5.3	900	2	Q6AX42_XENLA	Q6AX42	xenopus lae	1107	204.5	5.2	281	2	Q46137_LUMKU	Q46137	lumbricus r
1035	207.5	5.3	1010	2	Q4SO11_TETNG	Q4SO11	tetradon n	1108	204.5	5.2	311	2	Q4V3F4_DROME	Q4V3F4	drosophila
1036	207.5	5.3	1282	2	Q8TERO_HUMAN	Q8TERO	homo sapien	1109	204.5	5.2	367	2	Q4V3K5_DROME	Q4V3K5	drosophila
1037	207	5.2	225	2	Q5TAH7_HUMAN	Q5TAH7	homo sapien	1110	204.5	5.2	367	2	Q70169_MOUSE	Q70169	mus muscucu
1038	207	5.2	238	1	TRY5_AEDAE	P25787	aedes aegypt	1111	204.5	5.2	373	2	Q4V3X9_DROME	Q4V3X9	drosophila
1039	207	5.2	240	2	Q7SYO8_XENLA	Q7SYO8	xenopus lae	1112	204.5	5.2	449	2	Q95RA3_DROME	Q95RA3	drosophila
1040	207	5.2	260	1	NRPN_RAT	Q8B780	rattus norv	1113	204.5	5.2	470	2	Q661F4_XENTR	Q661F4	xenopus tro
1041	207	5.2	266	2	Q161D7_AEDAE	Q161D7	aedes aegypt	1114	204.5	5.2	752	1	CO2_PONPY	CO2	ponpy
1042	207	5.2	274	2	Q702X3_ANOGA	Q702X3	anopheles g	1115	204.5	5.2	768	2	Q5TF46_HUMAN	Q5TF46	homo sapien
1043	207	5.2	426	2	Q5T6B5_HUMAN	Q5T6B5	homo sapien	1116	204.5	5.2	1008	2	Q336F5_HUMAN	Q336F5	homo sapien
1044	207	5.2	1957	2	Q4SU28_TETNG	Q4SU28	tetradon n	1117	204.5	5.2	1497	2	Q8NB79_HUMAN	Q8NB79	homo sapien
1045	206.5	5.2	195	2	Q6SPC0_HUMAN	Q6SPC0	homo sapien	1118	204.5	5.2	2470	1	NOTC2_MOUSE	NOTC2	mouse
1046	206.5	5.2	247	2	Q171W1_AEDAE	Q171W1	aedes aegypt	1119	204.5	5.2	2483	1	Q29DR0_DROPS	Q29DR0	drosophila
1047	206.5	5.2	256	1	TRYA_MANSE	P35045	manduca sex	1120	204	5.2	190	2	Q5TT88_ANOGA	Q5TT88	anopheles g
1048	206.5	5.2	269	2	Q6ICV2_HUMAN	Q6ICV2	homo sapien	1121	204	5.2	220	2	Q4LIL5_9NEOP	Q4LIL5	9neopia non
1049	206.5	5.2	269	2	Q96OV5_HUMAN	Q96OV5	homo sapien	1122	204	5.2	248	2	Q16PR8_AEDAE	Q16PR8	aedes aegypt
1050	206.5	5.2	269	2	Q9Y929_DROME	Q9Y929	drosophila	1123	204	5.2	260	2	NRPN_HUMAN	NRPN	homo sapien
1051	206.5	5.2	270	2	Q27824_UCAPU	Q27824	uca pugiliat	1124	204	5.2	266	2	Q17FW5_AEDAE	Q17FW5	aedes aegypt
1052	206.5	5.2	274	2	Q70092_ANOGA	Q70092	anopheles g	1125	204	5.2	395	2	Q6R558_OSTUV	Q6R558	ostinia nu
1053	206.5	5.2	284	2	Q8NF86_HUMAN	Q8NF86	homo sapien	1126	204	5.2	417	1	TM1LD_RAT	TM1LD	m cranssemb

1127	204	5.2	645	2	05RG66 BRARE	051996 brachydanio	1200	201	5.1	484	2	0311V5 PANTR	0311V5 pan troglod
1128	203.5	5.2	195	2	081XB4 HUMAN	081XB4 homo sapien	1201	201	5.1	490	2	052KX2 MOUSE	052KX2 mus musculus
1129	203.5	5.2	238	2	070F40 ANOGA	070F40 anophelies g	1202	201	5.1	493	2	017064 AEDAE	017064 aedes aegypt
1130	203.5	5.2	247	1	TR12 HUMAN	TR12 homo sapien	1203	201	5.1	591	2	0176D9 AEDAE	0176D9 aedes aegypt
1131	203.5	5.2	247	2	03SY20 HUMAN	03SY20 homo sapien	1204	201	5.1	665	2	05SPB5 BRARE	05SPB5 brachydanio
1132	203.5	5.2	247	2	05NV56 HUMAN	05NV56 homo sapien	1205	200.5	5.1	148	2	05J326 OREMO	05J326 oreochromis
1133	203.5	5.2	261	2	0725F3 HUMAN	0725F3 homo sapien	1206	200.5	5.1	231	1	TRYP PIG	P00761 sus scrofa
1134	203.5	5.2	263	1	CFAD RAT	P32038 rattus norv	1207	200.5	5.1	246	2	0792Z1 MOUSE	0792Z1 mus musculus
1135	203.5	5.2	285	1	FA9 CAURO	P16295 cavia porce	1208	200.5	5.1	247	2	05H729 MACMU	05H729 macaca mula
1136	203.5	5.2	294	2	03V068 MOUSE	Q3V068 mus musculus	1209	200.5	5.1	249	2	09W7Q1 PAROL	09W7Q1 parailichthy
1137	203.5	5.2	309	2	Q27083 TACTR	Q27083 tachypneus	1210	200.5	5.1	260	2	017J19 AEDAE	017J19 aedes aegypt
1138	203.5	5.2	335	2	08V1F2 MOUSE	08V1F2 mus musculus	1211	200.5	5.1	281	2	06N8B4 HUMAN	06N8B4 homo sapien
1139	203.5	5.2	420	2	016076 AEDAE	016076 aedes aegypt	1212	200.5	5.1	288	2	016JN2 AEDAE	016JN2 aedes aegypt
1140	203.5	5.2	664	2	DLC BRARE	Q914C6 brachydanio	1213	200.5	5.1	351	2	017063 AEDAE	017063 aedes aegypt
1141	203.5	5.2	734	2	069D12 PIG	Q914D12 sus scrofa	1214	200.5	5.1	358	2	057434 FUGRI	057434 fugu rubrip
1142	203.5	5.2	750	2	09W653 CYPCA	Q9W653 cyprinus ca	1215	200.5	5.1	372	2	016PM8 AEDAE	016PM8 aedes aegypt
1143	203.5	5.2	1323	2	Q72387 HUMAN	Q72387 rattus norv	1216	200.5	5.1	415	1	PCOC2 HUMAN	PCOC2 homo sapien
1144	203.5	5.2	1432	1	ATRN RAT	Q99186 rattus norv	1217	200.5	5.1	583	2	016K16 AEDAE	016K16 aedes aegypt
1145	203.5	5.2	2067	2	059ED8 HUMAN	059ED8 homo sapien	1218	200.5	5.1	752	1	CO2 HUMAN	CO2 homo sapien
1146	203.5	5.2	2555	2	05XNM3 HUMAN	05XNM3 homo sapien	1219	200.5	5.1	752	2	053HP3 HUMAN	053HP3 homo sapien
1147	203.5	5.2	3398	2	Q29P22 DROPS	Q29P22 drosophila	1220	200.5	5.1	752	2	05UP69 HUMAN	05UP69 homo sapien
1148	203.5	5.2	3494	2	071C53 HUMAN	Q71C53 homo sapien	1221	200.5	5.1	810	1	PLMN MACMU	P12545 macaca mula
1149	203	5.1	254	2	05M8G2 XENTR	Q5M8G2 xenopus tro	1222	200.5	5.1	951	1	NAS39 CAERL	020176 caenorhabd
1150	203	5.1	255	2	Q70HS0 ANOGA	Q16TMI AEDAE	1223	200	5.1	247	2	042158 PETMA	042158 petromyzon
1151	203	5.1	266	2	016TMI AEDAE	Q16TMI aedes aegypt	1224	200	5.1	358	2	0171W3 AEDAE	0171W3 aedes aegypt
1152	203	5.1	370	2	09VA44 DROME	Q9VA44 drosophila	1225	200	5.1	385	1	TSP50 HUMAN	09U138 homo sapien
1153	203	5.1	403	2	Q9KS06 VIBCH	Q9KS06 vibrio chol	1226	200	5.1	454	2	046506 DROHE	046506 papio hamad
1154	203	5.1	520	2	Q21622 GLOMR	Q21622 glostina mo	1227	200	5.1	504	2	09VEMO DROHE	09VEMO drosophila
1155	203	5.1	680	2	01L8K4 BRARE	Q1L8K4 brachydanio	1228	200	5.1	564	2	07RTZ1 HUMAN	07RTZ1 homo sapien
1156	203	5.1	833	2	09Y1C5 CYPCA	09Y1C5 cyprinus ca	1229	200	5.1	2061	2	04SRM9 TETNG	04SRM9 tetraodon n
1157	202.5	5.1	239	2	08N1C9 HUMAN	Q8N1C9 homo sapien	1230	200	5.1	3564	2	016KG3 AEDAE	016KG3 aedes aegypt
1158	202.5	5.1	255	1	KLK15 SNGOE	Q7J166 saguinus oe	1231	199.5	5.1	223	2	09VBY4 DROME	09VBY4 drosophila
1159	202.5	5.1	274	2	016133 ANOST	Q61613 anophelies s	1232	199.5	5.1	243	2	05M902 XENTR	05M902 xenopus tiro
1160	202.5	5.1	339	2	Q6BD48 PENUP	Q6BD48 penaeus jap	1233	199.5	5.1	247	1	TRYP RAT	P08426 rattus norv
1161	202.5	5.1	347	2	05EBB4 RAT	Q5EBB4 rattus norv	1234	199.5	5.1	257	1	05X1Z0 BRARE	05X1Z0 brachydanio
1162	202.5	5.1	372	2	09W2C8 DROME	Q16PK6 drosophila	1235	199.5	5.1	257	1	KLK1 MACFA	007376 macaca fasc
1163	202.5	5.1	431	2	016PK6 AEDAE	Q16PK6 aedes aegypt	1236	199.5	5.1	258	2	05VANA CERTO	05VANA cercopithec
1164	202.5	5.1	1327	2	059ED1 HUMAN	Q59ED1 homo sapien	1237	199.5	5.1	258	2	Q28508 MACMU	Q28508 macaca mula
1165	202.5	5.1	3623	1	CUBN HUMAN	Q60494 homo sapien	1238	199.5	5.1	348	2	086W55 HUMAN	086W55 homo sapien
1166	202	5.1	241	1	TR1Y GADMO	P00752 sus scrofa	1239	199.5	5.1	378	2	Q9OWP0 TRASG	Q9OWP0 trachemys s
1167	202	5.1	249	2	KLK PIG	Q7Q9X5 anophelies g	1240	199.5	5.1	405	2	01ZEY4 GCAMM	01ZEY4 psychromona
1168	202	5.1	263	2	Q4L1K1 GNEOP	Q16Z81 sesamia non	1241	199.5	5.1	1193	2	090819 CHAMM	090819 gallus gall
1169	202	5.1	263	2	Q16Z81 AEDAE	Q16Z81 aedes aegypt	1242	199.5	5.1	2565	1	NOTC1 HUMAN	P46531 homo sapien
1170	202	5.1	312	2	Q32N63 XENTLA	Q32N63 xenopus lae	1243	1243	5.1	2633	2	Q25253 LUCCU	Q25253 lucilia cup
1171	202	5.1	331	2	Q68D21 HUMAN	Q68D21 homo sapien	1244	1244	5.0	191	2	Q5TW52 ANOGA	Q5TW52 anophelies g
1172	202	5.1	380	2	05MPB7 MANSE	Q5MPB7 manduca sex	1245	1245	5.0	254	2	05XG53 XENTLA	05XG53 xenopus lae
1173	202	5.1	488	2	081UV8 HUMAN	Q81UV8 homo sapien	1246	1246	5.0	260	2	016TMO AEDAE	016TMO aedes aegypt
1174	202	5.1	605	2	05MPB8 MANSE	Q5MPB8 manduca sex	1247	1247	5.0	263	2	062562 PENVA	062562 penaeus lae
1175	202	5.1	743	2	09YCE7 ONCHY	Q9YCE7 oncothynchu	1248	1248	5.0	264	2	06GPY5 XENTLA	06GPY5 xenopus lae
1176	202	5.1	797	2	Q501G6 ORYILA	Q501G6 oryzias lat	1249	1249	5.0	264	2	08QGf6 XENTLA	08QGf6 xenopus lae
1177	202	5.1	2321	1	NOTC3 HUMAN	Q9UW47 homo sapien	1250	1251	5.0	264	2	05MBV7 XENTR	05MBV7 xenopus tiro
1178	202	5.1	195	2	08J007 HUMAN	Q8J007 homo sapien	1251	1252	5.0	268	2	051S29 MAYDE	051S29 mayetolia d
1179	201.5	5.1	195	2	08J008 HUMAN	Q8J008 homo sapien	1252	1253	5.0	317	2	Q31MG7 MOUSE	Q31MG7 mus musculus
1180	201.5	5.1	195	2	08J008 HUMAN	P07146 mus musculu	1253	1254	5.0	355	2	Q176U9 AEDAE	Q176U9 aedes aegypt
1181	201.5	5.1	246	1	TR1Y MOUSE	Q792Y6 mus musculu	1254	1255	5.0	401	2	Q6LH17 PHOPR	Q6LH17 photobacter
1182	201.5	5.1	246	1	Q792Y6 MOUSE	Q61S10 homo sapien	1255	1256	5.0	441	2	Q9XXV0 BOMMO	Q9XXV0 bombyx mori
1183	201.5	5.1	255	2	Q61S10 HUMAN	Q9H2S5 xenopus tro	1256	1257	5.0	683	3	Q1ECY3 BRARE	Q1ECY3 brachydanio
1184	201.5	5.1	256	1	KLK15 HUMAN	Q9H2S5 xenopus tro	1257	1258	5.0	1303	2	Q66S84 OIRDI	Q66S84 oikopleura
1185	201.5	5.1	265	2	05HZU5 XENTR	Q16Z67 aedes aegypt	1258	1259	5.0	237	2	Q17035 ANOGA	Q17035 anophelies g
1186	201.5	5.1	293	2	016Z67 AEDAE	Q710X2 xenopus lae	1259	1260	5.0	243	1	TR1Y BOVIN	P00760 bos taurus
1187	201.5	5.1	320	2	Q7T0X2 XENTLA	Q640T8 xenopus lae	1260	1261	5.0	260	2	Q7S2C3 CHICK	Q7S2C3 gallus gall
1188	201.5	5.1	344	2	Q640F8 XENTLA	Q7PQ76 anophelies g	1261	1262	5.0	311	1	TRYP1 MOUSE	Q9U173 mus musculus
1189	201.5	5.1	383	2	Q7PQ76 ANOGA	Q53K66 homo sapien	1262	1263	5.0	357	2	Q7PQV3 ANOGA	Q7PQV3 anophelies g
1190	201.5	5.1	415	2	Q53K66 HUMAN	Q6ZWK6 homo sapien	1263	1264	5.0	364	2	Q7O1D1 ANOGA	Q7O1D1 aedes aegypt
1191	201.5	5.1	438	2	Q6ZWK6 HUMAN	Q6SMK3 tetraodon n	1264	1265	5.0	364	2	Q9NAS9 ANOGA	Q9NAS9 anophelies g
1192	201.5	5.1	497	2	Q4SMT3 TETNG	Q66105 xenopus lae	1265	1266	5.0	373	2	Q16GK3 AEDAE	Q16GK3 aedes aegypt
1193	201	5.1	247	2	Q42608 PETMA	Q66105 xenopus lae	1266	1267	5.0	382	2	Q179E4 AEDAE	Q179E4 aedes aegypt
1194	201	5.1	248	2	Q66105 XENTLA	Q66UD0 culicoides	1267	1268	5.0	461	2	Q44330 MANSE	Q44330 manduca sex
1195	201	5.1	260	2	Q81W69 HUMAN	Q816K0 holotrichia	1268	1269	5.0	752	1	CO2 GORGO	CO2 gorilla gor
1196	201	5.1	275	2	Q66UD0 YDIPR	Q9VMZ3 drosophila	1269	1270	5.0	829	2	05TF49 HUMAN	05TF49 homo sapien
1197	201	5.1	351	2	Q816K0 HOLDI	Q311V4 pan paniscu	1270	1271	5.0	829	2	Q4PPC3 MOUSE	Q4PPC3 mus musculus
1198	201	5.1	392	2	Q9VMZ3 DROME		1271	1272	5.0	829	2		
1199	201	5.1	484	2	Q311V4 PANPA		1272	1272	5.0	829	2		

1273	198.5	5.0	830	2	05T145_HUMAN	05t145 homo sapien	1346	195	4.9	262	2	0720G3_9DIPT	0720g3 phlebotomus
1274	198.5	5.0	1051	2	05U4U1_XENLA	05u4u1 xenopus lae	1347	195	4.9	336	2	03V0Q7_MOUSE	03v0q7 mus musculus
1275	198.5	5.0	1214	2	090YD2_XENLA	090yd2 xenopus lae	1348	195	4.9	432	1	UROC_RAT	P29598 r mus musculus
1276	198.5	5.0	1289	2	059FL3_HUMAN	059fl3 homo sapien	1349	194.5	4.9	246	1	TRYI_RAT	P00762 ratuus norv
1277	198	5.0	235	1	TRYD_HUMAN	09b2j3 homo sapien	1350	194.5	4.9	246	2	09ROT7_MOUSE	09rot7 mus musculus
1278	198	5.0	259	1	DERF3_DERFA	P49275 dermatophag	1351	194.5	4.9	247	2	0561Z7_BRAE	0561z7 brachydanio
1279	198	5.0	261	2	06QX60_9MAXI	06qx60 lepeophthei	1352	194.5	4.9	258	2	05VAN2_CERO	05van2 cercocobus
1280	198	5.0	268	2	05ISB8_MAYDE	05isb8 mayetiola d	1353	194.5	4.9	261	2	0725F4_HUMAN	0725f4 homo sapien
1281	198	5.0	427	2	05DI98_MANSE	05di98 manduca sex	1354	194.5	4.9	278	2	04SH19_TETNG	04sh19 tetraodon n
1282	198	5.0	427	2	06YX24_MANSE	06yx24 manduca sex	1355	194.5	4.9	283	2	095Y22_GANNE	095y22 lumbricus b
1283	198	5.0	760	1	CO2_MOUSE	P11180 mus musculu	1356	194.5	4.9	343	1	PLMN_SHEEP	P81286 ovib aries
1284	198	5.0	1024	1	SEZU_HUMAN	Q9byh1 homo sapien	1357	194.5	4.9	349	2	028GNI_XENTR	028gni xenopus tro
1285	198	5.0	1128	2	04S6G8_TETNG	Q4s6g8 tetraodon n	1358	194.5	4.9	359	2	04SPG0_TETNG	04spg0 tetraodon n
1286	197.5	5.0	220	2	016PV0_ABDAD	Q16pv0 aedes aegypt	1359	194.5	4.9	393	2	05MPC5_MANSE	05mpc5 manduca sex
1287	197.5	5.0	226	1	COGS_UCAPU	P00771 uca pugilat	1360	194.5	4.9	394	2	05TMN0_ANOGA	05tmn0 anopheles g
1288	197.5	5.0	242	2	06NTB8_HUMAN	06ntb8 homo sapien	1361	194.5	4.9	461	2	04VJ74_XENLA	04vj74 xenopus lae
1289	197.5	5.0	246	2	06IEE6_RAT	Q6iee6 ractus norv	1362	194.5	4.9	618	2	017J17_AEDAE	017j17 aedes aegypt
1290	197.5	5.0	248	1	KLKI2_HUMAN	Q9ukit0 homo sapien	1363	194.5	4.9	1374	2	09VSU0_DROME	09vsu0 drosoophila
1291	197.5	5.0	251	2	07Q4H6_ANOGA	Q7q4h6 anopheles g	1364	194.5	4.9	1449	2	09U112_DROME	09u112 drosoophila
1292	197.5	5.0	255	2	096RQ0_HUMAN	Q96rq0 homo sapien	1365	194.5	4.9	1450	2	08IQB8_DROME	08iqb8 drosoophila
1293	197.5	5.0	258	2	028805_PANTR	Q28805 pan troglod	1366	194.5	4.9	1458	2	01A5L1_BRAE	01a5l1 brachydanio
1294	197.5	5.0	263	2	06H319_PIG	Q6h319 sus scrofa	1367	194.5	4.9	1462	2	09U113_DROME	09u113 drosoophila
1295	197.5	5.0	428	2	01LYU7_BRAE	Q1lyv7 brachydanio	1368	194.5	4.9	2382	2	09B119_DROME	09b119 drosoophila
1296	197.5	5.0	752	2	03SGZ8_HUMAN	Q3sgz8 homo sapien	1369	194.5	4.9	2409	2	0960G6_DROME	0960g6 drosoophila
1297	197	5.0	222	2	091WZ0_RAT	Q91wz0 ractus norv	1370	194.5	4.9	2428	2	0816X6_BOONI	0816x6 boophilus m
1298	197	5.0	253	2	05OBG5_9DIPT	Q5qbg5 culicoides g	1371	194.5	4.9	2549	2	02L697_CIOIN	02l697 ciona intes
1299	197	5.0	258	2	07OKX6_ANOGA	Q7okxe anopheles g	1372	194.5	4.9	2786	2	09VSU2_DROME	09vsu2 drosoophila
1300	197	5.0	261	2	09VXC7_DROME	Q9vxc7 drosoophila	1373	194	4.9	243	2	07PFE7_ANOGA	07pfe7 anopheles g
1301	197	5.0	268	2	051V42_MAYDE	Q51v42 mayetiola d	1374	194	4.9	245	2	042160_PETMA	042160 petromyzon
1302	197	5.0	338	1	PLMN_HORSE	P80010 equus caball	1375	194	4.9	247	2	07OT74_HORSE	07ot74 equus caball
1303	197	5.0	382	2	029KZ8_DROPS	Q29kz8 drosoophila	1376	194	4.9	253	2	09VAG3_DROME	09vag3 drosoophila
1304	197	5.0	385	2	05U365_RAT	Q5u365 ractus norv	1377	194	4.9	259	1	CFAD_PIG	P51779 sus scrofa
1305	197	5.0	421	2	09SR86_DROME	Q9sr86 drosoophila	1378	194	4.9	276	2	016ID2_AEDAE	016id2 aedes aegypt
1306	197	5.0	585	2	09U0E2_TRICA	Q9u0e2 tribolium c	1379	194	4.9	301	2	016IO9_AEDAE	016io9 aedes aegypt
1307	197	5.0	745	2	091701_XENLA	Q91701 xenopus lae	1380	194	4.9	379	2	04SUW0_TETNG	04suw0 tetraodon n
1308	197	5.0	760	2	070J30_MOUSE	Q70j30 mus musculu	1381	194	4.9	356	2	080J35_BRAE	080j35 brachydanio
1309	196.5	5.0	219	2	091036_GADMO	Q91036 gadus morhu	1382	194	4.9	578	2	03USM6_MOUSE	03usm6 mus musculu
1310	196.5	5.0	223	2	029G71_DROPS	Q29g71 drosoophila	1383	194	4.9	806	1	PLMN_MACEU	Q18733 macropus eu
1311	196.5	5.0	231	2	06GY75_STRCA	Q6gy75 struchio ca	1384	193.5	4.9	183	2	06PLJ7_9EUC4	06plj7 fenneropena
1312	196.5	5.0	246	2	04SH18_TETNG	Q4sh18 tetraodon n	1385	193.5	4.9	235	2	070820_ANOGA	070820 anopheles g
1313	196.5	5.0	259	2	08IRE0_DROME	Q8ire0 drosoophila	1386	193.5	4.9	245	2	0792Y9_MOUSE	0792y9 mus musculu
1314	196.5	5.0	269	1	ELAZB_HUMAN	P88218 homo sapien	1387	193.5	4.9	246	2	09QUR9_MOUSE	09qur9 mus musculu
1315	196.5	5.0	270	2	08JUM8_AEDAE	Q8j8m8 aedes aegypt	1388	193.5	4.9	247	2	06T376_EISFO	06t376 eisenia foe
1316	196.5	5.0	298	2	08T4N4_RHAP	Q8t4n4 rhinipcephal	1389	193.5	4.9	247	2	09W705_PAROL	09w705 paralicthy
1317	196.5	5.0	362	2	0566K9_XENTR	Q566k9 xenopus tro	1390	193.5	4.9	256	2	027540_CHOIR	027540 choirosteneu
1318	196.5	5.0	370	2	0299U3_DROPS	Q299u3 drosoophila	1391	193.5	4.9	261	2	028Y25_DROPS	028y25 drosoophila
1319	196.5	5.0	570	1	BBP3_STRPU	P49013 strongyloce	1392	193.5	4.9	262	2	07Q144_ANOGA	07q144 anopheles g
1320	196.5	5.0	829	2	06NUL9_HUMAN	Q6nul9 homo sapien	1393	193.5	4.9	263	2	09V5X7_DROME	09v5x7 drosoophila
1321	196.5	5.0	2030	2	Q2MBY6_PLADU	Q2mby6 platyneleis	1394	193.5	4.9	269	2	05M925_XENTR	05m925 xenopus tro
1322	196.5	5.0	2524	1	NOTCH_XENLA	Q6gpx7 xenopus lae	1395	193.5	4.9	272	2	0290E7_DROME	0290e7 drosoophila
1323	196	5.0	248	2	06GPX7_XENLA	Q6gp7 xenopus lae	1396	193.5	4.9	317	2	09DGR3_XENLA	09dgr3 xenopus lae
1324	196	5.0	257	2	052KS8_XENLA	Q52ks8 xenopus lae	1397	193.5	4.9	347	2	070B73_ANOGA	070b73 anopheles g
1325	196	5.0	262	2	05XKPS_XENLA	Q5xkps xenopus lae	1398	193.5	4.9	375	2	028XQ9_DROPS	028xq9 drosoophila
1326	196	5.0	270	1	ELAZB_HUMAN	P08881 homo sapien	1399	193.5	4.9	389	2	0294U5_DROPS	0294u5 drosoophila
1327	196	5.0	275	2	066UC8_9DIPT	Q66uc8 culicoides	1400	193.5	4.9	789	2	08N1E9_HUMAN	08n1e9 homo sapien
1328	196	5.0	349	2	Q17N99_AEDAE	Q17n99 aedes aegypt	1401	193.5	4.9	1089	2	08T3A0_CIOIN	08t3a0 ciona intes
1329	196	5.0	400	2	09GRG2_TENMO	Q9grg2 tenobryo mo	1402	193.5	4.9	1235	2	06IO50_HUMAN	06io50 homo sapien
1330	196	5.0	418	2	04RJM2_TETNG	Q4rjm2 tetraodon n	1403	193.5	4.9	2471	1	NOTC2_RAT	09q470 ractus norv
1331	196	5.0	432	2	03XR76_RAT	Q3xr76 ractus norv	1404	193	4.9	239	2	0308Q8_EISFO	0308q8 eisenia foe
1332	196	5.0	484	2	Q11V3_PPRIM	Q31iv3 gorilla gor	1405	193	4.9	253	1	CAC3_BOVIN	030880 bos taurus
1333	196	5.0	850	2	Q11B23_BVARE	Q11b23 brachydanio	1406	193	4.9	258	1	ELAI_CANFA	086780 canis famli
1334	196	5.0	3623	1	CUBN_RAT	Q702d4 ractus norv	1407	193	4.9	268	2	09XY56_CTEFE	09xy56 ctenocephal
1335	195.5	5.0	247	2	05H730_MACMU	Q5h730 macaca mula	1408	193	4.9	269	2	095KM7_BOVIN	095km7 bos taurus
1336	195.5	5.0	257	1	GRAM_HUMAN	P51124 homo sapien	1409	193	4.9	272	2	052NWS_9DIPT	052nws anopheles c
1337	195.5	5.0	267	2	09GCP27_DROME	Q9gcp27 drosoophila	1410	193	4.9	305	2	017IQ6_AEDAE	017iq6 aedes aegypt
1338	195.5	5.0	274	2	Q170B6_ANOST	Q170b6 anopheles s	1411	193	4.9	315	2	05MGE3_LONON	05mge3 lononla obl
1339	195.5	5.0	276	2	Q18443_HELAM	Q18443 heilicoverpa	1412	193	4.9	319	2	016L26_AEDAE	016l26 aedes aegypt
1340	195.5	5.0	292	2	Q16N48_AEDAE	Q16n48 aedes aegypt	1413	193	4.9	357	2	017B40_AEDAE	017b40 aedes aegypt
1341	195.5	5.0	752	1	NOT2_PANTR	Q08q74 pan troglod	1414	193	4.9	379	2	0178V8_AEDAE	0178v8 aedes aegypt
1342	195.5	5.0	2471	1	NOTC2_HUMAN	Q04721 homo sapien	1415	193	4.9	392	2	Q1HRE9_AEDAE	01hre9 aedes aegypt
1343	195.5	5.0	2471	2	OSVTDO_HUMAN	Q5vtcd0 homo sapien	1416	193	4.9	393	2	Q7QAC0_ANOGA	07qac0 anopheles g
1344	195	4.9	242	2	Q4ADVA_SEROU	Q4adv4 seriola qui	1417	193	4.9	423	2	057433_FUGRU	057433 fugu rubrip
1345	195	4.9	261	1	KLKI_MOUSE	P15947 mus musculu	1418	193	4.9	447	2	Q499M3_MOUSE	Q499m3 mus musculu


```

1419 193 4.9 481 2 Q9H284_HUMAN
1420 193 4.9 543 2 Q6PHN6_MOUSE
1421 193 4.9 601 2 Q16S05_AEDAE
1422 193 4.9 601 2 Q16S05_AEDAE
1423 193 4.9 963 2 Q6P1D5_MOUSE
1424 193 4.9 1275 2 Q6P1D5_MOUSE
1425 193 4.9 2010 2 Q4RHF2_TETNG
1426 192.5 4.9 178 2 Q93594_DICLA
1427 192.5 4.9 222 2 Q94508_DERPA
1428 192.5 4.9 243 2 Q5M976_XENTR
1429 192.5 4.9 245 2 Q5TN68_ANOGA
1430 192.5 4.9 246 2 Q921R9_MOUSE
1431 192.5 4.9 247 2 Q8NHM4_HUMAN
1432 192.5 4.9 256 1 TRYP_CHOFU
1433 192.5 4.9 257 2 Q4QRH5_BRANE
1434 192.5 4.9 268 2 Q28276_DROPS
1435 192.5 4.9 276 1 KLK11_MOUSE
1436 192.5 4.9 381 2 Q8M0Y4_DROME
1437 192.5 4.9 438 2 Q9H804_HUMAN
1438 192.5 4.9 439 2 Q5RDX7_PONPY
1439 192.5 4.9 669 2 Q4SC13_TETNG
1440 192.5 4.9 754 2 P79816_ORYLA
1441 192.5 4.9 754 2 P79816_ORYLA
1442 192 4.9 244 2 Q42159_PETMA
1443 192 4.9 246 2 Q9BL17_LUMBU
1444 192 4.9 249 2 Q5TWT2_ANOGA
1445 192 4.9 254 2 Q9XY10_RHTIO
1446 192 4.9 256 2 Q6M0Y6_BDEBA
1447 192 4.9 265 2 Q4S848_TETNG
1448 192 4.9 304 2 Q16LR0_AEDAE
1449 192 4.9 354 2 Q7OKL3_ANOGA
1450 192 4.9 380 2 Q9Y1K5_ANOGA
1451 192 4.9 383 2 Q77102_MANSE
1452 192 4.9 333 2 Q175C8_AEDAE
1453 191.5 4.9 225 2 Q5TXH2_ANOGA
1454 191.5 4.9 243 2 Q5M959_XENTR
1455 191.5 4.9 247 1 TRYP_HUMAN
1456 191.5 4.9 247 2 Q5NV57_HUMAN
1457 191.5 4.9 247 2 Q17039_ANOGA
1458 191.5 4.9 265 2 Q6QX61_9MAKI
1459 191.5 4.9 270 2 Q4S520_TETNG
1460 191.5 4.9 279 2 Q155V8_DERPA
1461 191.5 4.9 281 2 Q76898_DROME
1462 191.5 4.9 284 2 Q81RX5_DROME
1463 191.5 4.9 285 2 Q7Q298_ANOGA
1464 191.5 4.9 316 2 Q29AX8_DROPS
1465 191.5 4.9 360 2 Q8SX54_DROME
1466 191.5 4.9 385 2 Q8SX54_DROME
1467 191.5 4.9 480 2 Q6STT1_KENLA
1468 191.5 4.9 713 2 Q80TP0_MOUSE
1469 191.5 4.9 830 1 LYAM3_HUMAN
1470 191.5 4.9 897 2 Q3V6S1_MOUSE
1471 191.5 4.9 2468 2 Q800E4_BRANE
1472 191.5 4.9 3396 2 Q9VM55_DROME
1473 191 4.8 228 2 Q6P6R8_HUMAN
1474 191 4.8 230 2 Q4RQD7_TETNG
1475 191 4.8 248 2 Q5H732_MACCU
1476 191 4.8 254 1 KLK4_HUMAN
1477 191 4.8 254 2 Q25227_LUCCU
1478 191 4.8 256 2 Q81BE5_9DIPF
1479 191 4.8 270 2 Q17BS3_AEDAE
1480 191 4.8 273 2 Q51Y40_MAYBE
1481 191 4.8 277 2 Q81Q10_DROME
1482 191 4.8 282 2 Q4VB11_BRANE
1483 191 4.8 317 2 Q8K4D1_MOUSE
1484 191 4.8 317 2 Q8K4D1_MOUSE
1485 191 4.8 415 2 Q9GRM0_HOUDI
1486 191 4.8 646 2 Q29097_TIG
1487 191 4.8 758 2 Q6MG73_RAT
1488 191 4.8 1006 2 Q29D77_DROPS
1489 190.5 4.8 245 2 Q4G0C2_MOUSE
1490 190.5 4.8 246 2 Q3V2G3_MOUSE
1491 190.5 4.8 246 2 Q79220_MOUSE

```

```

Q9H284 homo sapien
Q6PHN6 mus musculus
Q16S05 aedes aegypti
Q8C420 mus musculus
Q6P1D5 mouse
Q6P1D5 mouse
Q4RHF2 tetraodon
Q93594 dicentrarchus
Q94508 dermatophag
Q5M976 xenopus
Q5TN68 anopheles
Q921R9 mus musculus
Q8NHM4 homo sapien
P35042 choristoneura
Q4QRH5 brachydanio
Q28276 drosophila
Q9Y1K5 mus musculus
Q9H804 homo sapien
Q5RDX7 pongo
Q4SC13 tetraodon
P79816 oryza lat
Q7Q344 anopheles
Q42159 petiomys
Q9BL17 lumbricus
Q5TWT2 anopheles
Q9XY10 rhyzopertha
Q6M0Y6 bdellovibrio
Q4S848 tetraodon
Q16LR0 aedes aegypti
Q7OKL3 anopheles
Q9Y1K5 anopheles
Q77102 manduca
Q175C8 aedes aegypti
Q5TXH2 anopheles
Q5M959 xenopus
P07477 homo sapien
Q5NV57 homo sapien
Q17039 anopheles
Q6QX61 lepeophthei
Q4S520 tetraodon
Q155V8 dermatophag
Q76898 drosophila
Q81RX5 drosophila
Q7Q298 anopheles
Q29AX8 drosophila
Q8SX54 drosophila
Q8SX54 drosophila
Q6STT1 xenopus
Q80TP0 mus musculus
P16109 homo sapien
Q3V6S1 mus musculus
Q800E4 brachydanio
Q9VM55 drosophila
Q6P6R8 homo sapien
Q4RQD7 tetraodon
Q5H732 macaca
Q9Y5K2 homo sapien
Q25227 lucilia
Q81BE5 ochlerotatu
Q17BS3 aedes aegypti
Q51Y40 mayetioides
Q81Q10 drosophila
Q4VB11 brachydanio
Q8K4D1 mus musculus
Q8K4D1 mus musculus
Q9GRM0 holocricidia
Q29097 ratu scrofa
Q6MG73 rattus norvegicus
Q29D77 drosophila
Q4G0C2 mus musculus
Q3V2G3 mus musculus
Q79220 mus musculus

```

```

1492 190.5 4.8 257 2 Q81BE3_9DIPF
1493 190.5 4.8 314 2 Q28EV7_XENTR
1494 190.5 4.8 317 2 Q5PEM3_XENTR
1495 190.5 4.8 360 2 Q17HM7_AEDAE
1496 190.5 4.8 579 1 MFRP_HUMAN
1497 190.5 4.8 762 2 Q9Y1C6_CYPCA
1498 190.5 4.8 768 1 LYAM3_MOUSE
1499 190.5 4.8 768 2 Q32MFI_MOUSE
1500 190.5 4.8 1064 1 FBPI_STRPU

```

ALIGNMENTS

```

RESULT 1
Q6UXH9_HUMAN PRELIMINARY; PRT; 720 AA.
ID Q6UXH9_HUMAN
AC Q6UXH9;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 02-MAY-2006, entry version 14.
DE ELG69.
GN ORFNames=UNQ699;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorhini;
OC Catarrhini; Hominoidea; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22867296; PubMed=1295309; DOI=10.1101/gr.1293003;
RA Chen H.F., Gunney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,
RA Clark J., Chow B., Chui C., Crowley C., Currell B., Dowd P.,
RA Eaton D., Foster J.S., Grimaldi C., Gu Q., Hass P.E., Helens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schonfeld J.,
RA Sesbagli S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandien R.L., Watanabe C., Wleand D., Woods K., Xie M.-H.,
RA Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,
RA Wood W.I., Godowski P.J., Gray A.M.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment."
RL Genome Res. 13:2265-2270(2003).
CC -----
CC Copyrighted under the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NonDerivs License
CC -----
EMBL: A1358346; AA08712.1; -; mRNA.
DR UniGene; Hs.55044; -.
DR HSSP; P00734; 1BB0.
DR Ensemble; ENSG00000149090; Homo sapiens.
DR GO; GO:0004252; F:serine-type endopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis; IEA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR006210; EGF.
DR InterPro; IPR00742; EGF_3.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR013032; EGF_like_reg.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR InterPro; IPR01254; Peptidase_S1_S6.
DR InterPro; IPR01314; Peptidase_S1A.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00008; EGF; 1.
DR Pfam; PF00084; Sushi; 1.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00032; CCP; 2.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00181; EGF; 2.
DR SMART; SM00020; TRYP_SPC; 1.
DR PROSITE; PS01180; CUB; 1.

```

DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; 1.
 DR PROSITE; PS50026; EGF_3; 1.
 DR PROSITE; PS50923; SUSH1; 2.
 DR PROSITE; PS50240; TRYPsin_DOM; 1.
 SQ SEQUENCE 720 AA; 80199 MW; DC898BC7241289D3 CRC64;

Query Match 100.0%; Score 3945; DB 2; Length 720;
 Best Local Similarity 100.0%; Pred. No. 3 8e-288;
 Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MELGCMTQLGLTFLQILLISLPREYTVINEACPGAEMNIMCRCECYDQIECVCPGKRE 60
 DB 1 MELGCMTQLGLTFLQILLISLPREYTVINEACPGAEMNIMCRCECYDQIECVCPGKRE 60
 QY 61 VVGTTIPCCNNEECSCLIHPGCTTFENCKSCRNSWGGLDDFFVKGFFYCAECRAGW 120
 DB 61 VVGTTIPCCNNEECSCLIHPGCTTFENCKSCRNSWGGLDDFFVKGFFYCAECRAGW 120
 QY 121 YGSDCMRCGOVLRAPKQIILLESYPLNAHCEMTTHAKPGFVIOIRFVMLSLEPDMCOYD 180
 DB 121 YGSDCMRCGOVLRAPKQIILLESYPLNAHCEMTTHAKPGFVIOIRFVMLSLEPDMCOYD 180
 QY 121 YGSDCMRCGOVLRAPKQIILLESYPLNAHCEMTTHAKPGFVIOIRFVMLSLEPDMCOYD 180
 DB 121 YGSDCMRCGOVLRAPKQIILLESYPLNAHCEMTTHAKPGFVIOIRFVMLSLEPDMCOYD 180
 QY 181 YVEVRDGNRDGQIIKRVCGNERPAPIQSIGSSLHVLPHSDGSKNPFDFHAYIEBITACS 240
 DB 181 YVEVRDGNRDGQIIKRVCGNERPAPIQSIGSSLHVLPHSDGSKNPFDFHAYIEBITACS 240
 QY 241 SSPFHGTCVLDKAGSYKCACTAGTGRCENILLEERNCSDPGPGVNGYOKITGGGGLI 300
 DB 241 SSPFHGTCVLDKAGSYKCACTAGTGRCENILLEERNCSDPGPGVNGYOKITGGGGLI 300
 QY 301 NGRHAKIGTVSPFCNNSYVLSGNEKRTCOONGEMSGKOPICIAKCEPKISDLVRRVYL 360
 DB 301 NGRHAKIGTVSPFCNNSYVLSGNEKRTCOONGEMSGKOPICIAKCEPKISDLVRRVYL 360
 QY 301 NGRHAKIGTVSPFCNNSYVLSGNEKRTCOONGEMSGKOPICIAKCEPKISDLVRRVYL 360
 DB 301 NGRHAKIGTVSPFCNNSYVLSGNEKRTCOONGEMSGKOPICIAKCEPKISDLVRRVYL 360
 QY 361 PMQVOSRETPHQLYSAFSGKQLQSAPTKKPALPFGDLPMGYOHLTQLOYECISPFYR 420
 DB 361 PMQVOSRETPHQLYSAFSGKQLQSAPTKKPALPFGDLPMGYOHLTQLOYECISPFYR 420
 QY 421 RLSSSRRTCLRTGKMSGRABSCIPICGKIENITAPKTOGLKMPQOALVRRTSVHDSGL 480
 DB 421 RLSSSRRTCLRTGKMSGRABSCIPICGKIENITAPKTOGLKMPQOALVRRTSVHDSGL 480
 QY 481 HKGMFLVCSGALVNERTVVAHCVTDLGVKMTKTADLVKVGKFRDDDRDEKTIQS 540
 DB 481 HKGMFLVCSGALVNERTVVAHCVTDLGVKMTKTADLVKVGKFRDDDRDEKTIQS 540
 QY 541 LQISAILHPNYDPIILDADIAIKLIDKARISTRVOPICLAASRDLSFQESHITVAG 600
 DB 541 LQISAILHPNYDPIILDADIAIKLIDKARISTRVOPICLAASRDLSFQESHITVAG 600
 QY 601 MNVLADVRSPGKNDTLRSVSVVDLSLCEQHEDHGIPIVSYVDNMFCAWETAASDI 660
 DB 601 MNVLADVRSPGKNDTLRSVSVVDLSLCEQHEDHGIPIVSYVDNMFCAWETAASDI 660
 QY 661 CTATGTGIAAASPGRASPBPMMHLMGLVSNKYDCTSHSLSTAFYKVLPRKDMIERMK 720
 DB 661 CTATGTGIAAASPGRASPBPMMHLMGLVSNKYDCTSHSLSTAFYKVLPRKDMIERMK 720

RESULT 2
 OSJUP14 HUMAN PRELIMINARY; PRT; 720 AA.
 AC OSJUP14
 DT 15-FEB-2005, integrated into UniProtKB/TrEMBL.
 DT 02-MAY-2005, sequence version 1.
 DE Hypothetical protein DKFZp67H2312.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorhini;
 OC Catarrhini; Hominoidea; Homo.

OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Lymph node;
 RG The German cDNA Consortium;
 RA Koehler K., Beyer A., Mewes H.W., Well B., Amid C., Osanger A.,
 RA Pobo G., Han M., Wiemann S.;
 RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.

CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NonDerivs License

CC EMBL; AL632391; CA146203.1; -; mRNA.
 CC Ensemble; ENSG00000149090; Homo sapiens.

DR GO; GO:0004252; F:serine-type endopeptidase activity; IEA.
 DR GO; GO:0006508; P:proteolysis; IEA.

DR InterPro; IPR000859; CUB.
 DR InterPro; IPR006210; EGF.

DR InterPro; IPR000742; EGF_3.
 DR InterPro; IPR006209; EGF_like.

DR InterPro; IPR013032; EGF_like_reg.
 DR InterPro; IPR009003; Pept_Ser_Cys.

DR InterPro; IPR01254; Peptidase_S1_96.
 DR InterPro; IPR001314; Peptidase_S1A.

DR InterPro; IPR000436; Sush1_SCR_CCP.
 DR Pfam; PF00431; CUB; 1.

DR Pfam; PF00008; EGF; 1.
 DR Pfam; PF00084; Sush1; 2.

DR Pfam; PF00089; Trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.

DR SMART; SM00032; CCP; 2.
 DR SMART; SM00042; CUB; 1.

DR SMART; SM00181; EGF; 2.
 DR SMART; SM00020; TRYPSIN; 1.

DR PROSITE; PS01180; CUB; 1.
 DR PROSITE; PS00022; EGF; 1.

DR PROSITE; PS01186; EGF_2; 1.
 DR PROSITE; PS50026; EGF_3; 1.

DR PROSITE; PS50923; SUSH1; 2.
 DR PROSITE; PS50240; TRYPsin_DOM; 1.

DR Hypothetical protein.
 SQ SEQUENCE 720 AA; 80227 MW; 1C8A8A8C4BEE7767 CRC64;

Query Match 99.9%; Score 3941; DB 2; Length 720;
 Best Local Similarity 99.9%; Pred. No. 7 7e-288;
 Matches 719; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MELGCMTQLGLTFLQILLISLPREYTVINEACPGAEMNIMCRCECYDQIECVCPGKRE 60
 DB 1 MELGCMTQLGLTFLQILLISLPREYTVINEACPGAEMNIMCRCECYDQIECVCPGKRE 60
 QY 61 VVGTTIPCCNNEECSCLIHPGCTTFENCKSCRNSWGGLDDFFVKGFFYCAECRAGW 120
 DB 61 VVGTTIPCCNNEECSCLIHPGCTTFENCKSCRNSWGGLDDFFVKGFFYCAECRAGW 120
 QY 121 YGSDCMRCGOVLRAPKQIILLESYPLNAHCEMTTHAKPGFVIOIRFVMLSLEPDMCOYD 180
 DB 121 YGSDCMRCGOVLRAPKQIILLESYPLNAHCEMTTHAKPGFVIOIRFVMLSLEPDMCOYD 180
 QY 121 YGSDCMRCGOVLRAPKQIILLESYPLNAHCEMTTHAKPGFVIOIRFVMLSLEPDMCOYD 180
 DB 121 YGSDCMRCGOVLRAPKQIILLESYPLNAHCEMTTHAKPGFVIOIRFVMLSLEPDMCOYD 180
 QY 181 YVEVRDGNRDGQIIKRVCGNERPAPIQSIGSSLHVLPHSDGSKNPFDFHAYIEBITACS 240
 DB 181 YVEVRDGNRDGQIIKRVCGNERPAPIQSIGSSLHVLPHSDGSKNPFDFHAYIEBITACS 240
 QY 241 SSPFHGTCVLDKAGSYKCACTAGTGRCENILLEERNCSDPGPGVNGYOKITGGGGLI 300
 DB 241 SSPFHGTCVLDKAGSYKCACTAGTGRCENILLEERNCSDPGPGVNGYOKITGGGGLI 300
 QY 301 NGRHAKIGTVSPFCNNSYVLSGNEKRTCOONGEMSGKOPICIAKCEPKISDLVRRVYL 360
 DB 301 NGRHAKIGTVSPFCNNSYVLSGNEKRTCOONGEMSGKOPICIAKCEPKISDLVRRVYL 360
 QY 361 PMQVOSRETPHQLYSAFSGKQLQSAPTKKPALPFGDLPMGYOHLTQLOYECISPFYR 420
 DB 361 PMQVOSRETPHQLYSAFSGKQLQSAPTKKPALPFGDLPMGYOHLTQLOYECISPFYR 420

OX NCBI_TaxId=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Chondrosarcoma Lung Metastasis;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Topolinski S., Cantinici P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Mowley K.C., Harte S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywicki M.I., Skalek U., Smalins D.E.,
RA Schnerch A., Schein J.E., Jones S.U.M., Matra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Chondrosarcoma Lung Metastasis;
RA Director MGC Project;
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NonDerivative license
CC -----
CC EMBL: BC089434; AAH89434.1; -; mRNA.
DR UniGene; Hs.55044; -.
DR MEROPS; S01.998; -.
DR Ensembl; ENSG00000149090; Homo sapiens.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004252; F:serine-type endopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis; IEA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR006210; EGF.
DR InterPro; IPR000742; EGF_3.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR013032; EGF_like_reg.
DR InterPro; IPR009003; Pept_ser_Cys.
DR InterPro; IPR001254; Peptidase_S1_S6.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR000436; Sushi_SCR_CCP.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00008; EGF; 1.
DR Pfam; PF00084; Sushi; 2.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00032; CCP; 2.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00181; EGF; 2.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS00026; EGF_3; 1.
DR PROSITE; PSS0923; Sushi; 2.
DR PROSITE; PSS0240; TRYPSIN_DOM; 1.
DR PROSITE; PSS0240; TRYPSIN_DOM; 1.
KW Protease.
SQ SEQUENCE 737 AA; 81943 MW; PD3BACCFE47778FE CRC64;

Query March 99.5%; Score 1926.5; DB 2; Length 737;
Best Local Similarity 97.7%; Pred. No. 9.8e-287;
Matches 720; Conservative 0; Mismatches 0; Indels 17; Gaps 1;
QY 1 MELGCWTQGLTFLQLLISLIPREYTVINEACPGAENIMGRCCEYDQIEVCVCKRE 60

DB 1 MELGCWTQGLTFLQLLISLIPREYTVINEACPGAENIMGRCCEYDQIEVCVCKRE 60
QY 61 VGGYITPCCRNENEDSCLIHPGCTIFENCKSCRGSGGTLDDPYVKGFTYAEGRAG 120
DB 61 VGGYITPCCRNENEDSCLIHPGCTIFENCKSCRGSGGTLDDPYVKGFTYAEGRAG 120
QY 121 YGGDCRCGCVLAAPGQILLESYPLNACCEWTHAKPGFVQLRFVMLSLEFDYMCQYD 180
DB 121 YGGDCRCGCVLAAPGQILLESYPLNACCEWTHAKPGFVQLRFVMLSLEFDYMCQYD 180
QY 181 YVERDGDNRDQIIRKVGNERPAPISIGSSLHVLPHSDGSKNDFPAIYEETTACS 240
DB 181 YVERDGDNRDQIIRKVGNERPAPISIGSSLHVLPHSDGSKNDFPAIYEETTACS 240
QY 241 SSPCFHDTGTCVLDKAGSYKACLAGTTCQRCENL-----LEERNCSDP 283
DB 241 SSPCFHDTGTCVLDKAGSYKACLAGTTCQRCENL-----LEERNCSDP 300
QY 284 GGPVNGYOKITGGPGLINGRHAIGTVSPFCNNSYVLSGNEKRTCOQNGEMSGKPICT 343
DB 301 GGPVNGYOKITGGPGLINGRHAIGTVSPFCNNSYVLSGNEKRTCOQNGEMSGKPICT 360
QY 344 KACREPKISDLYRRVLPVQVQRETPHLQVSAFSSKQVQAPTKKPALPGDLPNGY 403
DB 361 KACREPKISDLYRRVLPVQVQRETPHLQVSAFSSKQVQAPTKKPALPGDLPNGY 420
QY 404 QHHTLOQYECISPFPRRLSSRRCTCLRTKSGRASPCTPIGKIENITAPTKQILRP 463
DB 421 QHHTLOQYECISPFPRRLSSRRCTCLRTKSGRASPCTPIGKIENITAPTKQILRP 480
QY 464 WQAIYRRTSGVMDGSLHKAMFLVCSGALVNRVTVAACHCTDAGKVTMTADLKV 523
DB 481 WQAIYRRTSGVMDGSLHKAMFLVCSGALVNRVTVAACHCTDAGKVTMTADLKV 540
QY 524 LGRFYRDDDEKTIQSLQISAILHPNYDPIILLDIALIKLDBKARISTRVQPICLAA 583
DB 541 LGRFYRDDDEKTIQSLQISAILHPNYDPIILLDIALIKLDBKARISTRVQPICLAA 600
QY 584 SRDLSTSFQSHITTVAGMNVLDVRSBPGKNDLTRSGVSVVDSLCEBQEHGHPVSV 643
DB 601 SRDLSTSFQSHITTVAGMNVLDVRSBPGKNDLTRSGVSVVDSLCEBQEHGHPVSV 660
QY 644 TDNMFCSMEPTAPSDICTAETGIAVSPRGAPEPRHMLGLVMSYDXTCSHRLST 703
DB 661 TDNMFCSMEPTAPSDICTAETGIAVSPRGAPEPRHMLGLVMSYDXTCSHRLST 720
QY 704 AFTKVLPEKDMIRNNK 720
DB 721 AFTKVLPEKDMIRNNK 737
RESULT 5
Q96JW2 HUMAN PRELIMINARY; PRT; 737 AA.
ID Q96JW2 HUMAN PRELIMINARY; PRT; 737 AA.
AC Q96JW2;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 02-MAY-2006, entry version 1.
DE CDNA FLJ14935 f1s, clone PLACE1009992, weakly similar to LIMULUS
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorhina;
OC Catarrhini; Hominoidea; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Placenta;
RX PubMed=14702039; DOI=10.1038/ng1285;
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Ohyashiki M., Nishi T., Shibahara T., Tanaka T., Ishii S.,

D	b		61	VGGTITPCCKRNEENCSCILHPECTTIFENCKSCRNSMGSTLDDFFVKGFYCAECRAW	120
O	y		121	YGGCQNRGCVLRAPKGOIILESEYPFLNAGEWTTHARPGFYTQLRFYMLSLFPDYMCOYD	180
D	b		121	YGGQWRMGCGVLARPKEQIILLSESPFLNAHEMTHTARPGFYIQARFMYLSLEPFYMCYD	180
O	y		181	YVEVRDGDNDFGQIIKRVCGNERPAPIQSIGSSLHLVLFHSDGSKNPDGFHAHYEETACS	240
D	b		181	YVEVRDGDNDNGOIIKRVCGERPAPIQSIGSSLHLVLFHSDGSKNFGDFHAHYEETACS	240
O	y		241	SSPCHGTCTVLDKASGYKACACLAGYGQRCENL-----LEERNCSDP	283
D	b		241	SSPCHGTCTVLDKAGPYKACACLAGYGQRCEMLEAKSKIKASEDSLVLIERNCSDP	300
O	y		284	GGPVNGYOKITGGPGLNGRHAKIGTVASFCCNNSYLISGENERTCOONGEMSGKOPICI	343
D	b		301	GGPVNGYOKITGGPGLNGRHAKIGTVASFCCNNSYLISGENERTCOONGEMSGKOPICI	360
O	y		344	KACEPKISDLVRRRLVMQVSRETEPHOLYSAAFSGOKLOSAPTCKPALPFGLPMGY	403
D	b		361	KACEPKISDLVRRRLVMQVSRETPLHQLYSAAFSGOKLOSAPTCKPALPFGLPMGY	420
O	y		404	QHLLTQQYECISPFYRLSSRTCLRTGKMSGRASCIPICGIENITPAKTQGLRP	463
D	b		421	QHLLTQQYECISPFYRLSSRTCLRTGKMSGRASCIPICGINITPAKTQGLRP	480
O	y		464	WOALIVRTSGVDHGSLHKGMFLVGCAGLVNESTVVAAHVCDLKVMTIKADLKV	523
D	b		481	WOALIVRTSGVDHGSLHKGMFLVGCAGLVNESTVVAAHVCDLGVMTIKADLKV	540
O	y		524	LGEFYRDDDRDEKTIQSLQISAILLHNBYDPIILDADIALLKLDKARISTRVPTCLAA	583
D	b		541	LGEFYRDDDRDEKTIQSLQISAITLHPNYDPIILDADIALLKLDKARISTRVPTCLAA	600
O	y		584	SRDLSTFOESHITVAGMNVLTADYRSFGFKNDTLRSQVSVYVDSLLCEBOEHEDGIPVS	643
D	b		601	SRDLSTFOESHITVAGMNVLTADYRSFGFKNDTLRSQVSVYVDSLLCEBOEHEDGIPVS	660
O	y		644	TDNMFCSWSBETAASDICTAETGGIAAVSPGRASPFRMHLMGLVMSVYKTSRHLST	703
D	b		661	TDNMFCSWSBETAASDICTAETGGIAAVSPGRASPFRMHLMGLVMSVYKTSRHLST	720
O	y		704	AFTKYLPFKDIERNMK 720	
D	b		721	AFTKYLPFKDIERNMK 737	
<hr/>					
RESULT 6					
OSRDII_PONPY PRELIMINARY, PRT; 720 AA.					
AC	OSRDII_PONPY				
DT	21-DEC-2004,	integrated into UniProtKB/TrEMBL.			
DT	21-DEC-2004,	sequence version 1.			
DT	02-MAY-2006,	entry version 8.			
DE	Hypothetical protein DKFZp468N1810.				
CN	Name=DKFZp468N1810;				
OS	Pongo pygmaeus (Orangutan).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Haplorhini;				
OC	Catarrhini; Hominoidea; Pongo.				
OX	NCBI_TaxId=9600;				
RN	[1]				
RP	NUCLEOTIDE SEQUENCE.				
RC	TISSUE=Heart.				
RG	The German cDNA Consortium,				
RA	Ottensmeyer B., Obermaier B., Deutscherbauer S., Schall A.,				
RA	Mewes H.W., Weil B., Auld C., Ossinger A., Fobo G., Han M., Wiemann S.;				
RL	Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.				
CC	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms				
CC	Distributed under the Creative Commons Attribution-NoDerivs License				
CC					

DR EMBL; CR857928; CA90176.1; -; mRNA.
 DR GO; GO:0004252; F:serine-type endopeptidase activity; IEA.
 DR GO; GO:0006508; P:proteolysis; IEA.
 DR InterPro; IPR000859; CUB.
 DR InterPro; IPR006210; EGF.
 DR InterPro; IPR007442; EGF_3.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR013032; EGF_like_reg.
 DR InterPro; IPR009003; Pept_Ser_Cys.
 DR InterPro; IPR001254; Peptidase_S1_S6.
 DR InterPro; IPR001314; Peptidase_S1A.
 DR InterPro; IPR000436; Sush1_SCR_CCP.
 DR Pfam; PF00431; CUB; 1.
 DR Pfam; PF00008; EGF; 1.
 DR Pfam; PF00008; EGF; 2.
 DR Pfam; PF00084; Trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM00032; CCP; 2.
 DR SMART; SM00042; CUB; 1.
 DR SMART; SM00181; EGF; 2.
 DR SMART; SM00020; Tryp_Spc; 1.
 DR PROSITE; PS01180; CUB; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; 1.
 DR PROSITE; PS00026; EGF_3; 1.
 DR PROSITE; PS00923; SUSH1; 2.
 DR PROSITE; PS02040; TRYPSIN_DOM; 1.
 DR Hypothetical protein.
 KW Hypothetical protein.
 SQ SEQUENCE 720 AA; 80041 MW; 3F83E2DAD41F4117 CRC64;
 Query Match Best Local Similarity 98.8%; Score 3898; DB 2; Length 720;
 Matches 709; Conservative 98.5%; Pred. No. 1.3e-264;
 Mismatches 9; Indels 0; Gaps 0;

QY 1 MELGCMWTQGLTFLVQLLLISLPREYVINEACFGAEWNINCRECEYDQIECVCPGKRE 60
 DB 1 MELGCMWTQGLTFLVQLLLISLPREYVINEACFGAEWNINCRECEYDQIECVCPGKE 60
 QY 61 VVGTTICCRNEECSCLIHPGCTI PENCKSRNGSGTLDFFVYKGFYCAECRAGW 120
 DB 61 VVGTTICCRNEECSCLIHPGCTI PENCKSRNGSGTLDFFVYKGFYCAECRAGW 120
 QY 121 YGDCMRCGQVLRAPKQIILLESYPLNAHCMTIHAKEGFIQLRFVLSLEFMYCQYD 180
 DB 121 YGDCMRCGQVLRAPKQIILLESYPLNAHCMTIHAKEGFIQLRFVLSLEFMYCQYD 180
 QY 181 YVEVRDGDNRDQIIRKVCNERNPAPIQSIGSSLHVLPHSDGSKNPDGFHA1YEETACS 240
 DB 181 YVEVRDGDNRDQIIRKVCNERNPAPIQSIGSSLHVLPHSDGSKNPDGFHA1FEETACS 240
 QY 241 SSPCFHGTGVLDRAGSYKCACLAGYTGQRCENLLEENNCSDPGGPVNGYKITGGPGLI 300
 DB 241 SSPCFHGTGVLDRAGSYKCACLAGYTGQRCENLLEENNCSDPGGPVNGYKITGGPGLI 300
 QY 301 NGRHAKIGTVVSPFCNNSYVLSSGNEKRTCOQNGEMSGKOPICIRACREPKISDLVRRVL 360
 DB 301 NGRHAKIGTVVSPFCNNSYVLSSGNEKRTCOQNGEMSGKOPICIRACREPKISDLVRRVL 360
 QY 361 PMQVQSRBTPHQIYSAAFSKQIQAAPTKKPALPFGDLPMGYQLHTQLDYECISPFYR 420
 DB 361 PMQVQSRBTPHQIYSAAFSKQIQAAPTKKPALPFGDLPMGYQLHTQLDYECISPFYR 420
 QY 421 RLGSRRRTCLATGKMSGAPSCIPICGKIENITAPKTGGLAMPWQAAIYRRTSGVHDSL 480
 DB 421 RLGSRRRTCLATGKMSGAPSCIPICGKIENITAPKTGGLAMPWQAAIYRRTSGVHDSL 480
 QY 481 HKGAMFLVCSGALVNERTVVAAACVTDLGKVTMTKTADLKYVKGKFRDDDRDEKTIQS 540
 DB 481 HKGAMFLVCSGALVNERTVVAAACVTDLGKVTMTKTADLKYVKGKFRDDDRDEKTIQS 540
 QY 541 LQISAIILHPNYDPLLDADIAILKLDKARISTRVQPICLAASRDLSTSGESHITVAG 600
 DB 541 LQISAIILHPNYDPLLDADIAILKLDKARISTRVQPICLAASRDLSTSGESHITVAG 600

QY 601 MNVLADVRSGPKNLTLRSQSVSVDSLCEQHEHGGIPVSYTDNNFCA5WEPTAPSDI 660
 DB 601 MNVLADVRSGPKNLTLRSQSVSVDSLCEQHEHGGIPVSYTDNNFCA5QPTAPSDI 660
 QY 661 CTAETGGIAVSPFGASPEPRMHLGLVSWSDKTC5HRL5TAFTKVLPEPKMIERNMK 720
 DB 661 CTAETGGIAVSPFGASPEPRMHLGLVSWSDKTC5HRL5TAFTKVLPEPKMIERNMK 720

RESULT 7
 Q5E9P5 BOVIN PRELIMINARY; PRT; 720 AA.
 AC Q5E9P5;
 DT 15-MAR-2005, integrated into UniProtKB/TrEMBL.
 DT 15-MAR-2005, sequence version 1.
 DT 18-APR-2006, entry version 8.
 DE Regeneration associated muscle protease isoform b.
 GN Name=DKFP56H2123;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
 OC Pecora; Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Poolled.
 RX MEDLINE=21180013; PubMed=11282978; DOI=10.1101/gr.170101;
 RA Smith T.P.L., Grose W.M., Freking B.A., Roberts A.J., Stone R.T.,
 RA Caas E., Wray J.E., White J., Cho J., Fahrenkrug S.C., Bennett G.L.,
 RA Heaton M.P., Laegreid W.W., Rohrer G.A., Chikow-Mckown C.G.,
 RA Petrea G., Holt I., Karamycheva S., Liang F., Quackenbush J.,
 RA Keele J.W.,
 RT "Sequence evaluation of four pooled-tissue normalized bovine CDNA
 RT libraries and construction of a gene index for cattle."
 RL Genome Res. 11:626-630(2001).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Poolled;
 RA Hatnay G.P., Sonstegard T.S., Clawson M.L., Heaton M.P., Keele J.W.,
 RA Snelling W.M., Weidmann R.T., Smith T.P.L.,
 RT "Sequencing and analysis of Bos taurus full-length insert CDNA
 RT clones."
 RL Submitted (FE8-2005) to the EMBL/GenBank/DBJ databases.

CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 CC EMBL; BT020875; AAX08892.1; -; mRNA.
 DR UniGene; Bt.6021; -.
 DR MEROPS; S01.998; -.
 DR GO; GO:0008233; F:peptidase activity; IEA.
 DR GO; GO:0004252; F:serine-type endopeptidase activity; IEA.
 DR GO; GO:0006508; P:proteolysis; IEA.
 DR InterPro; IPR000859; CUB.
 DR InterPro; IPR006210; EGF.
 DR InterPro; IPR000742; EGF_3.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR013032; EGF_like_reg.
 DR InterPro; IPR009003; Pept_Ser_Cys.
 DR InterPro; IPR001254; Peptidase_S1_S6.
 DR InterPro; IPR001314; Peptidase_S1A.
 DR InterPro; IPR000436; Sush1_SCR_CCP.
 DR Pfam; PF00431; CUB; 1.
 DR Pfam; PF00008; EGF; 1.
 DR Pfam; PF00008; EGF; 2.
 DR Pfam; PF00084; Trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM00032; CCP; 2.
 DR SMART; SM00042; CUB; 1.
 DR SMART; SM00181; EGF; 2.
 DR SMART; SM00020; Tryp_Spc; 1.
 DR PROSITE; PS01180; CUB; 1.

DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; 1.
 DR PROSITE; PS00026; EGF_3; 1.
 DR PROSITE; PS00923; SUSH1; 2.
 DR PROSITE; PS00240; TRYPsin_DOM; 1.
 KM PROTEASE.
 SQ SEQUENCE 720 AA; 80057 MW; 69DA098FF95037E1 CRC64;
 Query Match 91.7%; Score 3616; DB 2; Length 720;
 Best Local Similarity 90.6%; Pred. No. 2.4e-263;
 Matches 652; Conservative 30; Mismatches 38; Indels 0; Gaps 0;
 QY 1 MEIGCTQTGLTLPQLLLISSLPREYTVINEACGAGMNMCECCEDYDIECVCPKRE 60
 1 MEIGMWPQLGLAFQLLLISSLPREYTVINEACGAGMNMCECCEDYDIECVCPKRE 60
 DB 1 MEIGMWPQLGLAFQLLLISSLPREYTVINEACGAGMNMCECCEDYDIECVCPKRE 60
 QY 61 VVGVTTPCCNNEECSCLIHQCTTFENCCKSRNGSGGTLDDFYVKGPFYCAECRAGW 120
 61 VVGVTTPCCNNEECSCLIHQCTTFENCCKSRNGSGGTLDDFYVKGPFYCAECRAGW 120
 DB 61 VVGVTTPCCNNEECSCLIHQCTTFENCCKSRNGSGGTLDDFYVKGPFYCAECRAGW 120
 QY 121 YGSDCMRCGQVLRAPKQGLLESYPLNAHCEMTTHAKPGFVIOLRPMVLSLEFDYMOYD 180
 121 YGSDCMRCGQVLRAPKQGLLESYPLNAHCEMTTHAKPGFVIOLRPMVLSLEFDYMOYD 180
 DB 121 YGSDCMRCGQVLRAPKQGLLESYPLNAHCEMTTHAKPGFVIOLRPMVLSLEFDYMOYD 180
 QY 181 YVEVRDGDNRDGOIIRKVCNENRPAPIQSISSILHVFHSDGSKNFDGFAIYEETACS 240
 181 YVEVRDGDNRDGOIIRKVCNENRPAPIQSISSILHVFHSDGSKNFDGFAIYEETACS 240
 DB 181 YVEVRDGDNRDGOIIRKVCNENRPAPIQSISSILHVFHSDGSKNFDGFAIYEETACS 240
 QY 241 SSGCFHDGTCVLDKASGYKACLAGYTGRCENILLEERNCSDPGPNVGYOKITGGPGLI 300
 241 SSGCFHDGTCVLDKASGYKACLAGYTGRCENILLEERNCSDPGPNVGYOKITGGPGLI 300
 DB 241 SSGCFHDGTCVLDKASGYKACLAGYTGRCENILLEERNCSDPGPNVGYOKITGGPGLI 300
 QY 301 NGHAKITGVTFPCNNSVYLSGNERKTCQONGEMSKOICICAKCEPKISDLVRRRL 360
 301 NGHAKITGVTFPCNNSVYLSGNERKTCQONGEMSKOICICAKCEPKISDLVRRRL 360
 DB 301 NGHAKITGVTFPCNNSVYLSGNERKTCQONGEMSKOICICAKCEPKISDLVRRRL 360
 QY 361 PMOVOSRETFPHOLYSNAFSGKQKQAPTKKPAIPFGDLPMGYOHLTOLQVECTISPFYR 420
 361 PMOVOSRETFPHOLYSNAFSGKQKQAPTKKPAIPFGDLPMGYOHLTOLQVECTISPFYR 420
 DB 361 PMOVOSRETFPHOLYSNAFSGKQKQAPTKKPAIPFGDLPMGYOHLTOLQVECTISPFYR 420
 QY 421 RLGSRRRTCLRTGKWSGRAPSCIPICGKINENTAPKTQGLRMPQAAIYRTSGVHDSL 480
 421 RLGSRRRTCLRTGKWSGRAPSCIPICGKINENTAPKTQGLRMPQAAIYRTSGVHDSL 480
 DB 421 RLGSRRRTCLRTGKWSGRAPSCIPICGKINENTAPKTQGLRMPQAAIYRTSGVHDSL 480
 QY 481 HKGAWFLVCSGALVNESTVVAACHCTDGLKTMITKADLKVVLGKRYRDPDDEKTIQS 540
 481 HKGAWFLVCSGALVNESTVVAACHCTDGLKTMITKADLKVVLGKRYRDPDDEKTIQS 540
 DB 481 HKGAWFLVCSGALVNESTVVAACHCTDGLKTMITKADLKVVLGKRYRDPDDEKTIQS 540
 QY 541 LQISATILHENVDPILLADIALIKLIDKARISTRVOPICLAASRLDSTFQESHITVAG 600
 541 LQISATILHENVDPILLADIALIKLIDKARISTRVOPICLAASRLDSTFQESHITVAG 600
 DB 541 LQISATILHENVDPILLADIALIKLIDKARISTRVOPICLAASRLDSTFQESHITVAG 600
 QY 601 WNTLADVRSPFGKNDTLRSQVSVVDSLCEQHEHGHIPVSYTDNMFCAWEPAPASDI 660
 601 WNTLADVRSPFGKNDTLRSQVSVVDSLCEQHEHGHIPVSYTDNMFCAWEPAPASDI 660
 DB 601 WNTLADVRSPFGKNDTLRSQVSVVDSLCEQHEHGHIPVSYTDNMFCAWEPAPASDI 660
 QY 661 CTAFETGGIAVSPFGRASEPFRWHLGLVSWSDTKTSRHLSTAFKTVLPFKMIERNMK 720
 661 CTAFETGGIAVSPFGRASEPFRWHLGLVSWSDTKTSRHLSTAFKTVLPFKMIERNMK 720
 DB 661 CTAFETGGIAVSPFGRASEPFRWHLGLVSWSDTKTSRHLSTAFKTVLPFKMIERNMK 720
 RESULT 8
 OBBU25_MOUSE PRELIMINARY; PRT; 720 AA.
 AC OBBU25;
 DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.
 DT 01-MAR-2003, sequence version 1.
 DT 18-APR-2006, entry version 27.
 DE 2 days neonate thymus thymic cells cDNA, RIKEN full-length enriched
 DE library, clone:843002G05 product:hypothetical EGF-like domain, CUB
 DE domain, Sushi domain / SCR repeat / CCP module and Serine proteases,
 DE tryptsin family domain containing protein, full insert sequence.
 GN Name:E430002G05Rik;

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=NOD; TISSUE=Thymus;
 RX MEDLINE=99219253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.,
 RT "High-efficiency full-length cDNA cloning."
 RL Methods Enzymol. 303:19-44(1999).
 [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=NOD; TISSUE=Thymus;
 RX PubMed=16141072; DOI=10.1126/science.1112014;
 RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
 Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
 Bajic V.B., Bremner S.E., Batalov S., Forrest A.R., Zavolan M.,
 Davis M.J., Wilm M., Zeng L.G., Aldrich J., Allen J.E.,
 Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
 Banerji M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
 Chiu K.P., Choudhary V., Christofels A., Clutterbuck D.R.,
 Crowe M.L., Dailly E., Dairymple B.P., de Bono B., Della Gatta G.,
 di Bernardo D., Down T., Engstrom P., Faggiolini M., Faulkner G.,
 Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
 Georgi-Jacob M., Gingeras T.R., Gojobori T., Green R.E.,
 Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
 Hill D., Hummelbeck L., Iacono M., Ieko K., Iwama A., Ishikawa T.,
 Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kello J., Kitamura H.,
 Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
 Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
 Liun S., McWilliam S., Madan Babu M., Madera P., Marchionni L.,
 Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
 Mottagui-Tabar S., Mulder N., Nakano N., Nakaguchi H., Ng P.,
 Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ochara O.,
 Okazaki Y., Orlando V., Pang K.C., Pavan M.J., Pavoni G.,
 Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
 Rost B., Ruan Y., Salzberg S.L., Sanderlin A., Schneider C.,
 Schombach C., Sekiguchi K., Sempke C.A., Sene S., Sessa L., Sheng Y.,
 Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
 Sperling S., Stupka E., Sugita K., Sultana R., Takenaka Y., Taki K.,
 Tamajima K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
 Ueda H.R., Van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
 Yamashita H., Zabolovskiy E., Zhu S., Zimmer A., Hide W., Bult C.,
 Gilmour S.M., Teasdale R.D., Liu E.T., Brusic V., Quakenbush J.,
 Wilmstedt C., Mettlic J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
 Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
 Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
 Kawashima T., Kojima M., Kondo S., Kono H., Nakano K., Niimura N.,
 Nishio T., Okada M., Plessey C., Shibata K., Shiraki T., Suzuki S.,
 Tagami M., Waki K., Watanabe A., Okamura-Oho Y., Suzuki H., Kawai J.,
 Hayashizaki Y.,
 "The transcriptional landscape of the mammalian genome."
 Science 309:1159-1163(2005).
 [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=NOD; TISSUE=Thymus;
 RX PubMed=16141073; DOI=10.1126/science.1112009;
 RA RIKEN Genome Exploration Research Group, and Genome Science Group
 RG (Genome Network Core Team) and the FANTOM Consortium;
 RT "Antisense Transcription in the Mammalian Transcriptome."
 RL Science 309:1564-1566(2005).
 [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=NOD; TISSUE=Thymus;
 RX MEDLINE=22354663; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 Nakai I., Osato N., Saito R., Suzuki H., Yamashita H., Kiyosawa H.,
 Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schombach C., Gojobori T.,
 Baldarelli R., Hill D.P., Bult C., Hume D.A., Schombach C., Gojobori T.,
 Schiraldi L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 Blake J.A., Brad D., Bruscia V., Chothia C., Corbani L.E., Cousins S.,

RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaesslerland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Gilmond S., Guticlon S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglot D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Paven W.J., Petrea G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Sempile C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavalan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs";
 RL Nature 420:563-573(2002).
 [5]
 NP NUCLEOTIDE SEQUENCE.
 RC STRAIN=ND; TISSUE=Thymus;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi U., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleishmann W., Gaesslerland T., Gissi C., King B., Kochwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
 RA Schirral L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Baran G.,
 RA Blake J., Botfield D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita K., Gariboldi M.,
 RA Gustinich S., Hill D., Hofmann M., Hume D.A., Kanliya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Marzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weltz C., Whitaker C., Wilming L.,
 RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohetsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection";
 RL Nature 409:685-690(2001).
 [6]
 NP NUCLEOTIDE SEQUENCE.
 RC STRAIN=ND; TISSUE=Thymus;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes";
 RL Genome Res. 10:1617-1630(2000).
 [7]
 NP NUCLEOTIDE SEQUENCE.
 RC STRAIN=ND; TISSUE=Thymus;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitanaka T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer";
 RL Genome Res. 10:1757-1771(2000).
 [8]
 NP NUCLEOTIDE SEQUENCE.
 RC STRAIN=ND; TISSUE=Thymus;

RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,
 RA Horii F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Konda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Osato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akai H., Tanaka Y., Tanaka T.,
 RA Tomaru A., Toyota T., Yasunishi A., Yamamatsu M., Hayashizaki Y.,
 RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NonDerivative license
 CC
 DR EMBL, AK088017, BAC40098.1; -- mRNA.
 DR HSSP, P00736, 1GPZ.
 DR MEROPS, S01.998; --
 DR Ensembl, ENSMUSG00000027188; Mus musculus.
 DR MGI, MGI:2445082; E430002G05Rik.
 DR GO, GO:0005615; C:extracellular space; RCA.
 DR GO, GO:0004263; F:chymotrypsin activity; RCA.
 DR GO, GO:0004295; F:trypsin activity; RCA.
 DR GO, GO:0006508; P:proteolysis; RCA.
 DR InterPro, IPR006089; CUB.
 DR InterPro, IPR006210; EGF.
 DR InterPro, IPR000742; EGF_3.
 DR InterPro, IPR006209; EGF_like.
 DR InterPro, IPR013032; EGF_like_reg.
 DR InterPro, IPR009003; Pept_Ser_Cys.
 DR InterPro, IPR001254; Peptidase_S1_56.
 DR InterPro, IPR001314; Peptidase_S1A.
 DR InterPro, IPR000436; Sushi_SCR_CCP.
 DR Pfam, PF00431; CUB; 1.
 DR Pfam, PF00084; EGF; 1.
 DR Pfam, PF00084; Sushi; 2.
 DR Pfam, PF00089; Trypsin; 1.
 DR PRINTS, PR00722; CHYMOTRPSIN.
 DR SMART, SM00042; CUB; 2.
 DR SMART, SM00042; CUB; 1.
 DR SMART, SM00181; EGF; 2.
 DR SMART, SM00020; Tryp_Spc; 1.
 DR PROSITE, PS01180; CUB; 1.
 Query Match 91.6%; Score 3612; DB 2; Length 720;
 Best Local Similarity 90.1%; Pred. No. 4.7e-263;
 Matches 649; Conservative 33; Mismatches 38; Indels 0; Gaps 0;
 Oy 1 MELGCTQTGLTFLQILLISLPREYVINEACPGAEWMINICRECEYDQIECVPGKRE 60
 Db 1 MELDRAGQLVFLQLILLISLPREYVINEACPGAEWMINICRECEYDQIECVPGKRE 60
 Oy 61 VGGTIPCCNENECDSLIHPGCTTFENCKSCRNSWGCTLDDFFVKGFPYCAECRAGW 120
 Db 61 VGGTIPCCNENECDSLIHPGCTTFENCKSCRNSWGCTLDDFFVKGFPYCAECRAGW 120
 Oy 121 YGGDCMCGGVLRASKQILLISLPYNAHCEWTHAKPGVILQRFNMLSLFEDYKQYD 180
 Db 121 YGGDCMCGGVLRASKQILLISLPYNAHCEWTHAKPGVILQRFNMLSLFEDYKQYD 180
 Oy 181 YVEVRDDNDGQILIRKVCNENRPAPIQSGSSLHVLFHSDGSKNPFDAIYEETPACS 240
 Db 181 YVEVRDDNDSPILIRKVCNENRPAPIRSGSSLHVLFHSDGSKNPFDAIYEETPACS 240
 Oy 241 SSPCFHDTGVLDPKAGSKYKACLAGTGORCEMLLEBRNSDPGCPVNGYQKITGGPGLI 300
 Db 241 SSPCFHDTGVLDPKAGSKYKACLAGTGORCEMLLEBRNSDPGCPVNGYQKITGGPGLI 300
 Oy 301 NGRPAKIGTVVSPFCNNSYLSGNEKRTCOONGEMSKOPICIKACEPKISDLVRRRYL 360
 Db 301 NEHRVKGITGVVSPFCNNSYLSGNEKRTCOONGEMSKOPICIKACEPKISDLVRRRYL 360

QY	36	PMVOQSEETPLHOLYLSAASKCOLGSAPEKPKALPEFGLPMGYOHMLHOLYECISPEFYR	420
Db	361	SMVOQSEETPLHOLYLSAASKCOLGSAPEKPKALPEFGLPMGYOHMLHOLYECISPEFYR	4200
QY	421	RLGSSRRCTCLRTGKMSGRAPCSPICGKIENITAPRTGGLRMPOMAIYRRSTGVHDSGL	480
Db	421	RLGSSRRCTCLRTGKMSGRAPCSPICGKIENITAPRTGGLRMPOMAIYRRSTGVHDSGL	4800
QY	481	HKGAMFLVCSGALVNERIVVAACHCTYDGLKTYMTIKTADLKVYLAKGYRDDRDEKTIQS	540
Db	481	HKGAMFLVCSGALVNERIVVAACHCTYDGLKTYMTIKTADLKVYLAKGYRDDRDEKTIQS	5400
QY	541	LOISATIIHNNYDPIILLDDADIALIKLIDKARISTEYVOPICLAASRDISTSPQESHIVAG	6000
Db	541	LOISATIIHNNYDPIILLDDADIALIKLIDKARISTEYVOPICLAASRDISTSPQESHIVAG	6000
QY	601	WNYLADVRSFGFNQDPLRSGVSVVSDSLCEEQHEDHGIPIVSVDYNNFCASMEPTAPSDI	6600
Db	601	WNYLADVRSFGFNQDPLRSGVSVVSDSLCEEQHEDHGIPIVSVDYNNFCASMEPTAPSDI	6600
QY	661	CTAETGGIAALSPFGRAPEPRMHLVGLVMSYDXTKCSNGSLSTARTKVLPEKDWIERNMK	7200
Db	661	CTAETGGIAALSPFGRAPEPRMHLVGLVMSYDXTKCSNGSLSTARTKVLPEKDWIERNMK	7200
RESULT 9			
QK82B8_MOUSE			
ID	QK82B8_MOUSE	PREDIMINARY; PRT; 720 AA.	
AC	QK82B8_MOUSE		
DT	01-OCT-2002,	integrated into UniProtKB/TrEMBL.	
DT	01-OCT-2002,	sequence version 1.	
DT	18-APR-2006,	entry version 25.	
DE	Regeneration associated muscle protease.		
GN	Name=E43002G050Rik.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;		
OC	Muridea; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	NUCLEOTIDE SEQUENCE.		
RC	STRAIN=CECH II; TISSUE=Mammary tumor metastasized to lung. Tumor		
RC	arose spontaneously;		
RX	MEDLINE=22388251; PubMed=12477932; DOI=10.1073/pnas.242603899;		
RA	Strausberg R.L., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,		
RA	Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,		
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schefer C.F., Bhat N.K.,		
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,		
RA	DiCicco L., Marusina K., Farmer A., Rubin G.M., Hong L.,		
RA	Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,		
RA	Brownstein M.J., Udell T.B., Tohilyuki S., Carninci P., Prange C.,		
RA	Basa S.S., Loguella N.A., Peters G.J., Abramson R.D., Mullany S.J.,		
RA	Rosa S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,		
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,		
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,		
RA	Faley J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,		
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,		
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,		
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,		
RA	Butterfield Y.S.N., Krzywicki M.I., Skalska U., Smalins D.E.,		
RA	Scherer A., Schein J.E., Jones S.J.M., Marra M.A.,		
RT	"Generation and initial analysis of more than 15,000 full-length human		
RT	and mouse cDNA sequences."		
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).		
RN	[2]		
RP	NUCLEOTIDE SEQUENCE.		
RC	STRAIN=CECH II; TISSUE=Mammary tumor metastasized to lung. Tumor		
RC	arose spontaneously;		
RA	Strausberg R.		
RL	Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.		
RN	[3]		
RP	NUCLEOTIDE SEQUENCE.		
RC	STRAIN=CECH II; TISSUE=Mammary tumor metastasized to lung. Tumor		

Query Match	91.6%	Score 3612	DB 2	Length 720
Best local Similarity	90.1%	Pred. No. 4,7e-263		
Matches 649	Conservative 33	Mismatches 38	Indels	Gaps 0
DB	1	MELGCMTDLGTLFLOLLISSLPRYTYINACPGAEANNIMRECEYDQICVCPGKKE	60	
DB	1	MELDRMAQGLVFLQDLILSIIPRYTYINACPAEANNIMRECEYDQIECLCPGKKE	60	
DB	61	VVGYYTIPCCRNMBENBCDCLIHPCGTIFENCKSCRNWSGGLTDFFYVGFYCAECRAG	120	
DB	61	VVGYYTIPCCRNMBENBCDCLIHPCGTIFENCKSCRNWSGGLTDFFYVGFYCAECRAG	120	
DB	121	YGGDCMRGGOYLRAKQGLLESTYLANACETTHAKRGFVQLARFVMSLEFDYVCOYD	180	
DB	121	YGGDCMRGGOYLRAKQGLLESTYLANACETTHAKRGFVQLARFVMSLEFDYVCOYD	180	
DB	181	YVEVADGNGNRGOGLIKRIVCGNERPAPISIGSSLHYLFFPSDGSKNPFDGHAHYEETIACS	240	
DB	181	YVEVADGNGNSPIIKRFECGNERRAPISTGSSLHYLFFPSDGSKNPFDGHAHYEETIACS	240	
DB	241	SSPCFHDGTCVLDKASGYKACACLAGYTGQRCENTLLEERNCSDPGPGVANGYQKITGGPGLI	300	
DB	241	SSPCFHDGTCVLDLTGGSFKACACLAGYTGQRCENTLLEERNCSDLGGPVANGYKKITTEPGLI	300	
DB	301	NGRAHAKIGTVVSFFCNNSYVLSGNEKRTCCQNGEWSKQPCITAKCREPKISDLYARRVYL	360	
DB	301	NERHAKIGTVVSFFCNNGSYVLSGNEKRTCCQNGEWSKQPCVCMKACREPKISDLYARRVYL	360	

DR PROSITE; PS50923; SUSH1; 5.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW SIGNAL.
FT SIGNAL 1 25 Potential.
FT CHAIN 26 1019 factor C.
SQ SEQUENCE 1019 AA; 112249 MW; B8E51730AE595993 CRC64;

Query Match 17.2%; Score 678; DB 2; Length 1019;
Best Local Similarity 25.6%; Pred. No. 8.5e-42;
Matches 223; Conservative 117; Mismatches 308; Indels 222; Gaps 37;

QY 34 PGAEWNIM---CRECEYDQIE---CVCPKREVGVITPCCRNEENECDSLHPGCT 86
DB 184 PNGQMSFPKCKTRECCKAVSSPEHGKVTAAISGNMIEGATL-----PHYL 233
QY 87 IFENCKSCR-NGSWGTL----- 103
DB 234 IGGETTLTCCGNGQSGQIPQCKLVFCPDLDPVNHAEHGVKIGVEKYGQFPQGTETVYT 293
QY 104 --DDFYKGFYCAECR--AGHYGG--DCMR-----CGQVLR--APKG 137
DB 294 CSGNYFLMGFNTLKCNDLDSGSGQPSQVADREVDCSKAVDFLDVGEPEVRIHCPAG 353
QY 138 QILLES-----YPLNACEWTIHA---KPGFVI-----Q 163
DB 354 CSLTAGTVMGTATYHELSVCRATIHAGKLPNSGAVHVNVNGPYSDPLGSDLNGIKSEE 413
QY 164 LRFVWLSLEFDYM-----CQYDYVERD-----GDNRDQIIRKVCN--ERRAP 206
DB 414 LKSLARSPFRFDYVSSTAGRSGCPDGFVEVENCVVYTSKQRAWERAQGVCTNMAARLAV 473
QY 207 IQS--IGSSLHLVLFHSDG--SKNFDGF-----AIYEETIACSSSPCF 245
DB 474 LDKDVIPSSLTLEALRGKLTITWIGLRDLAEKPFWEMLDRSNVVLNDMLTFWASGEPG 533
QY 246 HDGTCV--LDRKAGS-----YKACLAGYTGQRCENLLEERN---CSDPGQPVNGYOKITGPR 297
DB 534 NETWCYVLDIRDQLOQPYWKYSQCFQPSFACMDLSDRNKAKCDDPSLENGHATLHGQS 593
QY 298 GLINGRAHAKIGTVVFFCNSVYLSGNEKRTQONGEMWCKOPICIK--ACREPKISDLV 355
DB 594 --IDGFYA--GSSIRYSCEVLHLSGETETVCTTNGTWSAPKPRCIKIVTCQNPVPVSYG 649
QY 356 RRRVLPMQVQSRRTPLQLYSAASFQKQLQ---SAPTKKPLPFGD-----LP 400
DB 650 SVEIKP--PSRTNISIRVGSPLRLPLPLARAAKPPKPRSSQPSQSTVDLASKVYLP 706
QY 401 MGYOHLHTOLQYECISPPYRLGSSRRTCARTGKMSGRAPSCIPICGKIENITAP----- 455
DB 707 EGHYRVSGRAIYTCESRYELLGSGQRCDNSGNMNSGRASCIPVCGRSDSPRSRPFITWG 766
QY 456 -KTQGLRMPQAAIYRTSGVHDSLHKGAWFLVCSGALVNERTVVAHCVTDLGKVTM 514
DB 767 NSTEIGMPWQAGISRWLA-----DHNMWFIQCGSLNEKMWLVTAHCVTYSATAEI 819
QY 515 IKTADLKVYLKGFYRDDDDREKTIQSLQISAIILHPNYDPIILLDADIAILKLLDKARIST 574
DB 820 IDPQFKIYLGKYYRDDSDDDYQVREALIHHVNPDPGNLNFIDIALIQLKTPVTLTT 879
QY 575 RVQPICLAASRDLSFQESH-----TVAGMVLADVRSPGFNDTLRSGVSVYDSL 628
DB 880 RVQPICLPT--DITL---REHLKEGTLAVVTGK---LNENNTYSEMTQOAVLPVAAS 930
QY 629 LCEQHEHDHGIPIVSVTDNMFCAWEPFAPSIDTAETGIAVSPFGRASPEPRWHLMLGL 688
DB 931 TCEEGYKPADLPLVYTEMFCAGYK--KGRYDACSGDSGG--PIVPAADSRTERRHVLGCI 987
QY 689 VSAASYDKTCSH--RLSTATKVLPRFDWIER 717
DB 988 VSWGSPSGCGKANQYGGFTKVNVLFWLWIRQ 1017

Search completed: April 4, 2007, 22:04:11
Job time : 399 secs

GenCore version 6.2
Copyright (c) 1993 - 2007 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: April 4, 2007, 21:55:04 ; Search time 30 Seconds
(without alignments)
2100.735 Million cell updates/sec

Title: US-10-063-546-38

Perfect score: 3945

Sequence: 1 MELGCTGTGLRFLQLLLS.....LSRAFTKVLPEKDMIRNMK 720

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database :

1: Issued Patents AA:*

2: /EMC_Celerra_SIDS3/prodata/2/iaa/5 COMB.pep:*

3: /EMC_Celerra_SIDS3/prodata/2/iaa/6 COMB.pep:*

4: /EMC_Celerra_SIDS3/prodata/2/iaa/7 COMB.pep:*

5: /EMC_Celerra_SIDS3/prodata/2/iaa/8 COMB.pep:*

6: /EMC_Celerra_SIDS3/prodata/2/iaa/9 COMB.pep:*

7: /EMC_Celerra_SIDS3/prodata/2/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3945	100.0	720	2	US-09-991-181-231
2	3945	100.0	720	2	US-09-990-444-231
3	3945	100.0	720	2	US-09-997-333-231
4	3945	100.0	720	2	US-09-992-598-231
5	3945	100.0	720	2	US-09-989-735-231
6	3945	100.0	720	3	US-09-989-726-231
7	3945	100.0	720	3	US-09-997-514-231
8	3945	100.0	720	3	US-09-989-728-231
9	3945	100.0	720	3	US-09-987-449-231
10	3945	100.0	720	3	US-09-987-553-231
11	3945	100.0	720	3	US-09-989-293A-231
12	2946.5	74.7	570	2	US-10-067-422-9
13	672	17.0	1019	1	US-10-183-992-4
14	665	16.9	1019	1	US-08-296-014A-4
15	665	16.9	1019	1	US-08-596-405-4
16	665	16.9	1019	1	US-08-877-620-4
17	665	16.9	1019	1	US-09-287-568-4
18	665	16.9	1019	2	US-09-626-795-4
19	665	16.9	1019	2	US-10-183-992-8
20	665	16.9	1083	1	US-08-296-014A-2
21	665	16.9	1083	1	US-08-596-405-2
22	665	16.9	1083	1	US-08-877-620-2
23	665	16.9	1083	2	US-09-287-568-2
24	665	16.9	1083	2	US-09-626-795-2
25	665	16.9	1083	2	US-10-183-992-6
26	482	12.2	699	2	US-09-949-016-6138

27	475	12.0	717	2	US-09-949-016-11182	Sequence 11182, A
28	469.5	11.9	679	2	US-09-874-198-6	Sequence 6, App1
29	403.5	10.2	708	2	US-09-874-198-7	Sequence 7, App1
30	403.5	10.2	705	2	US-09-949-002-326	Sequence 326, App
31	401.5	10.2	686	2	US-09-874-198-2	Sequence 2, App1
32	399.5	10.1	691	2	US-09-949-016-7775	Sequence 7775, Ap
33	334	8.5	673	2	US-09-874-198-8	Sequence 8, App1
34	332	8.4	855	2	US-10-037-417-132	Sequence 132, App
35	328	8.3	855	2	US-09-410-362-2	Sequence 2, App1
36	327	8.3	855	1	US-09-027-337-2	Sequence 2, App1
37	327	8.3	855	2	US-09-644-600-2	Sequence 2, App1
38	327	8.3	855	2	US-09-654-600A-2	Sequence 2, App1
39	327	8.3	855	3	US-09-421-213-2	Sequence 2, App1
40	321	8.1	460	7	5270178-16	Patent No. 5270178
41	317.5	8.0	798	1	US-08-200-900A-2	Sequence 2, App1
42	317.5	8.0	798	2	US-08-794-042-2	Sequence 2, App1
43	317.5	8.0	798	5	PCT-US94-00616-2	Sequence 2, App1
44	312	7.9	419	2	US-10-168-407-5	Sequence 5, App1
45	311.5	7.9	461	7	5460953-3	Patent No. 5460953
46	311	7.9	419	2	US-10-168-407-3	Sequence 3, App1
47	311	7.9	419	2	US-10-168-407-6	Sequence 6, App1
48	310.5	7.9	409	2	US-09-665-872-2	Sequence 2, App1
49	310.5	7.9	409	2	US-09-667-570A-2	Sequence 2, App1
50	310.5	7.9	410	2	US-09-665-872-1	Sequence 1, App1
51	310.5	7.9	419	1	US-09-667-570A-1	Sequence 1, App1
52	310.5	7.9	419	1	US-08-295-411-1	Sequence 1, App1
53	310.5	7.9	419	1	US-08-955-471-1	Sequence 1, App1
54	310.5	7.9	419	2	US-09-667-570A-3	Sequence 3, App1
55	310.5	7.9	419	2	US-10-182-263-1	Sequence 1, App1
56	310.5	7.9	419	2	US-10-168-407-1	Sequence 1, App1
57	310.5	7.9	419	2	US-09-997-623-4	Sequence 4, App1
58	310.5	7.9	419	2	US-09-719-911-3	Sequence 3, App1
59	310.5	7.9	419	2	US-09-719-911-3	Sequence 3, App1
60	310.5	7.9	419	5	PCT-US92-10242-1	Sequence 2, App1
61	310.5	7.9	460	1	US-08-756-506-2	Sequence 2, App1
62	310.5	7.9	460	1	US-08-756-506-4	Sequence 4, App1
63	310.5	7.9	461	2	US-10-182-263-2	Sequence 2, App1
64	310.5	7.9	461	2	US-09-054-272-32	Sequence 32, App1
65	310.5	7.9	461	2	US-09-949-016-5921	Sequence 5921, Ap
66	310.5	7.9	461	2	US-10-168-407-2	Sequence 2, App1
67	310.5	7.9	461	2	US-09-997-623-2	Sequence 2, App1
68	310.5	7.9	461	2	US-09-719-911-2	Sequence 2, App1
69	310.5	7.9	461	7	5225537-2	Patent No. 5225537
70	310.5	7.9	485	2	US-09-949-016-10882	Sequence 10882, A
71	310	7.9	419	2	US-10-182-263-6	Sequence 6, App1
72	310	7.9	419	2	US-10-168-407-4	Sequence 4, App1
73	309.5	7.8	419	2	US-09-719-911-4	Sequence 4, App1
74	309.5	7.8	419	2	US-09-719-911-5	Sequence 5, App1
75	309	7.8	419	2	US-10-182-263-3	Sequence 3, App1
76	309	7.8	419	2	US-10-182-263-5	Sequence 5, App1
77	309	7.8	419	2	US-10-182-263-5	Sequence 5, App1
78	308	7.8	419	2	US-10-182-263-4	Sequence 4, App1
79	307	7.8	460	7	5270178-15	Patent No. 5270178
80	305	7.7	460	7	5270178-13	Patent No. 5270178
81	305	7.7	460	7	5270178-14	Patent No. 5270178
82	302.5	7.7	461	7	5270178-17	Patent No. 5270178
83	302.5	7.7	461	7	5270178-18	Patent No. 5270178
84	298	7.6	337	2	US-10-104-047-3904	Sequence 13904, Ap
85	296	7.6	230	2	US-10-037-417-135	Sequence 135, App
86	288.5	7.3	802	2	US-09-999-833A-169	Sequence 169, App
87	288.5	7.3	802	2	US-10-020-445A-169	Sequence 169, App
88	288.5	7.3	802	2	US-09-978-189-169	Sequence 169, App
89	288.5	7.3	802	2	US-10-017-085A-169	Sequence 169, App
90	288.5	7.3	802	3	US-10-145-129A-169	Sequence 169, App
91	288.5	7.3	802	3	US-10-013-929A-169	Sequence 169, App
92	288.5	7.3	802	3	US-10-013-917A-169	Sequence 169, App
93	288.5	7.3	902	2	US-09-644-600-10	Sequence 10, App
94	288.5	7.3	902	2	US-09-654-600A-10	Sequence 10, App
95	288.5	7.3	902	3	US-09-421-213-10	Sequence 10, App
96	287.5	7.3	356	2	US-09-054-272-18	Sequence 18, App
97	284.5	7.2	254	2	US-09-856-319B-2	Sequence 2, App1
98	283.5	7.2	587	2	US-09-949-016-11501	Sequence 11501, A
99	282	7.1	527	7	5520913-1	Patent No. 5520913

100	281	7.1	487	1	US-08-469-486-53	Sequence 53, Appl	173	271.5	6.9	244	3	US-09-936-271C-84	Sequence 84, Appl
101	281	7.1	487	1	US-08-469-558-53	Sequence 53, Appl	174	271.5	6.9	335	2	US-09-949-016-773	Sequence 773, Ap
102	281	7.1	488	2	US-09-367-777-44	Sequence 44, Appl	175	270.5	6.9	415	1	US-08-295-411-2	Sequence 2, Appl
103	281	7.1	488	2	US-09-367-791A-27	Sequence 27, Appl	176	270.5	6.9	415	1	US-08-955-471-2	Sequence 2, Appl
104	281	7.1	488	2	US-10-348-504-44	Sequence 44, Appl	177	270.5	6.9	415	1	PCT-US92-10242-2	Sequence 2, Appl
105	281	7.1	488	2	US-09-632-722-2	Sequence 2, Appl	178	269.5	6.8	239	3	US-09-936-771C-71	Sequence 71, Appl
106	281	7.1	492	1	US-08-469-486-2	Sequence 2, Appl	179	269	6.8	633	2	US-10-099-122-113	Sequence 113, App
107	281	7.1	492	1	US-08-469-658-2	Sequence 2, Appl	180	269	6.8	643	2	US-10-044-564-113	Sequence 113, App
108	280.5	7.1	267	2	US-09-949-016-5575	Sequence 9575, Ap	181	268.5	6.8	406	1	US-08-293-778-24	Sequence 24, Appl
109	280	7.1	527	1	US-07-609-5108-16	Sequence 16, Appl	182	264.5	6.7	445	1	US-08-073-531B-1	Sequence 1, Appl
110	280	7.1	527	1	US-08-811-949-39	Sequence 39, Appl	183	264.5	6.7	415	1	US-08-766-288-1	Sequence 1, Appl
111	280	7.1	527	2	US-09-600-985-1	Sequence 1, Appl	184	263	6.7	431	2	US-09-101-272G-1	Sequence 1, Appl
112	280	7.1	527	2	US-09-612-314A-51	Sequence 51, Appl	185	263	6.7	431	2	US-09-949-002-345	Sequence 345, App
113	280	7.1	527	2	US-10-360-101-203	Sequence 203, App	186	263	6.7	417	7	5188829-1	Sequence 415, App
114	280	7.1	527	2	US-10-705-633-1	Sequence 1, Appl	187	263	6.7	437	2	US-09-949-002-415	Sequence 2, Appl
115	280	7.1	527	5	PCT-US91-01025A-19	Sequence 19, Appl	188	262.5	6.7	441	2	US-08-742-877-2	Sequence 21, Appl
116	280	7.1	527	5	PCT-US91-01025A-2	Sequence 2, Appl	189	262.5	6.7	441	2	US-09-053-871A-21	Sequence 21, Appl
117	280	7.1	527	5	5185259-8	Patent No. 5185259	190	262.5	6.7	461	2	US-10-133-907-5	Sequence 5, Appl
118	280	7.1	562	1	US-08-811-949-43	Sequence 43, Appl	191	262.5	6.7	461	7	5521070-2	Sequence 1123, A
119	280	7.1	562	1	US-08-560-098A-50	Sequence 50, Appl	192	262.5	6.7	480	2	US-09-949-016-11123	Sequence 2, Appl
120	280	7.1	562	1	US-08-883-795A-38	Sequence 38, Appl	193	262.5	6.7	1042	2	US-09-959-192-2	Sequence 2, Appl
121	280	7.1	562	2	US-09-703-695A-4	Sequence 4, Appl	194	261.5	6.6	415	2	US-09-118-748-2	Sequence 2, Appl
122	280	7.1	562	2	US-10-443-701-4	Sequence 4, Appl	195	260.5	6.6	437	1	US-08-487-037-2	Sequence 2, Appl
123	280	7.1	562	7	5185259-3	Patent No. 5185259	196	260	6.6	437	1	US-08-560-098A-51	Sequence 51, Appl
124	280	7.1	562	7	5200340-2	Patent No. 5200340	197	258.5	6.6	411	1	US-08-087-163-1	Sequence 1, Appl
125	279	7.1	562	7	5344773-2	Patent No. 5344773	198	258.5	6.6	411	1	US-08-286-748B-18	Sequence 18, Appl
126	279	7.1	527	2	US-09-600-985-2	Sequence 2, Appl	199	258.5	6.6	411	1	US-08-153-799-18	Sequence 18, Appl
127	279	7.1	527	2	US-10-705-633-2	Sequence 2, Appl	200	258.5	6.6	411	2	US-09-181-816-1	Sequence 1, Appl
128	279	7.1	932	2	US-10-363-937-6	Sequence 6, Appl	201	258.5	6.6	411	2	US-09-880-503-3	Sequence 3, Appl
129	278.5	7.1	466	1	US-07-882-202A-4	Sequence 4, Appl	202	257.5	6.5	410	7	5219569-2	Sequence 136, App
130	278.5	7.1	466	1	US-08-021-615A-4	Sequence 4, Appl	203	257	6.5	217	2	US-10-037-417-136	Sequence 4, Appl
131	278.5	7.1	466	1	US-08-321-777-4	Sequence 4, Appl	204	256.5	6.5	264	2	US-09-856-119B-4	Sequence 2, Appl
132	278.5	7.1	466	2	US-09-009-217-14	Sequence 14, Appl	205	256.5	6.5	411	2	US-09-403-736-2	Sequence 2, Appl
133	278.5	7.1	466	2	US-09-009-656-14	Sequence 14, Appl	206	256.5	6.5	410	1	US-07-942-157A-3	Sequence 3, Appl
134	278.5	7.1	466	5	PCT-US93-04493-4	Sequence 4, Appl	207	255.5	6.5	244	2	US-09-618-359-11	Sequence 11, Appl
135	278.5	7.1	483	2	US-09-949-016-9523	Sequence 9523, Ap	208	254.5	6.5	437	1	US-08-487-037-3	Sequence 3, Appl
136	278	7.0	448	5	PCT-US92-10068-1	Sequence 1, Appl	209	254	6.4	261	7	5270178-21	Patent No. 5270178
137	278	7.0	496	2	US-09-949-016-9524	Sequence 9524, Ap	210	251	6.4	261	7	5270178-5	Patent No. 5270178
138	276.5	7.0	655	1	US-08-448-937A-12	Sequence 12, Appl	211	250.5	6.3	229	1	US-08-557-146-13	Sequence 13, Appl
139	276.5	7.0	448	1	US-08-295-411-3	Sequence 3, Appl	212	250.5	6.3	229	1	US-09-154-344-13	Sequence 13, Appl
140	276	7.0	448	1	US-08-955-471-3	Sequence 3, Appl	213	250.5	6.3	411	1	US-08-560-098A-48	Sequence 48, Appl
141	276	7.0	448	5	PCT-US92-10242-3	Sequence 3, Appl	214	249.5	6.3	966	2	US-09-880-503-6	Sequence 6, Appl
142	276	7.0	527	2	US-09-600-985-3	Sequence 3, Appl	215	249.5	6.3	251	2	US-09-285-185C-19	Sequence 19, Appl
143	276	7.0	527	2	US-10-705-633-3	Sequence 3, Appl	216	249	6.3	251	2	US-08-944-483-47	Sequence 47, Appl
144	276	7.0	405	2	US-10-360-101-225	Sequence 225, App	217	248.5	6.3	250	2	US-08-944-483-51	Sequence 51, Appl
145	275.5	7.0	406	1	US-08-295-411-5	Sequence 5, Appl	218	248.5	6.3	261	7	5270178-19	Patent No. 5270178
146	275.5	7.0	406	1	US-08-955-471-5	Sequence 5, Appl	219	248.5	6.3	261	7	5270178-20	Patent No. 5270178
147	275.5	7.0	406	2	US-09-782-587B-1	Sequence 1, Appl	220	248.5	6.3	262	1	US-07-720-189-1	Sequence 1, Appl
148	275.5	7.0	406	2	US-09-782-587B-3	Sequence 3, Appl	221	248	6.3	230	2	US-08-944-483-62	Sequence 62, Appl
149	275.5	7.0	406	2	US-09-969-357B-3	Sequence 3, Appl	222	248	6.3	230	3	US-09-410-162F-8	Sequence 8, Appl
150	275.5	7.0	406	2	US-09-969-357B-1	Sequence 1, Appl	223	248	6.3	230	3	US-09-410-162F-40	Sequence 40, Appl
151	275.5	7.0	406	2	US-10-669-537-1	Sequence 1, Appl	224	248	6.3	231	1	US-09-027-337-6	Sequence 6, Appl
152	275.5	7.0	406	2	US-10-281-727-1	Sequence 1, Appl	225	248	6.3	231	2	US-09-644-600-6	Sequence 6, Appl
153	275.5	7.0	406	5	PCT-US92-10242-5	Sequence 5, Appl	226	248	6.3	231	2	US-09-654-600A-6	Sequence 6, Appl
154	275.5	7.0	444	1	US-08-475-845-2	Sequence 2, Appl	227	248	6.3	231	3	US-09-421-213-6	Sequence 6, Appl
155	275.5	7.0	444	1	US-08-327-690-2	Sequence 2, Appl	228	248	6.3	638	2	US-10-099-122-111	Sequence 111, App
156	275.5	7.0	444	1	US-08-660-289-2	Sequence 2, Appl	229	247	6.3	638	2	US-10-044-564-111	Sequence 111, App
157	275.5	7.0	444	1	US-08-537-807-2	Sequence 2, Appl	230	247	6.3	638	2	US-10-099-122-30	Sequence 30, Appl
158	275.5	7.0	444	1	US-08-871-003-2	Sequence 2, Appl	231	247	6.3	638	2	US-10-044-564-30	Sequence 30, Appl
159	275.5	7.0	444	1	US-08-464-233-2	Sequence 2, Appl	232	247	6.3	764	1	US-08-177-109A-2	Sequence 2, Appl
160	275.5	7.0	444	2	US-09-189-607-2	Sequence 2, Appl	233	247	6.3	764	1	US-08-687-706-2	Sequence 2, Appl
161	275.5	7.0	444	2	US-09-378-907-2	Sequence 2, Appl	234	247	6.3	764	2	US-09-949-002-325	Sequence 325, App
162	275.5	7.0	444	5	PCT-US94-05779-2	Sequence 2, Appl	235	247	6.3	798	2	US-09-949-016-11021	Sequence 11021, A
163	275.5	7.0	461	2	US-09-949-016-8839	Sequence 8839, App	236	247	6.3	798	2	US-09-949-002-544	Sequence 544, App
164	275	7.0	562	7	5244676-5	Patent No. 5244676	237	247	6.3	986	2	US-09-949-016-6690	Sequence 6690, App
165	275	7.0	562	7	5244676-5	Patent No. 5244676	238	246.5	6.2	259	2	US-08-944-483-52	Sequence 2, Appl
166	273	6.9	560	2	US-09-949-016-6458	Sequence 6458, App	239	246.5	6.2	376	2	US-08-338-168-2	Sequence 10, Appl
167	273	6.9	560	2	US-09-912-559-3	Sequence 3, Appl	240	246.5	6.2	376	2	US-08-558-269-10	Sequence 10, Appl
168	273	6.9	560	2	US-09-912-559-4	Sequence 4, Appl	241	246.5	6.2	376	2	US-09-410-882-10	Sequence 10, Appl
169	272	6.9	488	1	US-08-487-037-1	Sequence 1, Appl	242	246.5	6.2	579	1	US-08-235-411-4	Sequence 4, Appl
170	271.5	6.9	488	1	US-09-856-050-15	Sequence 15, Appl	243	246.5	6.2	579	1	US-08-955-471-4	Sequence 4, Appl
171	271.5	6.9	223	3	US-08-361-395-1	Sequence 1, Appl	244	246.5	6.2	579	2	US-09-117-708-14	Sequence 14, Appl
172	271.5	6.9	244	1	US-08-361-395-1	Sequence 1, Appl	245	246.5	6.2	579	5	PCT-US92-10242-4	Sequence 4, Appl

246	246.5	6.2	615	1	US-07-998-972A-3	Sequence 3, Appl1	319	236.5	6.0	416	2	US-10-099-323-138	Sequence 138, App
247	246.5	6.2	615	1	US-08-463-953-3	Sequence 3, Appl1	320	236.5	6.0	416	2	US-10-044-564-138	Sequence 138, App
248	246.5	6.2	615	1	US-08-462-261-3	Sequence 3, Appl1	321	236.5	6.0	416	2	US-08-811-949-63	Sequence 63, Appl
249	246.5	6.2	615	5	PCT-US92-11357-3	Sequence 3, Appl1	322	236.5	6.0	871	2	US-09-245-041-19	Sequence 19, Appl
250	246.5	6.2	622	2	US-08-952-967-8	Sequence 42, Appl1	323	236.5	6.0	871	2	US-09-358-055B-19	Sequence 19, Appl
251	246.5	6.2	622	2	US-09-054-272-42	Sequence 42, Appl1	324	236.5	6.0	871	2	US-09-893-238-19	Sequence 19, Appl
252	246	6.2	812	2	US-08-991-761A-7	Sequence 7, Appl1	325	236.5	6.0	1013	1	US-08-866-600-8	Sequence 3, Appl1
253	245.5	6.2	638	2	US-10-099-322-112	Sequence 112, App	326	236.5	6.0	1013	1	US-09-021-287-3	Sequence 3, Appl1
254	245.5	6.2	638	2	US-10-044-564-112	Sequence 112, App	327	236.5	6.0	1013	2	US-09-240-473-3	Sequence 3, Appl1
255	245	6.2	228	1	US-08-278-091-10	Sequence 10, Appl	328	236.5	6.0	1350	2	US-09-245-041-17	Sequence 17, Appl
256	245	6.2	228	1	US-08-483-859-10	Sequence 10, Appl	329	236.5	6.0	1350	2	US-09-358-055B-17	Sequence 17, Appl
257	245	6.2	228	1	US-08-472-173-10	Sequence 10, Appl	330	236.5	6.0	1350	2	US-09-893-238-17	Sequence 17, Appl
258	245	6.2	228	1	US-08-487-167-10	Sequence 10, Appl	331	236	6.0	355	1	US-08-811-949-53	Sequence 53, Appl
259	245	6.2	228	1	US-08-482-816-10	Sequence 10, Appl	332	236	6.0	355	1	US-08-811-949-59	Sequence 59, Appl
260	245	6.2	228	1	US-08-396-149-10	Sequence 10, Appl	333	235	6.0	270	1	US-08-978-408-8	Sequence 8, Appl1
261	245	6.2	228	1	US-08-801-499-10	Sequence 10, Appl	334	233.5	5.9	252	2	US-08-944-483-72	Sequence 72, Appl
262	245	6.2	228	1	US-08-615-271-10	Sequence 10, Appl	335	233.5	5.9	253	1	US-09-027-337-8	Sequence 8, Appl1
263	245	6.2	228	2	US-09-074-660-10	Sequence 10, Appl	336	233.5	5.9	253	2	US-09-644-600-8	Sequence 8, Appl1
264	245	6.2	228	2	US-09-074-659-10	Sequence 10, Appl	337	233.5	5.9	253	2	US-09-654-600A-8	Sequence 8, Appl1
265	245	6.2	228	2	US-09-106-468-10	Sequence 10, Appl	338	233.5	5.9	253	2	US-09-421-213-8	Sequence 8, Appl1
266	245	6.2	228	2	US-09-106-468A-10	Sequence 10, Appl	339	233.5	5.9	268	2	US-09-987-455A-18	Sequence 18, Appl
267	245	6.2	228	2	US-09-106-467-10	Sequence 10, Appl	340	233.5	5.9	383	1	US-08-558-269-6	Sequence 6, Appl1
268	245	6.2	445	2	US-10-360-101-266	Sequence 266, App	341	233.5	5.9	383	2	US-09-410-882-6	Sequence 6, Appl1
269	244.5	6.2	259	2	US-09-715-994-2	Sequence 2, Appl1	342	233.5	5.9	546	7	5200340-6	Patent No. 5200340
270	244	6.2	638	2	US-10-099-322-114	Sequence 114, App	343	232.5	5.9	259	2	US-10-165-442-2	Sequence 2, Appl1
271	244	6.2	638	2	US-10-044-564-114	Sequence 114, App	344	232.5	5.9	295	2	US-10-165-442-1	Sequence 1, Appl1
272	242.5	6.1	436	1	US-09-000-846-2	Sequence 2, Appl1	345	232.5	5.9	1013	1	US-08-866-650-5	Sequence 5, Appl1
273	242	6.1	322	3	US-10-114-270-134	Sequence 134, App	346	232.5	5.9	1013	1	US-09-021-287-5	Sequence 5, Appl1
274	242	6.1	730	2	US-08-872-757-2	Sequence 2, Appl1	347	232.5	5.9	1013	2	US-08-991-408-2	Sequence 2, Appl1
275	242	6.1	730	2	US-09-850-048A-2	Sequence 2, Appl1	348	232.5	5.9	1013	2	US-09-240-473-5	Sequence 5, Appl1
276	241.5	6.1	347	1	US-08-811-949-1	Sequence 1, Appl1	349	232.5	5.9	1013	2	US-09-432-473-2	Sequence 2, Appl1
277	241.5	6.1	788	1	US-08-572-225-1	Sequence 1, Appl1	350	232.5	5.9	1013	2	US-09-285-385C-20	Sequence 20, Appl
278	241	6.1	354	1	US-08-811-949-61	Sequence 61, Appl	351	232	5.9	416	2	US-10-099-322-137	Sequence 137, App
279	241	6.1	966	2	US-08-872-757-4	Sequence 4, Appl1	352	232	5.9	638	1	US-10-044-564-137	Sequence 137, App
280	241	6.1	966	2	US-09-850-048A-4	Sequence 4, Appl1	353	232	5.9	638	2	US-08-681-151-3	Sequence 3, Appl1
281	240.5	6.1	356	1	US-08-427-640-8	Sequence 8, Appl1	354	232	5.9	638	2	US-10-099-322-115	Sequence 115, App
282	240.5	6.1	3571	2	US-09-911-842A-2	Sequence 2, Appl1	355	232	5.9	638	2	US-10-044-564-115	Sequence 115, App
283	240	6.1	432	2	US-09-959-392-34	Sequence 34, Appl1	356	231.5	5.9	389	1	US-08-811-949-65	Sequence 65, Appl
284	240	6.1	432	1	US-08-560-098A-47	Sequence 47, Appl	357	231.5	5.9	417	2	US-09-820-002-4	Sequence 4, Appl1
285	239.5	6.1	1015	2	US-09-285-385C-2	Sequence 2, Appl1	358	231	5.9	365	1	US-08-944-483-63	Sequence 63, Appl
286	239.5	6.1	3594	2	US-09-911-842A-4	Sequence 4, Appl1	359	231	5.9	365	1	US-08-720-012-83	Sequence 83, Appl
287	239	6.1	230	2	US-09-601-318-3	Sequence 3, Appl1	360	231	5.9	393	1	US-08-560-098A-44	Sequence 44, Appl
288	239	6.1	356	1	US-08-681-151-1	Sequence 1, Appl1	361	231	5.9	393	2	US-08-967-024C-24	Sequence 24, Appl
289	239	6.1	389	1	US-08-811-949-67	Sequence 67, Appl	362	231	5.9	393	2	US-08-967-024C-25	Sequence 25, Appl
290	238.5	6.0	437	1	US-08-811-949-49	Sequence 49, Appl	363	231	5.9	1012	2	US-09-285-385C-4	Sequence 4, Appl1
291	238.5	6.0	437	1	US-08-811-949-51	Sequence 51, Appl	364	230.5	5.8	259	2	US-10-165-442-4	Sequence 4, Appl1
292	238.5	6.0	437	1	US-08-811-949-55	Sequence 55, Appl	365	230.5	5.8	295	2	US-10-165-442-4	Sequence 4, Appl1
293	238.5	6.0	437	1	US-08-811-949-57	Sequence 57, Appl	366	230.5	5.8	302	2	US-09-220-731-26	Sequence 26, Appl
294	238	6.0	237	2	US-08-163-919A-3	Sequence 3, Appl1	367	230.5	5.8	302	2	US-09-242-999-22	Sequence 22, Appl
295	238	6.0	237	2	US-08-462-515-3	Sequence 3, Appl1	368	230	5.8	232	2	US-09-959-392-31	Sequence 31, Appl
296	238	6.0	237	5	PCT-US94-14073-3	Sequence 3, Appl1	369	230	5.8	248	2	US-08-944-483-63	Sequence 63, Appl
297	238	6.0	335	2	US-09-987-455A-14	Sequence 14, Appl	370	230	5.8	387	2	US-09-032-215-8	Sequence 8, Appl1
298	238	6.0	333	2	US-09-987-455A-16	Sequence 16, Appl	371	230	5.8	387	2	US-09-032-215-13	Sequence 13, Appl
299	236.5	6.0	274	1	US-08-978-404B-5	Sequence 5, Appl1	372	229	5.8	242	2	US-09-004-721-36	Sequence 36, Appl
300	236.5	6.0	308	2	US-09-987-455A-17	Sequence 17, Appl	373	229	5.8	242	2	US-08-749-699-36	Sequence 36, Appl
301	236.5	6.0	331	2	US-09-987-455A-12	Sequence 12, Appl	374	229	5.8	242	2	US-09-004-729-30	Sequence 30, Appl
302	236.5	6.0	339	2	US-09-987-455A-13	Sequence 13, Appl	375	229	5.8	400	2	US-09-004-729-36	Sequence 36, Appl
303	236.5	6.0	333	2	US-09-987-455A-15	Sequence 15, Appl	376	229	5.8	400	2	US-09-004-731-33	Sequence 33, Appl
304	236.5	6.0	334	2	US-09-987-455A-11	Sequence 11, Appl	377	229	5.8	400	2	US-08-749-699-30	Sequence 30, Appl
305	236.5	6.0	355	1	US-08-137-116-1	Sequence 1, Appl1	378	229	5.8	400	2	US-08-749-699-33	Sequence 33, Appl
306	236.5	6.0	355	1	US-08-217-618-1	Sequence 1, Appl1	379	229	5.8	400	2	US-09-004-729-30	Sequence 30, Appl
307	236.5	6.0	355	1	US-08-427-640-2	Sequence 2, Appl1	380	229	5.8	400	2	US-09-004-729-33	Sequence 33, Appl
308	236.5	6.0	355	1	US-08-427-640-6	Sequence 6, Appl1	381	228.5	5.8	235	2	US-08-807-151-3	Sequence 3, Appl1
309	236.5	6.0	355	1	US-08-217-617A-1	Sequence 1, Appl1	382	228.5	5.8	235	2	US-09-878-957-3	Sequence 3, Appl1
310	236.5	6.0	355	1	US-08-217-616-1	Sequence 1, Appl1	383	228.5	5.8	343	3	US-10-162-335-86	Sequence 86, Appl
311	236.5	6.0	355	1	US-08-811-949-45	Sequence 45, Appl	384	228	5.8	287	3	US-10-114-270-130	Sequence 130, App
312	236.5	6.0	355	2	US-08-811-949-47	Sequence 47, Appl	385	228	5.8	591	2	US-08-991-408-4	Sequence 4, Appl1
313	236.5	6.0	355	2	US-08-794-528-1	Sequence 47, Appl	386	228	5.8	591	2	US-09-432-473-4	Sequence 4, Appl1
314	236.5	6.0	355	7	5223256-1	Patent No. 5223256	387	228	5.8	809	2	US-08-991-761A-9	Sequence 9, Appl1
315	236.5	6.0	377	1	US-08-427-640-4	Sequence 4, Appl1	388	228	5.8	812	1	US-08-248-629A-1	Sequence 1, Appl1
316	236.5	6.0	377	1	US-09-987-455A-8	Sequence 8, Appl1	389	228	5.8	812	1	US-08-451-932-1	Sequence 1, Appl1
317	236.5	6.0	378	2	US-09-553-498-10	Sequence 10, Appl	390	228	5.8	812	1	US-08-452-260-1	Sequence 1, Appl1
318	236.5	6.0	378	2	US-09-618-869-10	Sequence 10, Appl	391	228	5.8	812	1	US-08-326-785-1	Sequence 1, Appl1

392	228	5.8	812	1	US-08-612-788-1	Sequence 1, Appl1	465	223	5.7	521	2	US-09-949-016-11081	Sequence 11081, A
393	228	5.8	812	1	US-08-605-598B-1	Sequence 1, Appl1	466	223	5.7	521	2	US-09-949-016-11082	Sequence 11082, A
394	228	5.8	812	1	US-08-429-743-1	Sequence 1, Appl1	467	223	5.7	521	2	US-09-949-016-11083	Sequence 11083, A
395	228	5.8	812	1	US-08-866-735-1	Sequence 1, Appl1	468	222.5	5.6	304	2	US-10-039-322-139	Sequence 139, App
396	228	5.8	812	2	US-09-066-028-1	Sequence 1, Appl1	469	222.5	5.6	304	2	US-10-044-564-139	Sequence 139, App
397	228	5.8	812	2	US-09-192-012-3	Sequence 3, Appl1	470	222.5	5.6	304	2	US-10-235-789C-2	Sequence 2, Appl1
398	228	5.8	812	2	US-09-335-325-1	Sequence 1, Appl1	471	222.5	5.6	417	2	US-10-099-892C-13	Sequence 40, Appl
399	228	5.8	812	2	US-08-991-761A-12	Sequence 12, Appl	472	222.5	5.6	417	2	US-10-099-322-136	Sequence 136, App
400	228	5.8	812	2	US-09-335-614-1	Sequence 1, Appl1	473	222.5	5.6	417	2	US-10-044-564-136	Sequence 40, Appl
401	228	5.8	812	5	PCT-US95-05107-1	Sequence 1, Appl1	474	222.5	5.6	417	2	US-10-044-564-136	Sequence 136, App
402	227.5	5.8	237	3	US-09-936-271C-66	Sequence 66, Appl	475	222.5	5.6	445	2	US-09-856-771A-8	Sequence 8, Appl1
403	227.5	5.8	251	3	US-09-936-271C-67	Sequence 67, Appl	476	222.5	5.6	445	2	US-09-949-016-7182	Sequence 7182, Ap
404	227	5.8	241	3	US-09-657-968B-2	Sequence 2, Appl1	477	222.5	5.6	790	2	US-08-991-761A-13	Sequence 13, Appl
405	227	5.8	241	3	US-09-410-362F-3	Sequence 3, Appl	478	222	5.6	224	1	US-09-016-666A-21	Sequence 21, Appl
406	227	5.8	241	3	US-09-410-362F-35	Sequence 35, Appl	479	222	5.6	224	1	US-08-978-404B-16	Sequence 16, Appl
407	227	5.8	285	2	US-09-023-942A-26	Sequence 26, Appl	480	222	5.6	407	2	US-09-734-675-4	Sequence 4, Appl1
408	227	5.8	308	2	US-08-705-875A-10	Sequence 10, Appl	481	222	5.6	407	2	US-10-060-333-4	Sequence 4, Appl1
409	227	5.8	308	2	US-09-242-999-10	Sequence 10, Appl	482	222	5.6	433	2	US-10-012-231A-269	Sequence 269, App
410	226.5	5.7	454	2	US-09-518-046-2	Sequence 2, Appl1	483	222	5.6	433	2	US-10-015-889A-269	Sequence 269, App
411	226.5	5.7	454	2	US-09-650-371-2	Sequence 2, Appl1	484	222	5.6	433	2	US-10-006-768A-269	Sequence 269, App
412	226.5	5.7	2787	2	US-09-245-041-15	Sequence 15, Appl	485	222	5.6	433	2	US-10-015-671A-269	Sequence 269, App
413	226.5	5.7	2787	2	US-09-358-055B-15	Sequence 15, Appl	486	222	5.6	433	2	US-10-015-393A-269	Sequence 269, App
414	226.5	5.7	2787	2	US-09-893-238-15	Sequence 15, Appl	487	222	5.6	433	2	US-10-011-833A-269	Sequence 269, App
415	226	5.7	406	2	US-09-851-588-6	Sequence 6, Appl1	488	222	5.6	433	2	US-10-006-041A-269	Sequence 269, App
416	226	5.7	423	2	US-09-656-002-2	Sequence 2, Appl1	489	222	5.6	433	2	US-10-012-064A-269	Sequence 269, App
417	226	5.7	432	2	US-10-012-231A-275	Sequence 275, App	490	222	5.6	433	2	US-10-015-392A-269	Sequence 269, App
418	226	5.7	432	2	US-10-015-389A-275	Sequence 275, App	491	222	5.6	433	3	US-10-011-795B-269	Sequence 269, App
419	226	5.7	432	2	US-10-006-768A-275	Sequence 275, App	492	222	5.6	433	3	US-10-015-386A-269	Sequence 269, App
420	226	5.7	432	2	US-10-006-768A-275	Sequence 275, App	493	222	5.6	433	3	US-10-012-121A-269	Sequence 269, App
421	226	5.7	432	2	US-10-015-671A-275	Sequence 275, App	494	222	5.6	433	3	US-10-006-485A-269	Sequence 269, App
422	226	5.7	432	2	US-10-015-333A-275	Sequence 275, App	495	222	5.6	433	3	US-10-006-466A-269	Sequence 269, App
423	226	5.7	432	2	US-10-011-833A-275	Sequence 275, App	496	222	5.6	433	3	US-10-012-752A-275	Sequence 275, App
424	226	5.7	432	2	US-10-006-041A-275	Sequence 275, App	497	222	5.6	433	3	US-10-012-752A-275	Sequence 275, App
425	226	5.7	432	2	US-10-012-064A-275	Sequence 275, App	498	222	5.6	433	3	US-10-012-752A-275	Sequence 275, App
426	226	5.7	432	2	US-10-015-392A-275	Sequence 275, App	499	222	5.6	433	3	US-10-015-519A-269	Sequence 269, App
427	226	5.7	432	3	US-10-011-795B-275	Sequence 275, App	500	222	5.6	433	3	US-10-015-519A-269	Sequence 269, App
428	226	5.7	432	3	US-10-015-386A-275	Sequence 275, App	501	221.5	5.6	433	3	US-10-007-233A-269	Sequence 269, App
429	226	5.7	432	3	US-10-012-121A-275	Sequence 275, App	502	221.5	5.6	433	3	US-09-999-873A-69	Sequence 69, Appl
430	226	5.7	432	3	US-10-006-485A-275	Sequence 275, App	503	221.5	5.6	433	2	US-10-020-445A-69	Sequence 69, Appl
431	226	5.7	432	3	US-10-006-746A-275	Sequence 275, App	504	221.5	5.6	433	2	US-09-978-189-69	Sequence 69, Appl
432	226	5.7	432	3	US-10-012-752A-275	Sequence 275, App	505	221.5	5.6	433	2	US-10-017-085A-69	Sequence 69, Appl
433	226	5.7	432	3	US-10-017-253A-275	Sequence 275, App	506	221.5	5.6	433	3	US-10-145-129A-69	Sequence 69, Appl
434	226	5.7	432	3	US-10-015-519A-275	Sequence 275, App	507	221.5	5.6	433	3	US-10-013-929A-69	Sequence 69, Appl
435	226	5.7	432	3	US-10-015-715A-275	Sequence 275, App	508	221.5	5.6	253	3	US-10-013-917A-69	Sequence 73, Appl
436	226	5.7	435	2	US-10-007-236A-275	Sequence 275, App	509	221	5.6	253	3	US-08-944-483-73	Sequence 73, Appl
437	226	5.7	435	2	US-09-608-271A-6	Sequence 6, Appl1	510	221	5.6	253	3	US-08-978-404B-6	Sequence 6, Appl1
438	226	5.7	435	2	US-09-607-745-2	Sequence 6, Appl1	511	221	5.6	300	2	US-08-705-875A-6	Sequence 6, Appl1
439	226	5.7	435	2	US-09-968-415-6	Sequence 6, Appl1	512	221	5.6	300	2	US-09-242-899-6	Sequence 6, Appl1
440	226	5.7	435	3	US-10-030-688-2	Sequence 2, Appl1	513	221	5.6	1135	2	US-09-949-016-10498	Sequence 10498, A
441	226	5.7	437	2	US-09-851-588-8	Sequence 8, Appl1	514	220.5	5.6	1355	2	US-09-787-097-16	Sequence 10, Appl
442	226	5.7	481	2	US-09-949-016-9238	Sequence 9238, Ap	515	220	5.6	273	1	US-09-820-002-2	Sequence 2, Appl1
443	226	5.7	481	2	US-09-949-016-9239	Sequence 9239, Ap	516	220	5.6	273	1	US-09-016-366A-19	Sequence 19, Appl
444	226	5.7	492	3	US-10-030-688-4	Sequence 4, Appl1	517	219.5	5.6	273	1	US-08-978-404B-14	Sequence 14, Appl
445	226	5.7	637	2	US-09-949-016-11538	Sequence 11538, A	518	219.5	5.6	245	3	US-09-410-462P-36	Sequence 36, Appl
446	225.5	5.7	637	2	US-09-949-016-11539	Sequence 11539, A	519	219.5	5.6	245	2	US-08-944-483-50	Sequence 50, Appl
447	225.5	5.7	348	2	US-09-949-016-5979	Sequence 6979, Ap	520	219.5	5.6	255	1	US-09-027-337-7	Sequence 7, Appl1
448	225.5	5.7	457	2	US-09-856-371A-510	Sequence 10, Appl	521	219.5	5.6	255	2	US-09-644-600-7	Sequence 7, Appl1
449	225.5	5.7	1272	2	US-09-787-097-18	Sequence 18, Appl	522	219.5	5.6	255	2	US-09-654-600A-7	Sequence 7, Appl1
450	225	5.7	1429	2	US-09-787-097-12	Sequence 12, Appl	523	219	5.6	255	3	US-09-421-213-7	Sequence 7, Appl1
451	225	5.7	615	2	US-09-949-002-101	Sequence 301, App	524	219	5.6	333	2	US-09-948-094-2	Sequence 2, Appl1
452	224.5	5.7	232	2	US-09-959-392-32	Sequence 32, Appl	525	218.5	5.5	333	2	US-10-037-417-130	Sequence 130, Appl
453	224.5	5.7	235	2	US-08-944-483-65	Sequence 65, Appl	526	218.5	5.5	244	2	US-09-601-318-5	Sequence 5, Appl1
454	224.5	5.7	235	3	US-09-410-362F-5	Sequence 5, Appl	527	218.5	5.5	244	2	US-09-601-318-6	Sequence 6, Appl1
455	224	5.7	275	1	US-09-016-362F-37	Sequence 37, Appl	528	218.5	5.5	244	2	US-09-601-318-7	Sequence 7, Appl1
456	224	5.7	275	1	US-09-016-366A-17	Sequence 17, Appl	529	218.5	5.5	245	2	US-09-017-970A-6	Sequence 6, Appl1
457	224	5.7	275	1	US-08-978-404B-12	Sequence 12, Appl	530	218.5	5.5	245	2	US-09-601-318-1	Sequence 1, Appl1
458	224	5.7	276	1	US-09-598-982C-52	Sequence 52, Appl	531	218.5	5.5	245	2	US-09-079-970A-6	Sequence 11, Appl
459	224	5.7	306	1	US-09-880-503-5	Sequence 5, Appl1	532	218.5	5.5	245	2	US-09-598-982C-11	Sequence 11, Appl
460	224	5.7	323	2	US-08-560-098A-45	Sequence 45, Appl	533	218.5	5.5	249	2	US-09-598-982C-9	Sequence 9, Appl1
461	224	5.7	331	1	US-09-880-503-7	Sequence 7, Appl1	534	217.5	5.5	245	2	US-09-598-982C-33	Sequence 33, Appl
462	223.5	5.7	323	1	US-08-560-098A-46	Sequence 46, Appl	535	217.5	5.5	249	2	US-09-598-982C-35	Sequence 35, Appl
463	223.5	5.7	245	1	US-08-944-483-49	Sequence 69, Appl	536	217.5	5.5	249	2	US-09-598-982C-25	Sequence 25, Appl
464	223	5.7	346	2	US-09-949-016-9000	Sequence 9000, Ap	537	217.5	5.5	249	2	US-09-598-982C-27	Sequence 27, Appl

538	217.5	5.5	1198	2	US-09-245-041-131	Sequence 131, App	611	214	5.4	254	1	US-08-560-098A-49	Sequence 49, App1
539	217.5	5.5	1198	2	US-09-794-236-3	Sequence 3, App1	612	214	5.4	292	2	US-09-607-745-9	Sequence 9, App1
540	217.5	5.5	1198	2	US-09-358-055B-132	Sequence 132, App	613	214	5.4	342	2	US-10-037-417-133	Sequence 133, App
541	217.5	5.5	1198	2	US-09-964-956-35	Sequence 35, App1	614	214	5.4	342	2	US-10-037-417-134	Sequence 134, App
542	217.5	5.5	1198	2	US-09-787-097-2	Sequence 2, App1	615	213.5	5.4	114	2	US-09-964-956-68	Sequence 68, App1
543	217.5	5.5	1429	2	US-09-245-041-130	Sequence 130, App	616	213.5	5.4	255	3	US-08-944-483-67	Sequence 67, App1
544	217.5	5.5	1429	2	US-09-358-055B-131	Sequence 131, App	617	213.5	5.4	255	3	US-09-410-362F-6	Sequence 6, App1
545	217.5	5.5	1429	2	US-08-944-483-61	Sequence 61, App1	618	213.5	5.4	255	3	US-09-410-362F-38	Sequence 38, App1
546	217	5.5	258	2	US-09-613-822B-2	Sequence 2, App1	619	213.5	5.4	256	1	US-09-027-337-3	Sequence 3, App1
547	217	5.5	234	1	US-08-978-404B-3	Sequence 4, App1	620	213.5	5.4	256	2	US-09-644-600-3	Sequence 3, App1
548	217	5.5	374	2	US-10-037-417-44	Sequence 44, App1	621	213.5	5.4	256	2	US-09-654-600A-3	Sequence 3, App1
549	217	5.5	357	2	US-10-037-417-46	Sequence 46, App1	622	213.5	5.4	256	3	US-09-421-213-3	Sequence 3, App1
550	217	5.5	791	1	US-08-643-219-1	Sequence 1, App1	623	212.5	5.4	250	2	US-09-205-258-427	Sequence 427, App
551	217	5.5	791	2	US-08-851-350-1	Sequence 19, App1	624	212.5	5.4	250	2	US-10-004-860-427	Sequence 427, App
552	217	5.5	2703	2	US-08-899-232-4	Sequence 4, App1	625	212.5	5.4	250	2	US-10-012-231A-170	Sequence 170, App
553	217	5.5	2703	2	US-08-899-232-4	Sequence 4, App1	626	212.5	5.4	250	2	US-10-015-389A-170	Sequence 170, App
554	216.5	5.5	2703	2	US-09-121-457-4	Sequence 4, App1	627	212.5	5.4	250	2	US-10-006-768A-170	Sequence 170, App
555	216.5	5.5	245	2	US-09-598-982C-2	Sequence 2, App1	628	212.5	5.4	250	2	US-10-015-671A-170	Sequence 170, App
556	216.5	5.5	498	2	US-09-598-982C-6	Sequence 6, App1	629	212.5	5.4	250	2	US-10-015-393A-170	Sequence 170, App
557	216.5	5.5	498	2	US-10-183-992-2	Sequence 2, App1	630	212.5	5.4	250	2	US-10-011-833A-170	Sequence 170, App
558	216	5.5	257	1	US-09-016-366A-23	Sequence 23, App1	631	212.5	5.4	250	2	US-10-006-041A-170	Sequence 170, App
559	216	5.5	257	1	US-08-978-404B-18	Sequence 18, App1	632	212.5	5.4	250	2	US-10-012-064A-170	Sequence 170, App
560	216	5.5	257	2	US-09-917-254-101	Sequence 101, App	633	212.5	5.4	250	2	US-10-012-064A-170	Sequence 170, App
561	216	5.5	258	1	US-08-568-031-2	Sequence 2, App1	634	212.5	5.4	250	3	US-10-015-392A-170	Sequence 170, App
562	216	5.5	258	1	US-08-966-119-2	Sequence 2, App1	635	212.5	5.4	250	3	US-09-936-271C-86	Sequence 86, App1
563	216	5.5	258	1	US-09-153-304-2	Sequence 2, App1	636	212.5	5.4	250	3	US-10-015-386A-170	Sequence 170, App
564	216	5.5	299	2	US-08-944-483-66	Sequence 66, App1	637	212.5	5.4	250	3	US-10-012-121A-170	Sequence 170, App
565	216	5.5	319	2	US-09-386-642-12	Sequence 12, App1	638	212.5	5.4	250	3	US-10-006-485A-170	Sequence 170, App
566	216	5.5	790	1	US-09-386-642-11	Sequence 11, App1	639	212.5	5.4	250	3	US-10-012-121A-170	Sequence 170, App
567	216	5.5	790	1	US-08-469-486-54	Sequence 54, App1	640	212.5	5.4	250	3	US-10-012-752A-170	Sequence 170, App
568	216	5.5	790	1	US-08-469-486-54	Sequence 54, App1	641	212.5	5.4	250	3	US-10-017-253A-170	Sequence 170, App
569	216	5.5	810	7	5200340-8	Patent No. 5200340	642	212.5	5.4	250	3	US-10-015-518A-170	Sequence 170, App
570	215.5	5.5	245	2	US-09-598-982C-49	Sequence 49, App1	643	212.5	5.4	250	3	US-10-015-518A-170	Sequence 170, App
571	215.5	5.5	245	2	US-09-598-982C-51	Sequence 51, App1	644	212.5	5.4	250	3	US-10-015-715A-170	Sequence 170, App
572	215.5	5.5	249	2	US-09-598-982C-41	Sequence 41, App1	645	212.5	5.4	282	2	US-09-025-059-1	Sequence 1, App1
573	215.5	5.5	317	2	US-09-598-982C-43	Sequence 43, App1	646	212.5	5.4	282	2	US-09-856-320A-2	Sequence 2, App1
574	215.5	5.5	317	2	US-09-386-629-7	Sequence 7, App1	647	212.5	5.4	289	2	US-09-386-642-14	Sequence 14, App1
575	215.5	5.5	317	2	US-09-907-794A-263	Sequence 263, App	648	212.5	5.4	289	2	US-10-162-335-4	Sequence 4, App1
576	215.5	5.5	317	2	US-09-905-125A-263	Sequence 263, App	649	212.5	5.4	289	3	US-10-162-335-8	Sequence 8, App1
577	215.5	5.5	317	2	US-09-902-775A-263	Sequence 263, App	650	212.5	5.4	289	3	US-09-025-059-3	Sequence 3, App1
578	215.5	5.5	317	2	US-09-902-775A-263	Sequence 263, App	651	212	5.4	260	2	US-09-618-259-8	Sequence 8, App1
579	215.5	5.5	317	2	US-09-903-603A-263	Sequence 263, App	652	212	5.4	260	2	US-08-915-659A-10	Sequence 10, App1
580	215.5	5.5	317	2	US-09-904-920A-263	Sequence 263, App	653	212	5.4	814	1	US-08-750-711-1	Sequence 1, App1
581	215.5	5.5	317	2	US-09-905-381A-263	Sequence 263, App	654	211.5	5.4	232	1	US-08-508-448B-19	Sequence 19, App1
582	215.5	5.5	317	2	US-09-905-381A-263	Sequence 263, App	655	211.5	5.4	235	3	US-09-410-362F-4	Sequence 4, App1
583	215.5	5.5	317	2	US-09-906-618-263	Sequence 263, App	656	211.5	5.4	266	3	US-10-162-335-6	Sequence 6, App1
584	215.5	5.5	317	2	US-10-040-803-7	Sequence 7, App1	657	211.5	5.4	266	3	US-10-162-335-10	Sequence 10, App1
585	215.5	5.5	317	2	US-09-906-646-263	Sequence 263, App	658	211.5	5.4	418	1	US-08-508-448C-25	Sequence 25, App1
586	215.5	5.5	317	2	US-09-904-462-263	Sequence 263, App	659	211.5	5.4	418	2	US-09-370-838-82	Sequence 82, App1
587	215.5	5.5	317	2	US-09-902-736A-263	Sequence 263, App	660	211.5	5.4	418	2	US-09-370-838-83	Sequence 83, App1
588	215.5	5.5	317	2	US-09-906-722A-263	Sequence 263, App	661	211.5	5.4	418	2	US-09-854-133-82	Sequence 82, App1
589	215.5	5.5	317	2	US-09-905-449-263	Sequence 263, App	662	211.5	5.4	418	2	US-09-854-133-83	Sequence 83, App1
590	215.5	5.5	317	2	US-09-903-562B-263	Sequence 263, App	663	211	5.3	276	1	US-09-016-366A-15	Sequence 15, App1
591	215.5	5.5	317	2	US-09-906-679A-263	Sequence 263, App	664	211	5.3	276	1	US-08-978-404B-21	Sequence 21, App1
592	215.5	5.5	317	3	US-09-907-841-263	Sequence 263, App	665	211	5.3	300	2	US-08-705-875A-4	Sequence 4, App1
593	215.5	5.5	1428	2	US-09-964-956-33	Sequence 33, App1	666	211	5.3	300	2	US-09-220-731-21	Sequence 21, App1
594	215	5.4	359	2	US-10-037-417-131	Sequence 131, App	667	211	5.3	300	2	US-09-242-999-4	Sequence 4, App1
595	215	5.4	733	3	US-09-949-016-9983	Sequence 9983, App	668	211	5.3	300	2	US-09-644-022A-10	Sequence 10, App1
596	215	5.4	733	3	US-09-657-431A-1	Sequence 1, App1	669	211	5.3	433	2	US-09-949-016-882A0	Sequence 820, App
597	215	5.4	791	1	US-09-131-995-1	Sequence 1, App1	670	211	5.3	1010	2	US-08-882-046-7	Sequence 7, App1
598	215	5.4	791	1	US-08-832-087B-1	Sequence 1, App1	671	211	5.3	1010	2	US-09-566-047-7	Sequence 7, App1
599	215	5.4	791	2	US-09-132-154-1	Sequence 1, App1	672	211	5.3	1036	2	US-09-068-740A-6	Sequence 6, App1
600	215	5.4	791	2	US-08-991-761A-6	Sequence 6, App1	673	211	5.3	1067	2	US-09-579-536C-18	Sequence 18, App1
601	215	5.4	791	2	US-08-924-287A-1	Sequence 1, App1	674	211	5.3	1187	2	US-09-068-740A-7	Sequence 7, App1
602	215	5.4	791	2	US-10-360-101-257	Sequence 257, App	675	211	5.3	1208	2	US-09-199-865-1	Sequence 1, App1
603	215	5.4	810	1	US-07-854-603-2	Sequence 2, App1	676	211	5.3	1208	2	US-10-213-329-1	Sequence 1, App1
604	215	5.4	810	2	US-08-147-000B-29	Sequence 29, App1	677	211	5.3	1218	1	US-08-400-159-6	Sequence 6, App1
605	215	5.4	810	2	US-09-086-514-1	Sequence 1, App1	678	211	5.3	1218	2	US-08-611-729A-6	Sequence 6, App1
606	215	5.4	810	2	US-09-192-012-5	Sequence 5, App1	679	211	5.3	1218	2	US-08-882-046-2	Sequence 2, App1
607	215	5.4	810	2	US-09-403-736-1	Sequence 1, App1	680	211	5.3	1218	2	US-09-214-278-7	Sequence 7, App1
608	215	5.4	810	2	US-09-701-265-1	Sequence 1, App1	681	211	5.3	1218	2	US-09-068-740A-11	Sequence 11, App1
609	215	5.4	810	3	US-09-946-893C-2	Sequence 2, App1	682	211	5.3	1218	2	US-09-855-722-7	Sequence 7, App1
610	214.5	5.4	1428	2	US-09-964-956-34	Sequence 34, App1	683	211	5.3	1218	2	US-09-566-047-2	Sequence 2, App1

684	211	5.3	1218	2	US-09-917-254-85	Sequence 85, Appl	757	204.5	5.2	439	2	US-09-949-016-9260	Sequence 9260, Ap
685	211	5.3	1218	2	US-09-195-524-6	Sequence 6, Appl1	758	204	5.2	260	2	US-09-070-526-2	Sequence 7, Appl1
686	211	5.3	1218	2	US-09-579-536C-1	Sequence 1, Appl1	759	204	5.2	260	2	US-09-618-259-7	Sequence 7, Appl1
687	211	5.3	1218	2	US-09-949-016-5902	Sequence 5902, Ap	760	204	5.2	260	2	US-09-999-883A-395	Sequence 395, App
688	211	5.3	1218	2	US-09-310-685-4	Sequence 4, Appl1	761	204	5.2	260	2	US-10-020-445A-395	Sequence 395, App
689	211	5.3	1254	2	US-09-949-016-10297	Sequence 10297, A	762	204	5.2	260	2	US-09-978-189-395	Sequence 395, App
690	210.5	5.3	245	2	US-09-598-982C-31	Sequence 31, Appl	763	204	5.2	260	2	US-10-017-085A-395	Sequence 395, App
691	210.5	5.3	249	2	US-09-598-982C-23	Sequence 23, Appl	764	204	5.2	260	3	US-08-915-659A-7	Sequence 7, Appl1
692	210.5	5.3	418	2	US-09-370-838-62	Sequence 62, Appl	765	204	5.2	260	3	US-10-145-129A-395	Sequence 395, App
693	210.5	5.3	418	2	US-09-854-133-62	Sequence 62, Appl	766	204	5.2	260	3	US-10-013-929A-395	Sequence 395, App
694	210.5	5.3	1219	2	US-08-882-046-5	Sequence 5, Appl1	767	204	5.2	260	3	US-09-936-271C-835	Sequence 83, Appl
695	210.5	5.3	1219	2	US-09-566-047-5	Sequence 5, Appl1	768	204	5.2	260	3	US-10-013-917A-395	Sequence 395, App
696	210	5.3	154	2	US-09-261-416-5	Sequence 5, Appl1	769	203.5	5.2	224	3	US-08-944-483-34	Sequence 34, Appl
697	210	5.3	248	2	US-08-944-483-24	Sequence 24, Appl	770	203.5	5.2	224	3	US-09-410-362F-39	Sequence 39, Appl1
698	210	5.3	446	2	US-10-177-661-4	Sequence 4, Appl1	771	203.5	5.2	224	3	US-09-410-362F-39	Sequence 39, Appl1
699	209.5	5.3	372	3	US-10-162-335-2	Sequence 2, Appl1	772	203.5	5.2	249	2	US-09-949-016-8770	Sequence 8770, Ap
700	209.5	5.3	477	2	US-10-177-661-2	Sequence 2, Appl1	773	203.5	5.2	3623	2	US-09-341-461-2	Sequence 2, Appl1
701	209.5	5.3	562	2	US-09-879-792-12	Sequence 12, Appl1	774	203	5.1	263	2	US-08-807-151-1	Sequence 1, Appl1
702	208.5	5.3	245	2	US-09-598-982C-29	Sequence 29, Appl	775	203	5.1	263	2	US-09-478-957-1	Sequence 1, Appl1
703	208.5	5.3	245	2	US-09-598-982C-47	Sequence 47, Appl	776	202.5	5.1	268	3	US-09-936-271C-73	Sequence 73, Appl
704	208.5	5.3	249	2	US-09-598-982C-21	Sequence 21, Appl	777	202.5	5.1	701	2	US-10-297-895A-19	Sequence 19, Appl
705	208.5	5.3	249	2	US-09-598-982C-39	Sequence 39, Appl	778	202.5	5.1	766	2	US-10-397-895A-21	Sequence 21, Appl
706	208.5	5.3	492	2	US-09-685-166A-895	Sequence 895, App	779	202.5	5.1	997	2	US-10-297-895A-10	Sequence 10, Appl
707	208.5	5.3	492	2	US-09-879-792-14	Sequence 14, Appl	780	202	5.1	2321	2	US-09-230-652-2	Sequence 2, Appl1
708	208.5	5.3	492	2	US-09-679-426-995	Sequence 895, App	781	202	5.1	2321	2	US-09-612-226B-2	Sequence 2, Appl1
709	208.5	5.3	492	2	US-09-759-143-895	Sequence 895, App	782	200.5	5.1	226	2	US-08-984-417-4	Sequence 4, Appl1
710	208.5	5.3	492	2	US-10-012-896-895	Sequence 895, App	783	200.5	5.1	226	2	US-08-378-091-8	Sequence 8, Appl1
711	208.5	5.3	492	3	US-10-144-678A-895	Sequence 895, App	784	200.5	5.1	232	1	US-08-378-091-8	Sequence 8, Appl1
712	208	5.3	238	2	US-09-856-371A-2	Sequence 895, App	785	200.5	5.1	232	1	US-08-483-859-8	Sequence 8, Appl1
713	208	5.3	268	1	US-08-270-564A-2	Sequence 2, Appl1	786	200.5	5.1	232	1	US-08-472-173-8	Sequence 8, Appl1
714	208	5.3	268	1	US-08-765-192-2	Sequence 2, Appl1	787	200.5	5.1	232	1	US-08-487-167-8	Sequence 8, Appl1
715	208	5.3	268	1	US-09-199-793-2	Sequence 2, Appl1	788	200.5	5.1	232	1	US-08-482-816-8	Sequence 8, Appl1
716	208	5.3	271	1	US-08-467-155A-10	Sequence 10, Appl	789	200.5	5.1	232	1	US-08-296-449-8	Sequence 8, Appl1
717	208	5.3	271	1	US-08-628-198-10	Sequence 10, Appl	790	200.5	5.1	232	1	US-08-801-699-8	Sequence 8, Appl1
718	208	5.3	271	2	US-09-201-038-10	Sequence 10, Appl	791	200.5	5.1	232	1	US-08-615-271-8	Sequence 8, Appl1
719	208	5.3	271	3	US-10-021-368-10	Sequence 10, Appl	792	200.5	5.1	232	2	US-09-074-660-8	Sequence 8, Appl1
720	208	5.3	271	5	PCT-US96-07343-10	Sequence 10, Appl	793	200.5	5.1	232	2	US-09-074-660-8	Sequence 8, Appl1
721	208	5.3	273	2	US-09-856-371A-4	Sequence 4, Appl1	794	200.5	5.1	232	2	US-09-106-469-8	Sequence 8, Appl1
722	208	5.3	275	2	US-09-856-320A-6	Sequence 6, Appl1	795	200.5	5.1	232	2	US-09-106-468-8	Sequence 8, Appl1
723	208	5.3	311	2	US-09-856-371A-6	Sequence 6, Appl1	796	200.5	5.1	232	2	US-09-106-467-8	Sequence 8, Appl1
724	207.5	5.3	241	2	US-09-944-883C-59	Sequence 59, Appl	797	200.5	5.1	247	1	US-08-956-267A-2	Sequence 2, Appl1
725	206.5	5.3	245	2	US-09-598-982C-45	Sequence 45, Appl	798	200.5	5.1	314	2	US-09-636-882A-2	Sequence 2, Appl1
726	206.5	5.2	249	2	US-09-598-982C-37	Sequence 37, Appl	799	200.5	5.1	415	2	US-09-907-794A-104	Sequence 104, App
727	206.5	5.2	255	1	US-08-650-129-5	Sequence 5, Appl1	800	200.5	5.1	415	2	US-09-905-125A-104	Sequence 104, App
728	206.5	5.2	255	2	US-08-984-417-5	Sequence 5, Appl1	801	200.5	5.1	415	2	US-09-902-775A-104	Sequence 104, App
729	206.5	5.2	284	2	US-09-387-375-7	Sequence 7, Appl1	802	200.5	5.1	415	2	US-09-906-700-104	Sequence 104, App
730	206.5	5.2	284	2	US-10-041-400A-7	Sequence 7, Appl1	803	200.5	5.1	415	2	US-09-903-603A-104	Sequence 104, App
731	206.5	5.2	284	2	US-10-042-091A-7	Sequence 7, Appl1	804	200.5	5.1	415	2	US-09-904-920A-104	Sequence 104, App
732	206.5	5.2	284	2	US-10-041-264B-7	Sequence 7, Appl1	805	200.5	5.1	415	2	US-09-909-664-104	Sequence 104, App
733	206.5	5.2	316	2	US-09-387-375-9	Sequence 9, Appl1	806	200.5	5.1	415	2	US-09-905-581A-104	Sequence 104, App
734	206.5	5.2	316	2	US-10-041-400A-9	Sequence 9, Appl1	807	200.5	5.1	415	2	US-09-906-618-104	Sequence 104, App
735	206.5	5.2	316	2	US-10-042-091A-9	Sequence 9, Appl1	808	200.5	5.1	415	2	US-09-906-646-104	Sequence 104, App
736	206.5	5.2	316	2	US-10-041-264B-9	Sequence 9, Appl1	809	200.5	5.1	415	2	US-09-906-646-104	Sequence 104, App
737	206	5.2	275	3	US-09-936-271C-72	Sequence 72, Appl	810	200.5	5.1	415	2	US-09-904-462-104	Sequence 104, App
738	206	5.2	1185	2	US-09-964-956-7	Sequence 7, Appl1	811	200.5	5.1	415	2	US-09-902-736A-104	Sequence 104, App
739	205.5	5.2	235	2	US-08-944-483-48	Sequence 48, Appl	812	200.5	5.1	415	2	US-09-906-722A-104	Sequence 104, App
740	205.5	5.2	269	1	US-08-978-404B-10	Sequence 10, Appl	813	200.5	5.1	415	2	US-09-905-449-104	Sequence 104, App
741	205.5	5.2	269	1	US-10-162-335-14	Sequence 14, Appl	814	200.5	5.1	415	2	US-09-903-662B-104	Sequence 104, App
742	205.5	5.2	288	2	US-10-360-101-331	Sequence 231, App	815	200.5	5.1	415	2	US-09-906-679A-104	Sequence 104, App
743	205.5	5.2	327	2	US-09-386-642-13	Sequence 13, Appl	816	200.5	5.1	415	3	US-09-907-841-104	Sequence 104, App
744	205.5	5.2	327	2	US-09-386-629-8	Sequence 8, Appl1	817	200.5	5.1	769	2	US-09-907-841-104	Sequence 104, App
745	205.5	5.2	360	3	US-10-040-803-8	Sequence 8, Appl1	818	200	5.1	810	2	US-09-949-016-11019	Sequence 11019, A
746	205.5	5.2	360	3	US-10-162-335-18	Sequence 18, Appl	819	200	5.1	110	2	US-09-964-956-69	Sequence 69, Appl
747	205.5	5.2	492	2	US-10-162-335-18	Sequence 18, Appl	820	200	5.1	385	2	US-09-163-951-16	Sequence 16, Appl
748	205.5	5.2	492	2	US-09-342-749-2	Sequence 2, Appl1	821	200	5.1	385	2	US-09-345-881-16	Sequence 16, Appl
749	205.5	5.2	492	2	US-09-691-840-2	Sequence 2, Appl1	822	199.5	5.1	385	3	US-10-000-512-14	Sequence 10, Appl
750	205.5	5.2	492	2	US-09-759-143-932	Sequence 932, App	823	199.5	5.1	1193	1	US-08-400-159-10	Sequence 10, Appl
751	205.5	5.2	492	3	US-10-012-896-932	Sequence 932, App	824	199.5	5.1	1193	2	US-08-611-729A-10	Sequence 10, Appl
752	205.5	5.2	510	2	US-10-144-678A-932	Sequence 932, App	825	199.5	5.1	1193	2	US-08-195-524-10	Sequence 10, Appl
753	205	5.2	393	2	US-09-949-016-11074	Sequence 11074, A	826	199.5	5.1	1275	2	US-09-310-685-8	Sequence 8, Appl1
754	205	5.2	393	2	US-09-759-143-934	Sequence 934, App	827	199.5	5.1	1256	1	US-09-964-956-36	Sequence 36, Appl
755	205	5.2	393	2	US-10-012-896-934	Sequence 934, App	828	199.5	5.1	2556	1	US-08-185-432-17	Sequence 17, Appl
756	204.5	5.2	393	3	US-10-144-678A-934	Sequence 934, App	829	199.5	5.1	2556	2	US-08-083-590A-20	Sequence 20, Appl
			360	3	US-10-162-335-12	Sequence 12, Appl							

830	199.5	5.1	2556	2	US-08-899-232-2	Sequence 2, Appl1	903	195.5	5.0	2471	1	US-08-083-590A-19	Sequence 19, Appl1
831	199.5	5.1	2556	2	US-09-121-457-2	Sequence 2, Appl1	904	195.5	5.0	2471	2	US-08-532-384-19	Sequence 19, Appl1
832	199.5	5.0	2556	2	US-09-949-016-8151	Sequence 8151, Ap	905	195.5	5.0	2471	2	US-08-899-232-1	Sequence 1, Appl1
833	199.5	5.0	260	2	US-09-008-271A-7	Sequence 7, Appl1	906	195.5	5.0	2471	2	US-09-121-457-1	Sequence 1, Appl1
834	199.5	5.0	260	2	US-09-968-415-7	Sequence 4, Appl1	907	195.5	4.9	258	3	US-09-936-271C-85	Sequence 85, Appl1
835	199.5	5.0	278	2	US-08-392-828C-4	Sequence 4, Appl1	908	194.5	4.9	246	1	US-08-978-404B-4	Sequence 44, Appl1
836	199.5	5.0	278	2	US-09-330-945-4	Sequence 9, Appl1	909	194.5	4.9	341	3	US-10-162-335-20	Sequence 20, Appl1
837	198.5	5.0	223	1	US-08-483-859-9	Sequence 9, Appl1	910	194.5	4.9	415	2	US-09-032-523-2	Sequence 2, Appl1
838	198.5	5.0	223	1	US-08-472-173-9	Sequence 9, Appl1	911	194.5	4.9	415	2	US-09-802-633-2	Sequence 2, Appl1
839	198.5	5.0	223	1	US-08-487-167-9	Sequence 9, Appl1	912	194	4.9	113	3	US-09-438-046-20	Sequence 26, Appl1
840	198.5	5.0	223	1	US-08-482-816-9	Sequence 9, Appl1	913	194	4.9	113	3	US-09-410-362F-26	Sequence 26, Appl1
841	198.5	5.0	223	1	US-08-296-149-9	Sequence 9, Appl1	914	194	4.9	233	2	US-09-821-255-4	Sequence 4, Appl1
842	198.5	5.0	223	1	US-08-801-499-9	Sequence 9, Appl1	915	193.5	4.9	225	2	US-10-036-371-8	Sequence 8, Appl1
843	198.5	5.0	223	1	US-08-615-271-9	Sequence 9, Appl1	916	193	4.9	228	2	US-08-944-483-44	Sequence 44, Appl1
844	198.5	5.0	223	2	US-09-074-660-9	Sequence 9, Appl1	917	193	4.9	228	2	US-10-202-676-6	Sequence 69, Appl1
845	198.5	5.0	223	2	US-09-074-659-9	Sequence 9, Appl1	918	193	4.9	253	3	US-09-936-271C-69	Sequence 69, Appl1
846	198.5	5.0	223	2	US-09-106-468-9	Sequence 9, Appl1	919	193	4.9	253	7	5223425-8	Patent No. 5223425
847	198.5	5.0	223	2	US-09-106-468-9	Sequence 9, Appl1	920	193	4.9	268	2	US-09-032-215-42	Sequence 42, Appl1
848	198.5	5.0	223	2	US-09-106-468-9	Sequence 9, Appl1	921	192.5	4.9	225	1	US-08-557-146-12	Sequence 12, Appl1
849	198.5	5.0	223	2	US-09-601-318-2	Sequence 2, Appl1	922	192.5	4.9	225	1	US-08-557-146-12	Sequence 12, Appl1
850	198.5	5.0	223	2	US-09-601-318-2	Sequence 2, Appl1	923	192.5	4.9	276	2	US-09-856-320A-4	Sequence 4, Appl1
851	198.5	5.0	229	2	US-09-120-582-2	Sequence 2, Appl1	924	192.5	4.9	281	1	US-08-467-155A-7	Sequence 7, Appl1
852	198.5	5.0	229	2	US-08-978-404B-45	Sequence 45, Appl1	925	192.5	4.9	281	1	US-08-628-198-7	Sequence 7, Appl1
853	198.5	5.0	849	2	US-09-949-016-10271	Sequence 10271, A	926	192.5	4.9	281	2	US-09-201-038-7	Sequence 7, Appl1
854	198.5	5.0	221	2	US-08-944-483-57	Sequence 57, Appl1	927	192.5	4.9	281	3	US-10-021-368-7	Sequence 7, Appl1
855	197.5	5.0	221	2	US-08-944-483-54	Sequence 54, Appl1	928	192.5	4.9	281	5	PCT-US86-07343-7	Sequence 7, Appl1
856	197.5	5.0	222	1	US-08-456-840-46	Sequence 46, Appl1	929	192	4.9	149	2	US-09-518-046-20	Sequence 20, Appl1
857	197.5	5.0	222	1	US-08-466-407A-46	Sequence 46, Appl1	930	192	4.9	149	2	US-09-518-046-20	Sequence 20, Appl1
858	197.5	5.0	222	1	US-08-892-544-46	Sequence 46, Appl1	931	191.5	4.9	221	2	US-09-959-392-33	Sequence 33, Appl1
859	197.5	5.0	248	2	US-10-012-231A-194	Sequence 194, App	932	191.5	4.9	221	2	US-09-959-392-33	Sequence 33, Appl1
860	197.5	5.0	248	2	US-10-012-231A-194	Sequence 194, App	933	191.5	4.9	224	2	US-08-944-483-36	Sequence 36, Appl1
861	197.5	5.0	248	2	US-10-006-768A-194	Sequence 194, App	934	191.5	4.9	224	2	US-08-944-483-36	Sequence 36, Appl1
862	197.5	5.0	248	2	US-10-015-671A-194	Sequence 194, App	935	191.5	4.9	225	1	US-09-027-337-5	Sequence 5, Appl1
863	197.5	5.0	248	2	US-10-011-833A-194	Sequence 194, App	936	191.5	4.9	225	2	US-09-644-600A-5	Sequence 5, Appl1
864	197.5	5.0	248	2	US-10-011-833A-194	Sequence 194, App	937	191.5	4.9	225	2	US-09-644-600A-5	Sequence 5, Appl1
865	197.5	5.0	248	2	US-10-006-041A-194	Sequence 194, App	938	191.5	4.9	225	2	US-09-421-213-5	Sequence 5, Appl1
866	197.5	5.0	248	2	US-10-012-064A-194	Sequence 194, App	939	191.5	4.9	233	2	US-09-636-382A-24	Sequence 24, Appl1
867	197.5	5.0	248	2	US-10-015-192A-194	Sequence 194, App	940	191.5	4.9	247	3	US-09-936-271C-82	Sequence 82, Appl1
868	197.5	5.0	248	3	US-10-011-795A-194	Sequence 194, App	941	191.5	4.9	579	2	US-10-094-744-1884	Sequence 1884, Ap
869	197.5	5.0	248	3	US-09-936-271C-60	Sequence 60, Appl1	942	191.5	4.9	830	1	US-08-110-158-4	Sequence 4, Appl1
870	197.5	5.0	248	3	US-10-012-121A-194	Sequence 194, App	943	191	4.8	250	7	5223425-4	Patent No. 5223425
871	197.5	5.0	248	3	US-10-015-186A-194	Sequence 194, App	944	191	4.8	254	2	US-09-439-311-525	Sequence 525, App
872	197.5	5.0	248	3	US-10-006-485A-194	Sequence 194, App	945	191	4.8	254	2	US-09-636-215-525	Sequence 525, App
873	197.5	5.0	248	3	US-10-006-485A-194	Sequence 194, App	946	191	4.8	254	2	US-09-685-166A-525	Sequence 525, App
874	197.5	5.0	248	3	US-10-012-752A-194	Sequence 194, App	947	191	4.8	254	2	US-09-679-426-525	Sequence 525, App
875	197.5	5.0	248	3	US-10-017-253A-194	Sequence 194, App	948	191	4.8	254	2	US-09-759-144-525	Sequence 525, App
876	197.5	5.0	248	3	US-10-015-519A-194	Sequence 194, App	949	191	4.8	254	2	US-09-651-236-525	Sequence 525, App
877	197.5	5.0	248	3	US-10-015-519A-194	Sequence 194, App	950	191	4.8	254	2	US-09-657-279-525	Sequence 525, App
878	197.5	5.0	248	3	US-10-007-236A-194	Sequence 194, App	951	191	4.8	254	2	US-10-012-896-525	Sequence 525, App
879	197.5	5.0	338	2	US-08-991-761A-10	Sequence 10, Appl	952	191	4.8	254	3	US-09-936-271C-3	Sequence 3, Appl1
880	196.5	5.0	241	2	US-08-944-483-60	Sequence 60, Appl	953	191	4.8	254	3	US-09-936-271C-3	Sequence 3, Appl1
881	196.5	5.0	241	2	US-08-944-483-71	Sequence 71, Appl	954	191	4.8	455	2	US-10-144-678A-525	Sequence 525, App
882	196.5	5.0	300	1	US-08-148-910-1	Sequence 1, Appl1	955	190.5	4.8	251	3	US-09-621-416-2	Sequence 2, Appl1
883	196.5	5.0	300	1	US-08-448-937A-1	Sequence 1, Appl1	956	190.5	4.8	251	3	US-09-936-271C-77	Sequence 77, Appl1
884	196.5	5.0	360	3	US-10-162-335-16	Sequence 16, Appl	957	190	4.8	253	2	US-10-202-676-4	Sequence 4, Appl1
885	196.5	5.0	2523	2	US-08-185-432-18	Sequence 18, Appl	958	189.5	4.8	254	3	US-09-936-271C-81	Sequence 81, Appl
886	196.5	5.0	2523	2	US-08-899-232-3	Sequence 3, Appl1	959	189.5	4.8	284	2	US-09-386-642-54	Sequence 54, Appl1
887	196.5	5.0	2523	2	US-09-121-457-3	Sequence 45, Appl1	960	189.5	4.8	341	3	US-10-026-606-1	Sequence 1, Appl1
888	196.5	5.0	232	2	US-08-944-483-45	Sequence 45, Appl1	961	189	4.8	220	2	US-09-439-311-327	Sequence 327, App
889	195.5	5.0	241	1	US-08-330-978-4	Sequence 4, Appl1	962	189	4.8	220	2	US-09-352-616A-327	Sequence 327, App
890	195.5	5.0	241	1	US-08-474-042-4	Sequence 4, Appl1	963	189	4.8	220	2	US-09-232-148A-327	Sequence 327, App
891	195.5	5.0	241	1	US-08-484-558-4	Sequence 4, Appl1	964	189	4.8	220	2	US-09-636-215-327	Sequence 327, App
892	195.5	5.0	241	1	US-08-774-592-3	Sequence 3, Appl1	965	189	4.8	220	2	US-09-636-215-327	Sequence 327, App
893	195.5	5.0	241	1	US-08-330-978-3	Sequence 3, Appl1	966	189	4.8	220	2	US-09-688-1166A-327	Sequence 327, App
894	195.5	5.0	254	1	US-08-474-042-3	Sequence 3, Appl1	967	189	4.8	220	2	US-09-688-489-327	Sequence 327, App
895	195.5	5.0	254	1	US-08-484-558-3	Sequence 3, Appl1	968	189	4.8	220	2	US-09-679-426-327	Sequence 327, App
896	195.5	5.0	364	1	US-08-774-592-3	Sequence 3, Appl1	969	189	4.8	220	2	US-09-759-143-327	Sequence 327, App
897	195.5	5.0	364	1	US-08-330-978-1	Sequence 1, Appl1	970	189	4.8	220	2	US-09-651-236-327	Sequence 327, App
898	195.5	5.0	366	1	US-08-474-042-1	Sequence 1, Appl1	971	189	4.8	220	2	US-09-657-279-327	Sequence 327, App
899	195.5	5.0	366	1	US-08-484-558-1	Sequence 1, Appl1	972	189	4.8	220	2	US-10-012-896-327	Sequence 327, App
900	195.5	5.0	306	1	US-08-774-592-1	Sequence 1, Appl1	973	189	4.8	224	2	US-10-144-678A-327	Sequence 327, App
901	195.5	5.0	309	2	US-08-360-101-233	Sequence 233, App	974	189	4.8	225	1	US-08-944-483-33	Sequence 33, Appl
902	195.5	5.0	2471	1	US-08-185-432-16	Sequence 16, Appl	975	189	4.8	225	2	US-09-027-337-4	Sequence 4, Appl1

976	189	4.8	225	2	US-09-654-600A-4	Sequence 4, Appl1	1049	185.5	4.7	256	2	US-09-032-215-27	Sequence 27, Appl1
977	189	4.8	225	3	US-09-421-213-4	Sequence 2, Appl1	1050	185.5	4.7	261	2	US-08-163-919A-2	Sequence 2, Appl1
978	189	4.8	237	3	US-09-936-271C-2	Sequence 2, Appl1	1051	185.5	4.7	261	2	US-08-462-515-2	Sequence 2, Appl1
979	189	4.8	238	7	5223425-5	Patient No. 5223425	1052	185.5	4.7	261	5	PCT-US94-1407-2	Sequence 2, Appl1
980	189	4.8	253	1	US-08-557-146-2	Sequence 2, Appl1	1053	185.5	4.7	306	2	US-09-386-642-53	Sequence 53, Appl1
981	189	4.8	253	1	US-08-824-874-3	Sequence 3, Appl1	1054	185.5	4.7	711	1	US-08-184-012C-8	Sequence 8, Appl1
982	189	4.8	253	1	US-09-154-344-2	Sequence 2, Appl1	1055	185.5	4.7	711	1	US-08-334-177-2	Sequence 2, Appl1
983	189	4.8	253	2	US-08-930-188-2	Sequence 2, Appl1	1056	185.5	4.7	711	1	US-08-666-082B-1	Sequence 1, Appl1
984	189	4.8	253	2	US-09-210-084-3	Sequence 3, Appl1	1057	185.5	4.7	713	5	PCT-US95-13830-2	Sequence 2, Appl1
985	189	4.8	253	2	US-09-764-762-3	Sequence 3, Appl1	1058	185.5	4.7	713	2	US-08-872-855-5	Sequence 5, Appl1
986	189	4.8	253	3	US-10-071-214-2	Sequence 2, Appl1	1059	185	4.7	217	2	US-08-944-483-49	Sequence 49, Appl1
987	189	4.8	253	3	US-10-071-214-8	Sequence 48, Appl1	1060	185	4.7	258	1	US-08-744-026-3	Sequence 3, Appl1
988	189	4.8	253	5	PCT-US96-04294-2	Sequence 2, Appl1	1061	185	4.7	258	1	US-09-102-32-3	Sequence 3, Appl1
989	189	4.8	265	2	US-09-949-016-7716	Sequence 7716, Ap	1062	185	4.7	258	2	US-09-261-767-3	Sequence 3, Appl1
990	189	4.8	312	2	US-09-023-942A-4	Sequence 4, Appl1	1063	185	4.7	314	2	US-09-023-942A-6	Sequence 6, Appl1
991	189	4.8	449	2	US-09-636-215-617	Sequence 617, App	1064	184	4.7	144	2	US-09-618-259-1	Sequence 1, Appl1
992	189	4.8	449	2	US-09-685-166A-617	Sequence 617, App	1065	184	4.7	144	3	US-08-915-659A-1	Sequence 1, Appl1
993	189	4.8	449	2	US-09-679-426-617	Sequence 617, App	1066	184	4.7	314	2	US-09-008-271A-3	Sequence 3, Appl1
994	189	4.8	449	2	US-09-759-143-617	Sequence 617, App	1067	184	4.7	314	2	US-09-907-794A-257	Sequence 257, App
995	189	4.8	449	2	US-09-651-236-617	Sequence 617, App	1068	184	4.7	314	2	US-09-905-125A-257	Sequence 257, App
996	189	4.8	449	2	US-09-657-279-617	Sequence 617, App	1069	184	4.7	314	2	US-09-902-775A-257	Sequence 257, App
997	189	4.8	449	2	US-10-012-896-617	Sequence 617, App	1070	184	4.7	314	2	US-09-906-700-257	Sequence 257, App
998	189	4.8	449	3	US-10-144-678A-617	Sequence 617, App	1071	184	4.7	314	2	US-09-903-603A-257	Sequence 257, App
999	189	4.8	585	3	US-10-144-678A-1020	Sequence 1020, Ap	1072	184	4.7	314	2	US-09-904-920A-257	Sequence 257, App
1000	188.5	4.8	290	2	US-09-386-653A-7	Sequence 7, Appl1	1073	184	4.7	314	2	US-09-909-064-257	Sequence 257, App
1001	188.5	4.8	290	2	US-10-040-655-7	Sequence 7, Appl1	1074	184	4.7	314	2	US-09-905-618A-257	Sequence 257, App
1002	188.5	4.8	290	2	US-10-041-054-7	Sequence 7, Appl1	1075	184	4.7	314	2	US-09-906-618-257	Sequence 257, App
1003	188	4.8	228	2	US-09-821-255-2	Sequence 2, Appl1	1076	184	4.7	314	2	US-09-906-646-257	Sequence 257, App
1004	188	4.8	248	1	US-08-744-026-1	Sequence 1, Appl1	1077	184	4.7	314	2	US-09-968-615-3	Sequence 3, Appl1
1005	188	4.8	248	1	US-09-102-732-1	Sequence 1, Appl1	1078	184	4.7	314	2	US-09-904-462-257	Sequence 257, App
1006	188	4.8	248	2	US-09-261-767-1	Sequence 1, Appl1	1079	184	4.7	314	2	US-09-902-736A-257	Sequence 257, App
1007	188	4.8	249	3	US-09-936-271C-68	Sequence 68, Appl1	1080	184	4.7	314	2	US-09-906-722A-257	Sequence 257, App
1008	188	4.8	254	2	US-10-202-676-2	Sequence 2, Appl1	1081	184	4.7	314	2	US-09-905-449-257	Sequence 257, App
1009	188	4.8	254	2	US-09-439-313-523	Sequence 523, App	1082	184	4.7	314	2	US-09-903-652B-257	Sequence 257, App
1010	188	4.8	254	2	US-09-636-215-523	Sequence 523, App	1083	184	4.7	314	2	US-09-906-679A-257	Sequence 257, App
1011	188	4.8	254	2	US-09-685-166A-523	Sequence 523, App	1084	184	4.7	314	3	US-09-907-841-257	Sequence 257, App
1012	188	4.8	254	2	US-09-679-426-523	Sequence 523, App	1085	183.5	4.7	502	2	US-10-099-322-140	Sequence 140, App
1013	188	4.8	254	2	US-09-759-143-523	Sequence 523, App	1086	183.5	4.7	512	2	US-10-044-564-140	Sequence 2, Appl1
1014	188	4.8	254	2	US-09-651-236-523	Sequence 523, App	1087	183.5	4.7	711	1	US-08-766-882-2	Sequence 2, Appl1
1015	188	4.8	254	2	US-09-657-279-523	Sequence 523, App	1088	183.5	4.7	711	2	US-09-296-619-2	Sequence 2, Appl1
1016	188	4.8	254	3	US-10-012-896-523	Sequence 523, App	1089	183.5	4.7	711	2	US-09-600-991-20	Sequence 20, Appl1
1017	188	4.8	254	3	US-10-144-678A-523	Sequence 523, App	1090	183.5	4.7	711	2	US-09-601-940A-12	Sequence 12, Appl1
1018	188	4.8	263	1	US-08-790-137-4	Sequence 4, Appl1	1091	183.5	4.7	711	2	US-09-949-016-6981	Sequence 6981, Ap
1019	188	4.8	263	1	US-08-824-874-5	Sequence 5, Appl1	1092	183.5	4.7	722	2	US-08-981-192-12	Sequence 12, Appl1
1020	188	4.8	263	2	US-08-807-151-5	Sequence 5, Appl1	1093	183.5	4.7	722	2	US-09-908-122-12	Sequence 12, Appl1
1021	188	4.8	263	2	US-09-210-084-5	Sequence 5, Appl1	1094	183	4.6	418	2	US-10-177-661-6	Sequence 6, Appl1
1022	188	4.8	263	2	US-09-478-957-5	Sequence 5, Appl1	1095	182.5	4.6	258	2	US-09-023-942A-8	Sequence 8, Appl1
1023	188	4.8	333	2	US-09-764-762-5	Sequence 8, Appl1	1096	182.5	4.6	484	1	US-08-252-193C-9	Sequence 9, Appl1
1024	188	4.8	333	2	US-08-991-761A-8	Sequence 8, Appl1	1097	182.5	4.6	484	2	US-09-276-197-9	Sequence 9, Appl1
1025	187.5	4.8	224	2	US-08-944-483-35	Sequence 35, Appl1	1098	182.5	4.6	750	2	US-08-872-855-4	Sequence 4, Appl1
1026	187.5	4.8	224	2	US-08-944-483-35	Sequence 35, Appl1	1099	182.5	4.6	722	2	US-09-310-685-14	Sequence 14, Appl1
1027	187.5	4.8	255	2	US-08-966-769-83	Sequence 83, Appl1	1100	182	4.6	405	2	US-09-734-675-2	Sequence 2, Appl1
1028	187.5	4.8	255	2	US-08-906-616-83	Sequence 83, Appl1	1101	182	4.6	721	2	US-10-060-333-2	Sequence 2, Appl1
1029	187.5	4.8	255	2	US-08-817-795-83	Sequence 83, Appl1	1102	182	4.6	405	2	US-08-872-855-7	Sequence 7, Appl1
1030	187.5	4.8	255	2	US-08-639-075A-83	Sequence 83, Appl1	1103	182	4.6	1055	2	US-09-214-728-2	Sequence 2, Appl1
1031	187.5	4.8	255	2	US-09-012-431-83	Sequence 83, Appl1	1104	182	4.6	1055	2	US-09-855-722-2	Sequence 2, Appl1
1032	187.5	4.8	255	2	US-09-012-692-83	Sequence 83, Appl1	1105	182	4.6	1065	1	US-08-400-159-8	Sequence 8, Appl1
1033	187.5	4.8	255	2	US-08-906-613-83	Sequence 83, Appl1	1106	182	4.6	1212	2	US-09-214-728-3	Sequence 3, Appl1
1034	187.5	4.8	255	5	PCT-US95-14442A-83	Sequence 83, Appl1	1107	182	4.6	1212	2	US-09-855-722-3	Sequence 3, Appl1
1035	187	4.7	296	3	US-09-936-271C-22	Sequence 22, Appl1	1108	182	4.6	1238	2	US-09-214-728-5	Sequence 5, Appl1
1036	187	4.7	693	3	US-10-297-895A-20	Sequence 20, Appl1	1109	182	4.6	1238	2	US-09-855-722-5	Sequence 5, Appl1
1037	187	4.7	1004	2	US-10-114-270-32	Sequence 32, Appl1	1110	182	4.6	1257	2	US-08-611-129A-8	Sequence 8, Appl1
1038	186	4.7	110	2	US-09-341-461-38	Sequence 38, Appl1	1111	182	4.6	1257	2	US-09-195-524-8	Sequence 8, Appl1
1039	186	4.7	230	1	US-08-456-840-47	Sequence 47, Appl1	1112	182	4.6	1257	2	US-09-310-685-6	Sequence 6, Appl1
1040	186	4.7	230	1	US-08-266-407A-47	Sequence 47, Appl1	1113	181.5	4.6	258	1	US-07-990-301A-2	Sequence 2, Appl1
1041	186	4.7	230	1	US-08-892-544-47	Sequence 47, Appl1	1114	181.5	4.6	258	1	US-08-467-155A-8	Sequence 8, Appl1
1042	186	4.7	230	1	US-08-766-982-12	Sequence 12, Appl1	1115	181.5	4.6	299	1	US-08-628-198-8	Sequence 8, Appl1
1043	186	4.7	230	2	US-08-944-483-53	Sequence 53, Appl1	1116	181.5	4.6	299	2	US-09-201-038-8	Sequence 8, Appl1
1044	186	4.7	230	2	US-09-296-219-12	Sequence 12, Appl1	1117	181.5	4.6	299	3	US-10-021-368-8	Sequence 8, Appl1
1045	186	4.7	232	1	US-08-897-340-31	Sequence 31, Appl1	1118	181.5	4.6	299	5	PCT-US96-07343-8	Sequence 8, Appl1
1046	186	4.7	232	2	US-09-252-329-31	Sequence 31, Appl1	1119	181	4.6	257	3	US-09-936-271C-87	Sequence 87, Appl1
1047	186	4.7	326	2	US-09-411-977-3	Sequence 3, Appl1	1120	181	4.6	396	2	US-09-800-729-86	Sequence 86, Appl1
1048	186	4.7	326	2	US-10-057-951-3	Sequence 3, Appl1	1121	180	4.6	249	3	US-10-071-214-47	Sequence 47, Appl1

1122	180	4.6	254	2	US-09-949-016-6948	Sequence 6948, App	1195	176.5	4.5	909	2	US-09-439-711C-10	Sequence 10, App1
1123	180	4.6	254	3	US-09-936-271C-59	Sequence 59, App1	1196	176.5	4.5	914	2	US-08-936-135-12	Sequence 12, App1
1124	180	4.6	260	7	5223425-10	Patent No. 5223425	1197	176.5	4.5	914	2	US-09-439-711C-12	Sequence 12, App1
1125	179.5	4.6	205	2	US-09-020-956-176	Sequence 176, App	1198	176.5	4.5	925	2	US-09-116-473-2	Sequence 2, App1
1126	179.5	4.6	205	2	US-09-030-607-176	Sequence 176, App	1199	176.5	4.5	925	2	US-08-936-135-14	Sequence 14, App1
1127	179.5	4.6	205	2	US-09-439-313-176	Sequence 176, App	1200	176.5	4.5	926	2	US-09-439-711C-11	Sequence 11, App1
1128	179.5	4.6	205	2	US-09-352-616A-176	Sequence 176, App	1201	176.5	4.5	931	2	US-08-936-135-16	Sequence 16, App1
1129	179.5	4.6	205	2	US-09-232-149A-176	Sequence 176, App	1202	176.5	4.5	931	2	US-09-439-711C-16	Sequence 16, App1
1130	179.5	4.6	205	2	US-09-159-812-176	Sequence 176, App	1203	176.5	4.5	931	2	US-09-004-731-27	Sequence 27, App1
1131	179.5	4.6	205	2	US-09-636-215-176	Sequence 176, App	1204	176	4.5	233	2	US-08-749-699-27	Sequence 27, App1
1132	179.5	4.6	205	2	US-09-685-166A-176	Sequence 176, App	1205	176	4.5	232	2	US-09-004-729-27	Sequence 27, App1
1133	179.5	4.6	205	2	US-09-115-453-176	Sequence 176, App	1206	176	4.5	242	2	US-08-944-483-58	Sequence 58, App1
1134	179.5	4.6	205	2	US-09-688-489-176	Sequence 176, App	1207	176	4.5	266	2	US-09-004-731-24	Sequence 24, App1
1135	179.5	4.6	205	2	US-09-679-426-176	Sequence 176, App	1208	176	4.5	266	2	US-08-749-699-24	Sequence 24, App1
1136	179.5	4.6	205	2	US-09-759-143-176	Sequence 176, App	1209	176	4.5	266	2	US-09-004-729-24	Sequence 24, App1
1137	179.5	4.6	205	2	US-08-651-236-176	Sequence 176, App	1210	175.5	4.4	243	3	US-09-004-729-24	Sequence 24, App1
1138	179.5	4.6	205	2	US-09-030-606-176	Sequence 176, App	1211	175.5	4.4	921	2	US-10-071-214-46	Sequence 46, App1
1139	179.5	4.6	205	2	US-09-657-279-176	Sequence 176, App	1212	175	4.4	112	2	US-09-439-711C-4	Sequence 4, App1
1140	179.5	4.6	205	2	US-10-012-896-176	Sequence 176, App	1213	175	4.4	909	2	US-08-936-135-18	Sequence 18, App1
1141	179.5	4.6	205	3	US-09-116-134-176	Sequence 176, App	1214	175	4.4	909	2	US-09-439-711C-18	Sequence 18, App1
1142	179.5	4.6	250	3	US-10-144-678A-176	Sequence 176, App	1215	175	4.4	926	2	US-08-936-135-20	Sequence 20, App1
1143	179.5	4.6	250	3	US-09-936-271C-23	Sequence 23, App	1216	175	4.4	926	2	US-09-439-711C-20	Sequence 20, App1
1144	179.5	4.6	259	7	5223425-2	Patent No. 5223425	1217	175	4.4	931	2	US-09-583-638-4	Sequence 4, App1
1145	179.5	4.6	728	2	US-08-981-392-2	Sequence 2, App1	1218	174	4.4	265	1	US-08-177-109A-57	Sequence 57, App1
1146	179.5	4.6	728	2	US-09-908-322-2	Sequence 2, App1	1219	174	4.4	265	1	US-08-687-706-57	Sequence 57, App1
1147	179.5	4.6	728	2	US-09-310-685-11	Sequence 11, App1	1220	174	4.4	266	1	US-08-687-155A-9	Sequence 9, App1
1148	179.5	4.6	830	5	PCT-US91-05059-2	Sequence 2, App1	1221	174	4.4	286	1	US-08-628-138-9	Sequence 9, App1
1149	179	4.5	220	1	US-08-379-621-2	Sequence 2, App1	1222	174	4.4	286	1	US-09-201-038-9	Sequence 9, App1
1150	179	4.5	220	1	US-08-147-000B-2	Sequence 2, App1	1223	174	4.4	286	3	US-10-021-368-9	Sequence 9, App1
1151	179	4.5	230	1	US-08-889-078-2	Sequence 2, App1	1224	174	4.4	286	3	PCT-US96-07343-9	Sequence 9, App1
1152	179	4.5	253	2	US-09-578-303-4	Sequence 4, App1	1225	173.5	4.4	220	2	US-10-360-101-222	Sequence 22, App
1153	179	4.5	384	2	US-09-032-215-22	Sequence 22, App1	1226	173.5	4.4	294	2	US-09-800-729-146	Sequence 146, App
1154	178.5	4.5	350	2	US-08-944-483-68	Sequence 68, App1	1227	173.5	4.4	414	2	US-09-670-767-46426	Sequence 46426, A
1155	178.5	4.5	315	2	US-09-386-653A-9	Sequence 9, App1	1228	173.5	4.4	717	2	US-08-872-855-9	Sequence 9, App1
1156	178.5	4.5	315	2	US-10-040-655-9	Sequence 9, App1	1229	173.5	4.4	414	2	US-09-320-731-25	Sequence 25, App1
1157	178.5	4.5	401	1	US-10-041-054-9	Sequence 9, App1	1230	173	4.4	211	2	US-09-242-999-20	Sequence 20, App1
1158	178.5	4.5	468	1	US-08-839-008-5	Sequence 9, App1	1231	172.5	4.4	449	1	US-08-839-008-2	Sequence 2, App1
1159	178.5	4.5	468	2	US-09-032-523-8	Sequence 8, App1	1232	172.5	4.4	449	1	US-09-819-497-89	Sequence 89, App1
1160	178.5	4.5	468	2	US-08-802-633-8	Sequence 8, App1	1233	172.5	4.4	458	2	US-09-949-016-7328	Sequence 7238, App
1161	178.5	4.5	468	2	US-09-802-633-8	Sequence 8, App1	1234	172.5	4.4	449	2	US-09-819-497-89	Sequence 89, App1
1162	178.5	4.5	922	2	US-09-116-473-4	Sequence 4, App1	1235	172.5	4.4	571	2	US-10-017-189-132	Sequence 132, App
1163	178.5	4.5	923	2	US-08-936-135-6	Sequence 6, App1	1236	172.5	4.4	571	3	US-10-145-129A-132	Sequence 132, App
1164	178.5	4.5	923	2	US-09-439-711C-6	Sequence 6, App1	1237	172.5	4.4	571	2	US-10-013-929A-132	Sequence 132, App
1165	177.5	4.5	248	1	US-08-851-974-3	Sequence 3, App1	1238	172.5	4.4	571	2	US-10-013-917A-132	Sequence 132, App
1166	177.5	4.5	248	1	US-09-213-390-3	Sequence 3, App1	1239	172.5	4.4	571	2	US-08-882-046-6	Sequence 132, App
1167	177.5	4.5	1964	2	US-09-467-997-1	Sequence 7, App1	1240	172.5	4.4	1248	2	US-09-566-047-6	Sequence 6, App1
1168	177.5	4.5	102	2	US-09-374-135-7	Sequence 7, App1	1241	172.5	4.4	250	2	US-09-270-767-43564	Sequence 43564, A
1169	177	4.5	110	2	US-09-341-461-29	Sequence 29, App1	1242	172.5	4.4	357	2	US-09-270-767-43564	Sequence 43564, A
1170	177	4.5	112	3	US-09-410-362F-27	Sequence 27, App1	1243	172.5	4.4	721	2	US-09-881-392-5	Sequence 85, App1
1171	177	4.5	223	2	US-09-270-767-45768	Sequence 45768, A	1244	172.5	4.4	259	2	US-08-944-483-39	Sequence 39, App1
1172	177	4.5	240	1	US-08-278-091-11	Sequence 11, App1	1245	172	4.4	259	2	US-08-906-769-190	Sequence 190, App
1173	177	4.5	240	1	US-08-463-859-11	Sequence 11, App1	1246	172	4.4	259	2	US-08-906-616-190	Sequence 190, App
1174	177	4.5	240	1	US-08-472-173-11	Sequence 11, App1	1247	172	4.4	259	2	US-08-639-075A-190	Sequence 190, App
1175	177	4.5	240	1	US-08-487-167-11	Sequence 11, App1	1248	172	4.4	259	2	US-09-012-431-190	Sequence 85, App1
1176	177	4.5	240	1	US-08-482-816-11	Sequence 11, App1	1249	172	4.4	259	2	US-09-012-431-190	Sequence 85, App1
1177	177	4.5	240	1	US-08-286-149-11	Sequence 11, App1	1250	171.5	4.3	259	2	US-08-749-699-85	Sequence 85, App1
1178	177	4.5	240	1	US-08-801-499-11	Sequence 11, App1	1251	171.5	4.3	259	2	US-09-012-692-190	Sequence 190, App
1179	177	4.5	240	1	US-08-615-271-11	Sequence 11, App1	1252	171.5	4.3	259	2	US-08-004-731-85	Sequence 85, App1
1180	177	4.5	240	1	US-09-074-660-11	Sequence 11, App1	1253	171.5	4.3	259	2	US-08-749-699-85	Sequence 85, App1
1181	177	4.5	240	1	US-09-074-659-11	Sequence 11, App1	1254	171.5	4.3	259	2	US-09-012-692-190	Sequence 190, App
1182	177	4.5	240	2	US-09-106-658-11	Sequence 11, App1	1255	171.5	4.3	259	2	US-08-004-731-85	Sequence 85, App1
1183	177	4.5	240	2	US-09-106-658-11	Sequence 11, App1	1256	171.5	4.3	259	2	US-08-749-699-85	Sequence 85, App1
1184	177	4.5	240	2	US-09-106-658-11	Sequence 11, App1	1257	171.5	4.3	259	2	US-09-012-692-190	Sequence 190, App
1185	177	4.5	729	2	US-08-106-467-11	Sequence 11, App1	1258	171.5	4.3	259	2	US-08-004-731-85	Sequence 85, App1
1186	177	4.5	830	7	US-08-872-855-8	Patent No. 5378464-2	1259	171.5	4.3	259	2	US-09-004-729-85	Sequence 85, App1
1187	176.5	4.5	232	1	US-07-990-301A-4	Sequence 4, App1	1260	171.5	4.3	262	1	US-08-790-137-1	Sequence 1, App1
1188	176.5	4.5	901	2	US-08-936-135-22	Sequence 22, App1	1261	171.5	4.3	262	1	US-08-790-137-3	Sequence 3, App1
1189	176.5	4.5	901	2	US-09-439-711C-22	Sequence 22, App1	1262	171.5	4.3	262	1	US-08-681-151-4	Sequence 4, App1
1190	176.5	4.5	906	2	US-08-936-135-24	Sequence 24, App1	1263	171.5	4.3	262	1	US-08-824-874-4	Sequence 4, App1
1191	176.5	4.5	906	2	US-09-439-711C-24	Sequence 24, App1	1264	171.5	4.3	262	2	US-08-807-151-4	Sequence 4, App1
1192	176.5	4.5	909	2	US-08-936-135-8	Sequence 8, App1	1265	171.5	4.3	262	2	US-09-210-084-4	Sequence 4, App1
1193	176.5	4.5	909	2	US-08-936-135-10	Sequence 10, App1	1266	171.5	4.3	262	2	US-09-478-957-4	Sequence 4, App1
1194	176.5	4.5	909	2	US-09-439-711C-8	Sequence 8, App1	1267	171.5	4.3	262	2	US-09-764-762-4	Sequence 4, App1

1268	171.5	4.3	262	2	US-09-618-259-9	Sequence 9, Appl1	1341	166	4.2	237	2	US-09-100-264-3	Sequence 3, Appl1
1269	171.5	4.3	666	2	US-09-341-587-1	Sequence 1, Appl1	1342	166	4.2	237	2	US-09-303-339-2	Sequence 2, Appl1
1270	171.5	4.3	1785	2	US-09-341-587-3	Sequence 3, Appl1	1343	166	4.2	237	2	US-08-843-0760-7	Sequence 7, Appl1
1271	171	4.3	256	3	US-09-936-271C-44	Sequence 44, Appl1	1344	166	4.2	237	2	US-09-303-208-1	Sequence 1, Appl1
1272	171	4.3	262	2	US-09-025-059-4	Sequence 4, Appl1	1345	166	4.2	237	2	US-08-944-483-70	Sequence 70, Appl1
1273	171	4.3	262	2	US-09-755-100A-14	Sequence 14, Appl1	1346	166	4.2	237	2	US-09-949-016-110792	Sequence 10792, A
1274	171	4.3	277	3	US-09-936-271C-45	Sequence 45, Appl1	1347	166	4.2	933	3	US-09-439-711C-2	Sequence 2, Appl1
1275	171	4.3	287	2	US-09-270-767-33263	Sequence 33263, A	1348	165.5	4.2	240	1	US-08-472-228A-1	Sequence 2, Appl1
1276	171	4.3	287	2	US-09-270-767-48480	Sequence 48480, A	1349	165.5	4.2	240	1	US-09-146-631-1	Sequence 1, Appl1
1277	171	4.3	290	2	US-09-949-016-8166	Sequence 8166, Ap	1350	165.5	4.2	240	5	PCT-US96-09303-1	Sequence 1, Appl1
1278	171	4.3	717	2	US-09-601-040A-6	Sequence 6, Appl1	1351	165.5	4.2	363	1	US-08-597-545-2	Sequence 2, Appl1
1279	171	4.3	729	2	US-09-601-040A-2	Sequence 2, Appl1	1352	165.5	4.2	363	1	US-08-457-135-2	Sequence 2, Appl1
1280	171	4.3	737	2	US-09-866-028-15	Sequence 15, Appl1	1353	165	4.2	101	1	US-09-374-135-4	Sequence 4, Appl1
1281	171	4.3	737	2	US-09-944-457-15	Sequence 15, Appl1	1354	164	4.2	351	2	US-09-245-041-11	Sequence 11, Appl1
1282	171	4.3	737	2	US-09-945-584-15	Sequence 15, Appl1	1355	164	4.2	351	2	US-09-358-055B-11	Sequence 11, Appl1
1283	171	4.3	737	2	US-09-944-944-15	Sequence 15, Appl1	1356	164	4.2	351	2	US-09-893-238-11	Sequence 11, Appl1
1284	171	4.3	737	2	US-09-945-587-15	Sequence 15, Appl1	1357	164	4.2	812	2	US-09-192-012-9	Sequence 9, Appl1
1285	171	4.3	737	3	US-09-944-884-15	Sequence 15, Appl1	1358	163.5	4.1	267	3	US-10-000-512-4	Sequence 4, Appl1
1286	170	4.3	213	2	US-08-906-769-149	Sequence 149, App	1359	163	4.1	441	2	US-09-949-016-11196	Sequence 11196, A
1287	170	4.3	213	2	US-08-906-616-149	Sequence 149, App	1360	163	4.1	607	2	US-09-907-794B-190	Sequence 190, App
1288	170	4.3	213	2	US-08-639-075A-149	Sequence 149, App	1361	163	4.1	607	2	US-09-905-125A-190	Sequence 190, App
1289	170	4.3	213	2	US-09-012-431-149	Sequence 149, App	1362	163	4.1	607	2	US-09-902-775A-190	Sequence 190, App
1290	170	4.3	213	2	US-09-012-692-149	Sequence 149, App	1363	163	4.1	607	2	US-09-906-700-190	Sequence 190, App
1291	170	4.3	213	2	US-08-906-613-149	Sequence 149, App	1364	163	4.1	607	2	US-09-903-603A-190	Sequence 190, App
1292	170	4.3	717	2	US-09-601-040A-8	Sequence 8, Appl1	1365	163	4.1	607	2	US-09-905-881A-190	Sequence 190, App
1293	170	4.3	729	2	US-09-601-040A-4	Sequence 4, Appl1	1366	163	4.1	607	2	US-09-909-064-190	Sequence 190, App
1294	170	4.3	1148	2	US-08-882-046-4	Sequence 4, Appl1	1367	163	4.1	607	2	US-09-904-820A-190	Sequence 190, App
1295	170	4.3	1148	2	US-09-566-047-4	Sequence 4, Appl1	1368	163	4.1	607	2	US-09-906-618-190	Sequence 190, App
1296	169	4.3	95	2	US-09-374-135-8	Sequence 8, Appl1	1369	163	4.1	607	2	US-09-906-646-190	Sequence 190, App
1297	169	4.3	110	2	US-09-341-461-25	Sequence 25, Appl1	1370	163	4.1	607	2	US-09-904-662-190	Sequence 190, App
1298	169	4.3	237	5	PCT-US94-07329-11	Sequence 11, Appl1	1371	163	4.1	607	2	US-09-902-736A-190	Sequence 190, App
1299	169	4.3	237	5	PCT-US95-06157-1	Sequence 11, Appl1	1372	163	4.1	607	2	US-09-906-722A-190	Sequence 190, App
1300	169	4.3	375	2	US-09-755-100A-11	Sequence 11, Appl1	1373	163	4.1	607	2	US-09-905-449-190	Sequence 190, App
1301	169	4.3	721	2	US-09-310-685-12	Sequence 12, Appl1	1374	163	4.1	607	2	US-09-903-662B-190	Sequence 190, App
1302	169	4.3	869	2	US-10-104-047-2532	Sequence 2532, Ap	1375	163	4.1	607	2	US-09-906-679A-190	Sequence 190, App
1303	169	4.3	222	7	5223425-6	Patent No. 5223425	1376	163	4.1	1290	1	US-08-907-841-190	Sequence 2, Appl1
1304	168.5	4.3	383	2	US-09-142-027A-12	Sequence 12, Appl1	1377	162.5	4.1	251	2	US-08-944-483-28	Sequence 28, Appl1
1305	168.5	4.3	470	2	US-10-915-160-4	Sequence 4, Appl1	1378	161.5	4.1	832	2	US-08-981-392-6	Sequence 6, Appl1
1306	168.5	4.3	245	2	US-08-906-769-121	Sequence 121, App	1379	161.5	4.1	832	2	US-09-908-322-6	Sequence 6, Appl1
1307	168	4.3	245	2	US-08-906-616-121	Sequence 121, App	1380	161.5	4.1	1025	2	US-09-834-309-5	Sequence 5, Appl1
1308	168	4.3	245	2	US-08-639-075A-121	Sequence 121, App	1381	161	4.1	270	2	US-09-949-016-7712	Sequence 7712, Ap
1309	168	4.3	245	2	US-09-012-431-121	Sequence 121, App	1382	161	4.1	293	2	US-09-509-908-2	Sequence 2, Appl1
1310	168	4.3	245	2	US-08-906-613-121	Sequence 121, App	1383	161	4.1	293	2	US-09-991-181-309	Sequence 309, App
1311	168	4.3	245	2	US-10-915-160-6	Sequence 6, Appl1	1384	161	4.1	293	2	US-09-990-444-309	Sequence 309, App
1312	168	4.3	255	3	US-09-936-271C-74	Sequence 74, Appl1	1385	161	4.1	293	2	US-09-987-333-309	Sequence 309, App
1313	167.5	4.2	256	3	US-08-744-026-5	Sequence 5, Appl1	1386	161	4.1	293	2	US-09-989-726-309	Sequence 309, App
1314	167.5	4.2	261	1	US-09-618-259-10	Sequence 10, Appl1	1387	161	4.1	293	2	US-09-989-735-309	Sequence 309, App
1315	167.5	4.2	261	2	US-09-936-271C-78	Sequence 78, Appl1	1388	161	4.1	293	3	US-09-989-293A-309	Sequence 309, App
1316	167.5	4.2	261	2	US-09-936-271C-80	Sequence 80, Appl1	1389	160.5	4.1	263	2	US-09-949-016-10776	Sequence 10776, A
1317	167.5	4.2	262	1	US-09-102-732-4	Sequence 4, Appl1	1390	160.5	4.1	263	2	US-09-992-995A-54	Sequence 54, Appl1
1318	167.5	4.2	262	1	US-09-102-732-4	Sequence 4, Appl1	1391	160.5	4.1	263	2	US-09-992-995B-54	Sequence 54, Appl1
1319	167.5	4.2	261	2	US-09-261-767-5	Sequence 5, Appl1	1392	161	4.1	293	3	US-10-000-986A-54	Sequence 54, Appl1
1320	167.5	4.2	261	2	US-09-261-767-5	Sequence 5, Appl1	1393	160.5	4.1	263	2	US-08-944-483-46	Sequence 46, Appl1
1321	167.5	4.2	261	2	US-09-907-402-1	Sequence 1, Appl1	1394	161	4.1	234	2	US-09-949-016-10712	Sequence 10712, A
1322	167.5	4.2	261	2	US-09-618-259-10	Sequence 10, Appl1	1395	160.5	4.1	268	2	US-09-949-016-1076	Sequence 1076, Appl1
1323	167.5	4.2	261	2	US-09-936-271C-78	Sequence 78, Appl1	1396	160.5	4.1	2871	2	US-08-766-982-11	Sequence 11, Appl1
1324	167.5	4.2	262	1	US-08-744-026-4	Sequence 4, Appl1	1397	160.5	4.1	228	2	US-09-296-619-11	Sequence 11, Appl1
1325	167.5	4.2	262	1	US-09-102-732-4	Sequence 4, Appl1	1398	160.5	4.1	228	2	US-09-296-619-11	Sequence 11, Appl1
1326	167.5	4.2	262	2	US-09-261-767-4	Sequence 4, Appl1	1399	160.5	4.1	276	2	US-09-270-767-32048	Sequence 32048, A
1327	167.5	4.2	262	3	US-09-936-271C-80	Sequence 80, Appl1	1400	160	4.1	276	2	US-09-270-767-47265	Sequence 2, Appl1
1328	167.5	4.2	923	3	US-09-583-638-2	Sequence 2, Appl1	1401	160	4.1	508	2	US-10-915-160-2	Sequence 2, Appl1
1329	167	4.2	103	2	US-09-374-135-5	Sequence 5, Appl1	1402	160	4.1	237	1	US-08-844-024-2	Sequence 2, Appl1
1330	166.5	4.2	520	2	US-09-068-740A-3	Sequence 3, Appl1	1403	160	4.1				
1331	166.5	4.2	702	2	US-09-068-740A-9	Sequence 9, Appl1	1404	160	4.1				
1332	166.5	4.2	723	2	US-09-423-753-27	Sequence 27, Appl1	1405	160	4.1				
1333	166.5	4.2	723	2	US-09-423-753-27	Sequence 27, Appl1	1406	160	4.1				
1334	166.5	4.2	723	3	US-10-241-476-27	Sequence 27, Appl1	1407	160	4.1				
1335	166.5	4.2	723	3	US-10-241-476-27	Sequence 27, Appl1	1408	159.5	4.0				
1336	166	4.2	237	7	US-08-768-859A-1	Sequence 1, Appl1	1409	159.5	4.0				
1337	166	4.2	237	2	US-08-767-820A-1	Sequence 1, Appl1	1410	159.5	4.0				
1338	166	4.2	237	2	US-08-622-046B-7	Sequence 7, Appl1	1411	159.5	4.0				
1339	166	4.2	237	2	US-08-622-046B-7	Sequence 7, Appl1	1412	159.5	4.0				
1340	166	4.2	237	2	US-08-944-483-38	Sequence 38, Appl1	1413	159	4.0				

1414	159	4.0	237	1	US-08-718-547-2
1415	159	4.0	287	3	US-09-936-271C-70
1416	158.5	4.0	287	3	US-09-244-111-2
1417	158.5	4.0	283	2	US-10-012-231A-111
1418	158.5	4.0	283	2	US-10-015-389A-111
1419	158.5	4.0	283	2	US-10-006-768A-111
1420	158.5	4.0	283	2	US-10-015-677A-111
1421	158.5	4.0	283	2	US-10-015-393A-111
1422	158.5	4.0	283	2	US-10-011-833A-111
1423	158.5	4.0	283	2	US-10-006-042A-111
1424	158.5	4.0	283	2	US-10-012-064A-111
1425	158.5	4.0	283	2	US-10-015-392A-111
1426	158.5	4.0	283	3	US-10-011-795E-111
1427	158.5	4.0	283	3	US-10-015-386A-111
1428	158.5	4.0	283	3	US-10-012-121A-111
1429	158.5	4.0	283	3	US-10-006-746A-111
1430	158.5	4.0	283	3	US-10-006-485A-111
1431	158.5	4.0	283	3	US-10-012-752A-111
1432	158.5	4.0	283	3	US-10-017-253A-111
1433	158.5	4.0	283	3	US-10-015-519A-111
1434	158.5	4.0	283	3	US-10-015-715A-111
1435	158.5	4.0	283	3	US-10-007-236A-111
1436	158.5	4.0	385	1	US-08-597-545-1
1437	158.5	4.0	385	1	US-08-457-135-1
1438	158.5	4.0	385	2	US-09-142-027A-10
1439	158.5	4.0	833	1	US-08-264-53A-6
1440	158.5	4.0	833	1	US-08-465-500-6
1441	158.5	4.0	833	1	US-08-346-126-6
1442	158.5	4.0	833	1	US-08-346-128-6
1443	158.5	4.0	833	1	US-08-532-38A-2
1444	158.5	4.0	833	2	US-08-532-38A-2
1445	158.5	4.0	833	2	US-08-893-828-6
1446	158.5	4.0	833	2	US-09-310-685-2
1447	158	4.0	156	2	US-09-261-416-6
1448	157.5	4.0	190	1	US-08-845-998-4
1449	157.5	4.0	190	2	US-09-206-537-4
1450	157.5	4.0	190	2	US-09-430-854-4
1451	157.5	4.0	226	2	US-09-601-040A-28
1452	157.5	4.0	228	2	US-08-944-483-55
1453	157.5	4.0	255	2	US-08-906-769-91
1454	157.5	4.0	255	2	US-08-906-616-91
1455	157.5	4.0	255	2	US-08-817-795-91
1456	157.5	4.0	255	2	US-08-639-075A-91
1457	157.5	4.0	255	2	US-09-012-431-91
1458	157.5	4.0	255	2	US-09-012-692-91
1459	157.5	4.0	255	2	US-08-906-616-91
1460	157.5	4.0	255	5	PC9-US95-1444A-91
1461	157	4.0	185	2	US-08-906-769-141
1462	157	4.0	185	2	US-08-906-616-141
1463	157	4.0	185	2	US-08-639-075A-141
1464	157	4.0	185	2	US-09-012-431-141
1465	157	4.0	185	2	US-09-012-692-141
1466	157	4.0	185	2	US-08-906-616-141
1467	157	4.0	610	7	5217870-2
1468	157	4.0	647	2	US-09-949-016-1027
1469	156.5	4.0	275	2	US-09-466-778-12
1470	156.5	4.0	312	2	US-09-636-382A-15
1471	156.5	4.0	3635	2	US-09-845-583A-2
1472	156.5	4.0	3635	2	US-10-037-417-47
1473	156.5	4.0	3635	2	US-10-037-182-4
1474	156	4.0	184	3	US-09-936-271C-57
1475	156	4.0	237	2	US-08-768-859A-16
1476	156	4.0	237	2	US-08-768-859A-

[illegible]

1487	156	4.0	238	2	US-08-767-820A-8	Sequence 8, Appl
1488	156	4.0	238	5	PCT-US55-06157-8	Sequence 8, Appl
1489	156	4.0	244	2	US-08-768-859A-10	Sequence 10, Appl
1490	156	4.0	244	2	US-08-767-820A-10	Sequence 10, Appl
1491	156	4.0	244	2	US-08-622-046B-5	Sequence 5, Appl
1492	156	4.0	244	2	US-08-622-046B-16	Sequence 16, Appl
1493	156	4.0	244	2	US-09-100-264-5	Sequence 5, Appl
1494	156	4.0	244	2	US-08-643-076D-5	Sequence 5, Appl
1495	156	4.0	244	5	PCT-US55-06157-10	Sequence 10, Appl
1496	156	4.0	255	3	US-09-936-627C-75	Sequence 75, Appl
1497	156	4.0	261	2	US-08-768-859A-6	Sequence 6, Appl
1498	156	4.0	261	2	US-08-768-859A-19	Sequence 19, Appl
1499	156	4.0	261	2	US-08-767-820A-6	Sequence 6, Appl
1500	156	4.0	261	2	US-08-767-820A-19	Sequence 19, Appl

ALIGNMENTS

```

RESULT 1
US-09-991-181-231
Sequence 231, Application US/09991181
Patent No. 6913919
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Deenoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertlisen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Guirney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C53
CURRENT APPLICATION NUMBER: US/09/991,181
CURRENT FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28

```


PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09
Query Match 100.0%; Score 3945; DB 2; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MELGCMWQGLTFLQILLISSLPREYVINEACPGAMNIMCECCYDIECVCKPKRE 60
DB 1 MELGCMWQGLTFLQILLISSLPREYVINEACPGAMNIMCECCYDIECVCKPKRE 60
QY 61 VVGSTTPCCNNEECSCLIHPGCTIFENCKSCRNMGSTLDDFVKGFCYACBAGW 120
DB 61 VVGSTTPCCNNEECSCLIHPGCTIFENCKSCRNMGSTLDDFVKGFCYACBAGW 120
QY 121 YGDDCMRCGQVLRAPKQOILLSEYPLNAHCEMTIHAKEFVILQRFVMSLEFDYMCQYD 180
DB 121 YGDDCMRCGQVLRAPKQOILLSEYPLNAHCEMTIHAKEFVILQRFVMSLEFDYMCQYD 180
QY 181 YVEVRDNDNDGQIKRVCNENRPAPIQSTGSSLHVLPHSDGSKNPFDAIYEBITACS 240
DB 181 YVEVRDNDNDGQIKRVCNENRPAPIQSTGSSLHVLPHSDGSKNPFDAIYEBITACS 240
QY 241 SSPCFHDGTCLVDKAGSYKACLAGYTGRCENLLEERNCSDPGPGVNGYQKITGGPGLI 300
DB 241 SSPCFHDGTCLVDKAGSYKACLAGYTGRCENLLEERNCSDPGPGVNGYQKITGGPGLI 300
QY 301 NGRHAKIGTVVSPFNNSYVLSGNEKRTCCQNGEMSGKOPICIKACREPKISDLVRRVL 360
DB 301 NGRHAKIGTVVSPFNNSYVLSGNEKRTCCQNGEMSGKOPICIKACREPKISDLVRRVL 360
QY 361 PMOVQSETEPLHQLYSAESKQKQSAPTKKPALPFBDLPMGQHLTQOYECISPFYR 420
DB 361 PMOVQSETEPLHQLYSAESKQKQSAPTKKPALPFBDLPMGQHLTQOYECISPFYR 420
QY 421 RLSSSRRTCLRTGKMSGRAPSCIPICGKIENITAPKQGRMPQOAIYRTSGVHDSL 480
DB 421 RLSSSRRTCLRTGKMSGRAPSCIPICGKIENITAPKQGRMPQOAIYRTSGVHDSL 480
QY 481 HKGAMFLVCSGALVNEKTVVAAHCVTLGKVTMIKTADLKVYLKGFYRDDDEKTIQS 540
DB 481 HKGAMFLVCSGALVNEKTVVAAHCVTLGKVTMIKTADLKVYLKGFYRDDDEKTIQS 540
QY 541 LQISATILHNPYPIILDADIAIKLIDKARISIRVOPICLAASRDISTFQESHITVAG 600
DB 541 LQISATILHNPYPIILDADIAIKLIDKARISIRVOPICLAASRDISTFQESHITVAG 600
QY 601 MNVLADVRSPGPKNDTLRSGVSVVDSILCEBQEHEDGIPVSTDNMFCAWEPASDI 660
DB 601 MNVLADVRSPGPKNDTLRSGVSVVDSILCEBQEHEDGIPVSTDNMFCAWEPASDI 660
QY 661 CTAEITGIAAVSPFGRASPEPRMIMGLVMSYDKTCSHRLSTFTVLPFKMIERNMK 720
DB 661 CTAEITGIAAVSPFGRASPEPRMIMGLVMSYDKTCSHRLSTFTVLPFKMIERNMK 720

RESULT 2
US-09-990-444-231
Sequence 231, Application US/09990444
Patent No. 6930170
GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gottfredsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C19
CURRENT APPLICATION NUMBER: US/09/990,444
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087609
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087759
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087827
PRIOR FILING DATE: 1998-06-03
PRIOR APPLICATION NUMBER: 60/088021
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088025
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088026
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088028
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088029
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088030
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088033
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088326
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088167
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088202
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088212
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088217
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088655
PRIOR FILING DATE: 1998-06-09
PRIOR APPLICATION NUMBER: 60/088734
PRIOR FILING DATE: 1998-06-10

PRIOR APPLICATION NUMBER: 60/088738
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088742
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088810
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088824
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088826
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088858
 PRIOR FILING DATE: 1998-06-11
 PRIOR APPLICATION NUMBER: 60/088861
 PRIOR FILING DATE: 1998-06-11
 PRIOR APPLICATION NUMBER: 60/088876
 PRIOR FILING DATE: 1998-06-11
 PRIOR APPLICATION NUMBER: 60/089105
 PRIOR FILING DATE: 1998-06-12
 PRIOR APPLICATION NUMBER: 60/089440
 PRIOR FILING DATE: 1998-06-16
 PRIOR APPLICATION NUMBER: 60/089512
 PRIOR FILING DATE: 1998-06-16
 PRIOR APPLICATION NUMBER: 60/089514
 PRIOR FILING DATE: 1998-06-16
 PRIOR APPLICATION NUMBER: 60/089532
 PRIOR FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: 60/089538
 PRIOR FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: 60/089598
 PRIOR FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: 60/089599
 PRIOR FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: 60/089600
 PRIOR FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: 60/089653
 PRIOR FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: 60/089801
 PRIOR FILING DATE: 1998-06-18
 PRIOR APPLICATION NUMBER: 60/089907
 PRIOR FILING DATE: 1998-06-18
 PRIOR APPLICATION NUMBER: 60/089908
 PRIOR FILING DATE: 1998-06-18
 PRIOR APPLICATION NUMBER: 60/089947
 PRIOR FILING DATE: 1998-06-19
 PRIOR APPLICATION NUMBER: 60/089948
 PRIOR FILING DATE: 1998-06-19
 PRIOR APPLICATION NUMBER: 60/089952
 PRIOR FILING DATE: 1998-06-19
 PRIOR APPLICATION NUMBER: 60/090246
 PRIOR FILING DATE: 1998-06-22
 PRIOR APPLICATION NUMBER: 60/090252
 PRIOR FILING DATE: 1998-06-22
 PRIOR APPLICATION NUMBER: 60/090254
 PRIOR FILING DATE: 1998-06-22
 PRIOR APPLICATION NUMBER: 60/090349
 PRIOR FILING DATE: 1998-06-23
 PRIOR APPLICATION NUMBER: 60/090355
 PRIOR FILING DATE: 1998-06-23
 PRIOR APPLICATION NUMBER: 60/090429
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090431
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090435
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090444
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090445
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090472
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090535
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090540

PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090542
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090557
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090676
 PRIOR FILING DATE: 1998-06-25
 PRIOR APPLICATION NUMBER: 60/090678
 PRIOR FILING DATE: 1998-06-25
 PRIOR APPLICATION NUMBER: 60/090690
 PRIOR FILING DATE: 1998-06-25
 PRIOR APPLICATION NUMBER: 60/090694
 PRIOR FILING DATE: 1998-06-25
 PRIOR APPLICATION NUMBER: 60/090695
 PRIOR FILING DATE: 1998-06-25
 PRIOR APPLICATION NUMBER: 60/090696
 PRIOR FILING DATE: 1998-06-25
 PRIOR APPLICATION NUMBER: 60/090662
 PRIOR FILING DATE: 1998-06-26
 PRIOR APPLICATION NUMBER: 60/090863
 PRIOR FILING DATE: 1998-06-26
 PRIOR APPLICATION NUMBER: 60/091360
 PRIOR FILING DATE: 1998-07-01
 PRIOR APPLICATION NUMBER: 60/091478
 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091544
 PRIOR FILING DATE: 1998-07-01
 PRIOR APPLICATION NUMBER: 60/091519
 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091626
 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091633
 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091978
 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/091982
 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/092182
 PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 3945; DB 2; Length 720;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MELGCTWGLTFLQILLSSLPREYTVINEACPGAENIMCECEYQIEVCGRKX 60
 1 MELGCTWGLTFLQILLSSLPREYTVINEACPGAENIMCECEYQIEVCGRKX 60
 61 VVGTTIPCCNENECDSCLHPGCTIFENCKSCRNGSGTLDYFYVGFYCAEGRAG 120
 61 VVGTTIPCCNENECDSCLHPGCTIFENCKSCRNGSGTLDYFYVGFYCAEGRAG 120
 121 YGDDCMRCGQVILAPKQIILLESYPLNAHCWTHAKPGFVQLREFVMSLEFDYMCQYD 180
 121 YGDDCMRCGQVILAPKQIILLESYPLNAHCWTHAKPGFVQLREFVMSLEFDYMCQYD 180
 121 YGDDCMRCGQVILAPKQIILLESYPLNAHCWTHAKPGFVQLREFVMSLEFDYMCQYD 180
 181 YVEVRDGNDRDQGIIRKVCNENEPAPIOSGSSHLVLFHSDGSKNFDGHAHYEETTAGS 240
 181 YVEVRDGNDRDQGIIRKVCNENEPAPIOSGSSHLVLFHSDGSKNFDGHAHYEETTAGS 240
 181 YVEVRDGNDRDQGIIRKVCNENEPAPIOSGSSHLVLFHSDGSKNFDGHAHYEETTAGS 240
 241 SSPCFHGTGCVLAKASYKACLAGYTGRCENLBERNCSDPGGVNGYQKXTGGPGL 300
 241 SSPCFHGTGCVLAKASYKACLAGYTGRCENLBERNCSDPGGVNGYQKXTGGPGL 300
 301 NGRHAKIGTVVSFFCNNSYVLSGNERKTCQONGEMSGKOPICAKAREKISLVARRVYL 360
 301 NGRHAKIGTVVSFFCNNSYVLSGNERKTCQONGEMSGKOPICAKAREKISLVARRVYL 360
 361 PMOVQSHETPLHQLYSAAPSKQKLGAPTKKPLPFGDLPMGYOHLHTQLQYECISPFYR 420
 361 PMOVQSHETPLHQLYSAAPSKQKLGAPTKKPLPFGDLPMGYOHLHTQLQYECISPFYR 420
 421 RLGSSRRTCRLRTKMGSGRAASCTPICGKIENITAPRTQGLRWQAAITKRTSGVHDGSL 480

Db 421 RLGSSRTCLRTGMSGRASCIPICCKIENITAPKTQGLRWPMQAIYRTSGVHDGL 480
Qy 481 HKGAMPLVCSGALVNBRTVVAAHCTYDLKNTMTKTDADLVYLGKFRDDDEXTIOG 540
Db 481 HKGAMPLVCSGALVNBRTVVAAHCTYDLKNTMTKTDADLVYLGKFRDDDEXTIOG 540
Qy 541 LQISAIILHNPYDPIILDADIALIKLDPKARISTRVOPICLASRPDSTSFOESHITVAG 600
Db 541 LQISAIILHNPYDPIILDADIALIKLDPKARISTRVOPICLASRPDSTSFOESHITVAG 600
Qy 601 WNYLADVRSPGFNDLTRSGVSVVDSLLCEQHEDHGIPIVSVTDNMFCASMEPTAPSDI 660
Db 601 WNYLADVRSPGFNDLTRSGVSVVDSLLCEQHEDHGIPIVSVTDNMFCASMEPTAPSDI 660
Qy 661 CTAFETGIAVSPFGRASPEPRWHLMGLVSWSYDKTCSHRLSTAFKTVLFPKMIERNMK 720
Db 661 CTAFETGIAVSPFGRASPEPRWHLMGLVSWSYDKTCSHRLSTAFKTVLFPKMIERNMK 720

RESULT 3
US-09-997-333-231
Sequence 231, Application US/09997333
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tuma, Daniel
APPLICANT: Williams, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PIC27
CURRENT APPLICATION NUMBER: US/09/997,333
PRIOR APPLICATION NUMBER: 2001-11-15
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106

PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087609
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087759
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087827
PRIOR FILING DATE: 1998-06-03
PRIOR APPLICATION NUMBER: 60/088021
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088025
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088026
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088028
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088029
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088030
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088033
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088326
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088167
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088202
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088212
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088217
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088655
PRIOR FILING DATE: 1998-06-09
PRIOR APPLICATION NUMBER: 60/088734
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088738
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088742
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088810
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088824
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088826
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088858
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088861
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088876
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/089105
PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/089440
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089512
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089514
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089532
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089538
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089598
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089599
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089600
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089653
PRIOR FILING DATE: 1998-06-17

```

; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/089907
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/089908
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/089947
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: 60/089948
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: 60/089952
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: 60/090246
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: 60/090252
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: 60/090254
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: 60/090349
; PRIOR FILING DATE: 1998-06-23
; PRIOR APPLICATION NUMBER: 60/090355
; PRIOR FILING DATE: 1998-06-23
; PRIOR APPLICATION NUMBER: 60/090429
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090431
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090435
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090444
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090445
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090472
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090535
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090540
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090542
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090676
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090678
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090690
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090694
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090695
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090696
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090862
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/090863
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982

```

```

; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match      100.0%; Score 3945; DB 2; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  MELGCTWQGLTFLQGLLISLIPREYTVINEACPGAEMNIMCECEYOIECVCPKKE 60
        1  MELGCTWQGLTFLQGLLISLIPREYTVINEACPGAEMNIMCECEYOIECVCPKKE 60
Db      1  MELGCTWQGLTFLQGLLISLIPREYTVINEACPGAEMNIMCECEYOIECVCPKKE 60
Qy      61  VVGYYTIPCCNNEBECDSCLHPGCTTFENCKSCRNKSGTGLDPFYVKGFCACBRAGH 120
        61  VVGYYTIPCCNNEBECDSCLHPGCTTFENCKSCRNKSGTGLDPFYVKGFCACBRAGH 120
Db      61  VVGYYTIPCCNNEBECDSCLHPGCTTFENCKSCRNKSGTGLDPFYVKGFCACBRAGH 120
Qy      121  YGSDCMRCGOVLAAPKQILLESYPUNACCEWTHAKPGFVIOARVVMLSLEFDYMCQVD 180
        121  YGSDCMRCGOVLAAPKQILLESYPUNACCEWTHAKPGFVIOARVVMLSLEFDYMCQVD 180
Db      121  YGSDCMRCGOVLAAPKQILLESYPUNACCEWTHAKPGFVIOARVVMLSLEFDYMCQVD 180
Qy      181  YVEYRDGDNNDGQIIKRVCGNERPAPIOSIGSSLHYLFHSDGSKNFDGFAIYEETIAGS 240
        181  YVEYRDGDNNDGQIIKRVCGNERPAPIOSIGSSLHYLFHSDGSKNFDGFAIYEETIAGS 240
Db      181  YVEYRDGDNNDGQIIKRVCGNERPAPIOSIGSSLHYLFHSDGSKNFDGFAIYEETIAGS 240
Qy      241  SSPCFHDGTCVLDKAGSYKACIAGYTGQRCENLLEBRNCSDBGVNGYQKITGGPGLI 300
        241  SSPCFHDGTCVLDKAGSYKACIAGYTGQRCENLLEBRNCSDBGVNGYQKITGGPGLI 300
Db      241  SSPCFHDGTCVLDKAGSYKACIAGYTGQRCENLLEBRNCSDBGVNGYQKITGGPGLI 300
Qy      301  NGRHAKIGTVVSFFCNNSYVLSGNEKRTCOQNEBWSGKOPICIKACREPKISDLVRRVL 360
        301  NGRHAKIGTVVSFFCNNSYVLSGNEKRTCOQNEBWSGKOPICIKACREPKISDLVRRVL 360
Db      301  NGRHAKIGTVVSFFCNNSYVLSGNEKRTCOQNEBWSGKOPICIKACREPKISDLVRRVL 360
Qy      361  PMQVOSRETPHOLYSASFQKLOSAPTKPPALPMGQDLPMGQHLHTLOLEYCISPPFYR 420
        361  PMQVOSRETPHOLYSASFQKLOSAPTKPPALPMGQDLPMGQHLHTLOLEYCISPPFYR 420
Db      361  PMQVOSRETPHOLYSASFQKLOSAPTKPPALPMGQDLPMGQHLHTLOLEYCISPPFYR 420
Qy      421  RLSSRRRTCLRTKWSGRAPSCIPICGKIENITAPTKOGLRMPWQAAYRTISGVHDGSL 480
        421  RLSSRRRTCLRTKWSGRAPSCIPICGKIENITAPTKOGLRMPWQAAYRTISGVHDGSL 480
Db      421  RLSSRRRTCLRTKWSGRAPSCIPICGKIENITAPTKOGLRMPWQAAYRTISGVHDGSL 480
Qy      481  HKGAMFLVCSGALVNETVVAAHCVTDLGRKVTMKTADIKVYLGKFRYRDDDEKTIOS 540
        481  HKGAMFLVCSGALVNETVVAAHCVTDLGRKVTMKTADIKVYLGKFRYRDDDEKTIOS 540
Db      481  HKGAMFLVCSGALVNETVVAAHCVTDLGRKVTMKTADIKVYLGKFRYRDDDEKTIOS 540
Qy      541  LQISATILHPNYPIILDADIALIKLDPKARISTRVOPICLASRDLSTSFQESHITVAG 600
        541  LQISATILHPNYPIILDADIALIKLDPKARISTRVOPICLASRDLSTSFQESHITVAG 600
Db      541  LQISATILHPNYPIILDADIALIKLDPKARISTRVOPICLASRDLSTSFQESHITVAG 600
Qy      601  MNVLADYRSPGFNDTLRSQVSVVDSLLCEQHEHDGIPVSYTDNMFCASWEPTAPSDI 660
        601  MNVLADYRSPGFNDTLRSQVSVVDSLLCEQHEHDGIPVSYTDNMFCASWEPTAPSDI 660
Db      601  MNVLADYRSPGFNDTLRSQVSVVDSLLCEQHEHDGIPVSYTDNMFCASWEPTAPSDI 660
Qy      661  CTATETGIAAVSPFGRASEPBRWHLGLVWSYDXTCSHRLSTAFKTVLPFKMIERNMK 720
        661  CTATETGIAAVSPFGRASEPBRWHLGLVWSYDXTCSHRLSTAFKTVLPFKMIERNMK 720
Db      661  CTATETGIAAVSPFGRASEPBRWHLGLVWSYDXTCSHRLSTAFKTVLPFKMIERNMK 720

RESULT 4
US-09-992-598-231
; Sequence 231, Application US/09992598
; Patent No. 6956108
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gettitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.

```

APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC20
CURRENT APPLICATION NUMBER: US/09/992,598
PRIOR FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087609
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087759
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087827
PRIOR FILING DATE: 1998-06-03
PRIOR APPLICATION NUMBER: 60/088021
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088025
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088026
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088028
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088029
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088030
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088033
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088326
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088167
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088202
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088212
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088217
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088655
PRIOR FILING DATE: 1998-06-09
PRIOR APPLICATION NUMBER: 60/088734

PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088738
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088742
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088810
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088824
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088826
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088858
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088861
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088876
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/089105
PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/089440
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089512
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089514
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089532
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089538
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089598
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089599
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089600
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089653
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089907
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089908
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089947
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089948
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089952
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/090246
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090252
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090254
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090349
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090355
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090429
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090431
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090435
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090444
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090445
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090472
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090535
PRIOR FILING DATE: 1998-06-24


```
; PRIOR APPLICATION NUMBER: 60/090540
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090542
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090676
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090678
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090690
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090694
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090695
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090696
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090862
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/090863
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09
```

```
Query Match 100.0%; Score 3945; DB 2; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 MELGCMQQLGLTFQLQLISLPREYTYINACGAEENINMCRCCCEYDOIECYCPGRRE 60
DB 1 MELGCMQQLGLTFQLQLISLPREYTYINACGAEENINMCRCCCEYDOIECYCPGRRE 60
QY 61 VVGVTIIPCCRNENECDSCLIHPCGTFIFENCKSGRNGSWGTLDPFYKGFYCAECRAGW 120
DB 61 VVGVTIIPCCRNENECDSCLIHPCGTFIFENCKSGRNGSWGTLDPFYKGFYCAECRAGW 120
QY 121 YGSCCMRGQYLRAPKGQILLESYPLNAHCWTHAKGFYIQLRFVWLSLEFDYMCQYD 180
DB 121 YGSCCMRGQYLRAPKGQILLESYPLNAHCWTHAKGFYIQLRFVWLSLEFDYMCQYD 180
QY 121 YGSCCMRGQYLRAPKGQILLESYPLNAHCWTHAKGFYIQLRFVWLSLEFDYMCQYD 180
DB 121 YGSCCMRGQYLRAPKGQILLESYPLNAHCWTHAKGFYIQLRFVWLSLEFDYMCQYD 180
QY 181 YVEVRDGNRGGQIIKRVCGNERPAPLOSISLSLHVLFHSGSKNPFOSFHAIVEBITACS 240
DB 181 YVEVRDGNRGGQIIKRVCGNERPAPLOSISLSLHVLFHSGSKNPFOSFHAIVEBITACS 240
QY 241 SSPCFHDTCVLDKXGSKYKACLAGYTGRCENILLEENNCSDPGAPVNGYOKITGPGILI 300
DB 241 SSPCFHDTCVLDKXGSKYKACLAGYTGRCENILLEENNCSDPGAPVNGYOKITGPGILI 300
QY 301 NGRRAKIGTVVSPFCNNSYVLSGNEKRTCOONGEMSGKOPICIRAKREPKISDLVRRVVL 360
DB 301 NGRRAKIGTVVSPFCNNSYVLSGNEKRTCOONGEMSGKOPICIRAKREPKISDLVRRVVL 360
QY 361 PMOVOSRRTPLHOLYSAAFSKOKLOSAPTKKRALPFGSLPMGYQHLHQLQYECISPYR 420
DB 361 PMOVOSRRTPLHOLYSAAFSKOKLOSAPTKKRALPFGSLPMGYQHLHQLQYECISPYR 420
```

```
QY 421 RLGSSRRCTLRKMGSGRAPSCIPICGKIENITAPKTQGLRPMQAAIYRRTSGVHDSL 480
DB 421 RLGSSRRCTLRKMGSGRAPSCIPICGKIENITAPKTQGLRPMQAAIYRRTSGVHDSL 480
QY 481 HKGAWFLVCSGALVNRRTVVAAHCTTDLGKTMITADLKVYLGFYRDDDRDEKTIOS 540
DB 481 HKGAWFLVCSGALVNRRTVVAAHCTTDLGKTMITADLKVYLGFYRDDDRDEKTIOS 540
QY 541 LQISATILHPNYPIILLDDIALILKLDKARISTRVQPICLAASRLSTSPQESHITVAG 600
DB 541 LQISATILHPNYPIILLDDIALILKLDKARISTRVQPICLAASRLSTSPQESHITVAG 600
QY 601 MWNLADVRSPGFNDTLRSGVSVSDSLCEEQHEHDGILPVSVYTDNMFCASMEPTAPSDI 660
DB 601 MWNLADVRSPGFNDTLRSGVSVSDSLCEEQHEHDGILPVSVYTDNMFCASMEPTAPSDI 660
QY 661 CTAEITGIIAIVSPFGASPEPRWHLNGLYSWSTDCKSRSLSTAFKVLPEKWIERRNK 720
DB 661 CTAEITGIIAIVSPFGASPEPRWHLNGLYSWSTDCKSRSLSTAFKVLPEKWIERRNK 720
```

RESULT 5

```
US-09-989-735-231
; Sequence 231, Application US/09989735
; Patent No. 6972185
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerlsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Steward, Timothy A.
; APPLICANT: Tuma, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1c61
; CURRENT APPLICATION NUMBER: US/09/989, 735
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
```


;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 3945; DB 2; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 MELGCMWQLGLTFLIQLLLISLPREYVINEACGAEWMNMCRCCEYDQIECCPKRE 60
DB 1 MELGCMWQLGLTFLIQLLLISLPREYVINEACGAEWMNMCRCCEYDQIECCPKRE 60
QY 61 VGGTITPCRNNEECSCLIHPGCTIFENCKSCRNSMGCTLDDFVYKGFYCAECAGW 120
DB 61 VGGTITPCRNNEECSCLIHPGCTIFENCKSCRNSMGCTLDDFVYKGFYCAECAGW 120
QY 121 YGDDCMRCGOVLRAPKQIILLESYPLNAHCMTIHAKEPVYQLRFYMLSLFPDYMCOYD 180
DB 121 YGDDCMRCGOVLRAPKQIILLESYPLNAHCMTIHAKEPVYQLRFYMLSLFPDYMCOYD 180
QY 181 YVEVRDDNBDGQIKKVCNGERAPFIOISGSLHVLPHSDGSKNPFQFAIYEITACS 240
DB 181 YVEVRDDNBDGQIKKVCNGERAPFIOISGSLHVLPHSDGSKNPFQFAIYEITACS 240
QY 241 SSPCFHDTGCVLDKAGSYKACLAGYTGRCENLLEBRNCSDPGAPNGYOKITGGFGLI 300
DB 241 SSPCFHDTGCVLDKAGSYKACLAGYTGRCENLLEBRNCSDPGAPNGYOKITGGFGLI 300
QY 301 NGRHAKITGVVSPFCNNSYVLSGNEKRTCOQNGEMSGKOPICIVACEPKISDLVRRVL 360
DB 301 NGRHAKITGVVSPFCNNSYVLSGNEKRTCOQNGEMSGKOPICIVACEPKISDLVRRVL 360
QY 361 PMOVQSEETPLHOUYSAFSSKQKQSAPTKKPALPFQDLPMGYOHLTQLOECISPYR 420
DB 361 PMOVQSEETPLHOUYSAFSSKQKQSAPTKKPALPFQDLPMGYOHLTQLOECISPYR 420
QY 421 RLGSRRRTCLRTGKMSGRAPSCIPICGKIENITAPKTQGLRMPQAAIYRRTSGVHGSGL 480
DB 421 RLGSRRRTCLRTGKMSGRAPSCIPICGKIENITAPKTQGLRMPQAAIYRRTSGVHGSGL 480
QY 481 HKGMFLVCSGALVNERTVVVAACHCVTDLGKVTMIKTADLKVLGKCYRDDDRDEKTIQS 540
DB 481 HKGMFLVCSGALVNERTVVVAACHCVTDLGKVTMIKTADLKVLGKCYRDDDRDEKTIQS 540
QY 541 LQISAIIHPYVDIILDDADIAIKLIDKARISTRVQPICLAARDLSTSQESHITVAG 600
DB 541 LQISAIIHPYVDIILDDADIAIKLIDKARISTRVQPICLAARDLSTSQESHITVAG 600
QY 601 MNVLADVRSPGFKNDTLRSQVSVVDSLLCEQHEHDGIPVSYDNMFCAWMEPTAPSDI 660
DB 601 MNVLADVRSPGFKNDTLRSQVSVVDSLLCEQHEHDGIPVSYDNMFCAWMEPTAPSDI 660
QY 661 CTAAETGGIAAVSPGRASPPEPRMHLMGVLSWSYDKTCSHRLSTAFTVKLPFKDNIERNMK 720
DB 661 CTAAETGGIAAVSPGRASPPEPRMHLMGVLSWSYDKTCSHRLSTAFTVKLPFKDNIERNMK 720
```

RESULT 6
US-09-989-726-231
; Sequence 231, Application US/09989726
; Patent No. 7018811
; GENERAL INFORMATION:

;; APPLICANT: Ashkenazi, Avi J.
;; APPLICANT: Baker, Kevin P.
;; APPLICANT: Botstein, David
;; APPLICANT: Deenoyers, Luc
;; APPLICANT: Eacon, Dan L.
;; APPLICANT: Ferrara, Napoleone
;; APPLICANT: Fong, Sherman
;; APPLICANT: Gerber, Hanspeter
;; APPLICANT: Gettitsen, Mary E.
;; APPLICANT: Goddard, Audrey

```
;; APPLICANT: Godowski, Paul J.  
;; APPLICANT: Grimaldi, J. Christopher  
;; APPLICANT: Gurney, Austin L.  
;; APPLICANT: Kijavlin, Ivar J.  
;; APPLICANT: Napier, Mary A.  
;; APPLICANT: Pan, James  
;; APPLICANT: Paoni, Nicholas F.  
;; APPLICANT: Roy, Margaret Ann  
;; APPLICANT: Stewart, Timothy A.  
;; APPLICANT: Thomas, Daniel  
;; APPLICANT: Watanabe, Colin K.  
;; APPLICANT: Williams, P. Mickey  
;; APPLICANT: Wood, William I.  
;; APPLICANT: Zhang, Zemin  
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
;; TITLE OF INVENTION: Acids Encoding the Same  
;; FILE REFERENCE: P27301C60  
;; CURRENT APPLICATION NUMBER: US/09/989,726  
;; CURRENT FILING DATE: 2001-11-19  
;; PRIOR APPLICATION NUMBER: 60/049787  
;; PRIOR FILING DATE: 1997-06-16  
;; PRIOR APPLICATION NUMBER: 60/062250  
;; PRIOR FILING DATE: 1997-10-17  
;; PRIOR APPLICATION NUMBER: 60/065186  
;; PRIOR FILING DATE: 1997-11-12  
;; PRIOR APPLICATION NUMBER: 60/065311  
;; PRIOR FILING DATE: 1997-11-13  
;; PRIOR APPLICATION NUMBER: 60/066770  
;; PRIOR FILING DATE: 1997-11-24  
;; PRIOR APPLICATION NUMBER: 60/075945  
;; PRIOR FILING DATE: 1998-02-25  
;; PRIOR APPLICATION NUMBER: 60/078910  
;; PRIOR FILING DATE: 1998-03-20  
;; PRIOR APPLICATION NUMBER: 60/083322  
;; PRIOR FILING DATE: 1998-04-28  
;; PRIOR APPLICATION NUMBER: 60/084600  
;; PRIOR FILING DATE: 1998-05-07  
;; PRIOR APPLICATION NUMBER: 60/087106  
;; PRIOR FILING DATE: 1998-05-28  
;; PRIOR APPLICATION NUMBER: 60/087607  
;; PRIOR FILING DATE: 1998-06-02  
;; PRIOR APPLICATION NUMBER: 60/087609  
;; PRIOR FILING DATE: 1998-06-02  
;; PRIOR APPLICATION NUMBER: 60/087759  
;; PRIOR FILING DATE: 1998-06-02  
;; PRIOR APPLICATION NUMBER: 60/087827  
;; PRIOR FILING DATE: 1998-06-03  
;; PRIOR APPLICATION NUMBER: 60/088021  
;; PRIOR FILING DATE: 1998-06-04  
;; PRIOR APPLICATION NUMBER: 60/088025  
;; PRIOR FILING DATE: 1998-06-04  
;; PRIOR APPLICATION NUMBER: 60/088026  
;; PRIOR FILING DATE: 1998-06-04  
;; PRIOR APPLICATION NUMBER: 60/088028  
;; PRIOR FILING DATE: 1998-06-04  
;; PRIOR APPLICATION NUMBER: 60/088029  
;; PRIOR FILING DATE: 1998-06-04  
;; PRIOR APPLICATION NUMBER: 60/088030  
;; PRIOR FILING DATE: 1998-06-04  
;; PRIOR APPLICATION NUMBER: 60/088033  
;; PRIOR FILING DATE: 1998-06-04  
;; PRIOR APPLICATION NUMBER: 60/088326  
;; PRIOR FILING DATE: 1998-06-04  
;; PRIOR APPLICATION NUMBER: 60/088167  
;; PRIOR FILING DATE: 1998-06-05  
;; PRIOR APPLICATION NUMBER: 60/088202  
;; PRIOR FILING DATE: 1998-06-05  
;; PRIOR APPLICATION NUMBER: 60/088212  
;; PRIOR FILING DATE: 1998-06-05  
;; PRIOR APPLICATION NUMBER: 60/088217  
;; PRIOR FILING DATE: 1998-06-05  
;; PRIOR APPLICATION NUMBER: 60/088655  
;; PRIOR FILING DATE: 1998-06-09
```


QY 421 RLSSRRCTURTGKWSGRAPSCIPICGKINENTAPKTOGLRMPQOAIYRTSGVHDGSL 480
DB 421 RLSSRRCTURTGKWSGRAPSCIPICGKINENTAPKTOGLRMPQOAIYRTSGVHDGSL 480
QY 481 HKGAMFLVCGALVNEKTVVAHCVTDLCKVMTIKTADLKVYLGKPYRDDDEKTIQS 540
DB 481 HKGAMFLVCGALVNEKTVVAHCVTDLCKVMTIKTADLKVYLGKPYRDDDEKTIQS 540
QY 541 LQISATILHNPYDILADIALIKLIDKARISRPVOPICLAASRDLSFQESHITVAG 600
DB 541 LQISATILHNPYDILADIALIKLIDKARISRPVOPICLAASRDLSFQESHITVAG 600
QY 601 MNVLADVRSPGKNDTLRSQVSVVDSLCEBOHEDHGIPIVSYDNMFCSAWEPTASDI 660
DB 601 MNVLADVRSPGKNDTLRSQVSVVDSLCEBOHEDHGIPIVSYDNMFCSAWEPTASDI 660
QY 661 CTMETGCIAAVSPGRASPEPRMHLMGLVMSYDKTCSHRLSTAFYVLPDKMIEHNMK 720
DB 661 CTMETGCIAAVSPGRASPEPRMHLMGLVMSYDKTCSHRLSTAFYVLPDKMIEHNMK 720

RESULT 7
US-09-997-514-231
Sequence 231, Application US/09997514
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertlisen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Thomas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secretd and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC46
CURRENT APPLICATION NUMBER: US/09/997, 514
PRIOR FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600

PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087609
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087759
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087827
PRIOR FILING DATE: 1998-06-03
PRIOR APPLICATION NUMBER: 60/088021
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088025
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088026
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088028
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088029
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088030
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088033
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088326
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088167
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088202
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088212
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088217
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088655
PRIOR FILING DATE: 1998-06-09
PRIOR APPLICATION NUMBER: 60/088734
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088738
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088742
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088810
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088824
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088826
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088858
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088861
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088876
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/089105
PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/089440
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089512
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089514
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089532
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089538
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089598
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089599
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089600
PRIOR FILING DATE: 1998-06-17

; PRIOR APPLICATION NUMBER: 60/089653
 ; PRIOR FILING DATE: 1998-06-17
 ; PRIOR APPLICATION NUMBER: 60/089801
 ; PRIOR FILING DATE: 1998-06-18
 ; PRIOR APPLICATION NUMBER: 60/089907
 ; PRIOR FILING DATE: 1998-06-18
 ; PRIOR APPLICATION NUMBER: 60/089908
 ; PRIOR FILING DATE: 1998-06-18
 ; PRIOR APPLICATION NUMBER: 60/089947
 ; PRIOR FILING DATE: 1998-06-19
 ; PRIOR APPLICATION NUMBER: 60/089948
 ; PRIOR FILING DATE: 1998-06-19
 ; PRIOR APPLICATION NUMBER: 60/089952
 ; PRIOR FILING DATE: 1998-06-19
 ; PRIOR APPLICATION NUMBER: 60/090246
 ; PRIOR FILING DATE: 1998-06-22
 ; PRIOR APPLICATION NUMBER: 60/090252
 ; PRIOR FILING DATE: 1998-06-22
 ; PRIOR APPLICATION NUMBER: 60/090254
 ; PRIOR FILING DATE: 1998-06-22
 ; PRIOR APPLICATION NUMBER: 60/090349
 ; PRIOR FILING DATE: 1998-06-23
 ; PRIOR APPLICATION NUMBER: 60/090355
 ; PRIOR FILING DATE: 1998-06-23
 ; PRIOR APPLICATION NUMBER: 60/090429
 ; PRIOR FILING DATE: 1998-06-24
 ; PRIOR APPLICATION NUMBER: 60/090431
 ; PRIOR FILING DATE: 1998-06-24
 ; PRIOR APPLICATION NUMBER: 60/090435
 ; PRIOR FILING DATE: 1998-06-24
 ; PRIOR APPLICATION NUMBER: 60/090444
 ; PRIOR FILING DATE: 1998-06-24
 ; PRIOR APPLICATION NUMBER: 60/090445
 ; PRIOR FILING DATE: 1998-06-24
 ; PRIOR APPLICATION NUMBER: 60/090472
 ; PRIOR FILING DATE: 1998-06-24
 ; PRIOR APPLICATION NUMBER: 60/090555
 ; PRIOR FILING DATE: 1998-06-24
 ; PRIOR APPLICATION NUMBER: 60/090540
 ; PRIOR FILING DATE: 1998-06-24
 ; PRIOR APPLICATION NUMBER: 60/090542
 ; PRIOR FILING DATE: 1998-06-24
 ; PRIOR APPLICATION NUMBER: 60/090557
 ; PRIOR FILING DATE: 1998-06-24
 ; PRIOR APPLICATION NUMBER: 60/090676
 ; PRIOR FILING DATE: 1998-06-25
 ; PRIOR APPLICATION NUMBER: 60/090678
 ; PRIOR FILING DATE: 1998-06-25
 ; PRIOR APPLICATION NUMBER: 60/090690
 ; PRIOR FILING DATE: 1998-06-25
 ; PRIOR APPLICATION NUMBER: 60/090694
 ; PRIOR FILING DATE: 1998-06-25
 ; PRIOR APPLICATION NUMBER: 60/090695
 ; PRIOR FILING DATE: 1998-06-25
 ; PRIOR APPLICATION NUMBER: 60/090696
 ; PRIOR FILING DATE: 1998-06-25
 ; PRIOR APPLICATION NUMBER: 60/090862
 ; PRIOR FILING DATE: 1998-06-26
 ; PRIOR APPLICATION NUMBER: 60/090863
 ; PRIOR FILING DATE: 1998-06-26
 ; PRIOR APPLICATION NUMBER: 60/091360
 ; PRIOR FILING DATE: 1998-07-01
 ; PRIOR APPLICATION NUMBER: 60/091478
 ; PRIOR FILING DATE: 1998-07-02
 ; PRIOR APPLICATION NUMBER: 60/091544
 ; PRIOR FILING DATE: 1998-07-01
 ; PRIOR APPLICATION NUMBER: 60/091519
 ; PRIOR FILING DATE: 1998-07-02
 ; PRIOR APPLICATION NUMBER: 60/091626
 ; PRIOR FILING DATE: 1998-07-02
 ; PRIOR APPLICATION NUMBER: 60/091633
 ; PRIOR FILING DATE: 1998-07-02
 ; PRIOR APPLICATION NUMBER: 60/091978

; PRIOR FILING DATE: 1998-07-07
 ; PRIOR APPLICATION NUMBER: 60/091982
 ; PRIOR FILING DATE: 1998-07-07
 ; PRIOR APPLICATION NUMBER: 60/092182
 ; PRIOR FILING DATE: 1998-07-09
 Query Match 100.0%; Score 3945; DB 3; Length 720;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MELGCTWQGLTFLQLLISSLPREYTVINEACPGAENWIMCECEYDOIECVGPKKE 60
 DB 1 MELGCTWQGLTFLQLLISSLPREYTVINEACPGAENWIMCECEYDOIECVGPKKE 60
 QY 61 VVGYYTPCCRNENECDSCLHHPCTTFENCKSCRNCSVGTLDFFYKGYCAECRAGM 120
 DB 61 VVGYYTPCCRNENECDSCLHHPCTTFENCKSCRNCSVGTLDFFYKGYCAECRAGM 120
 QY 121 YGDDCMRCGQVLRAPRGQILLESYPINACEWTTHAKPGFVQLRFVMLSLBFDVWCQYD 180
 DB 121 YGDDCMRCGQVLRAPRGQILLESYPINACEWTTHAKPGFVQLRFVMLSLBFDVWCQYD 180
 QY 181 YVEVRDGDNRDQIIRKVCNRPAPRISGSLHVLFFSDSKNPDGFHAHYEETTACS 240
 DB 181 YVEVRDGDNRDQIIRKVCNRPAPRISGSLHVLFFSDSKNPDGFHAHYEETTACS 240
 QY 241 SSPCFHDGTGCVLDKAGSYKACLAGYTGRCENTLEERNCSDPGPFVNGYOKITGGPGLI 300
 DB 241 SSPCFHDGTGCVLDKAGSYKACLAGYTGRCENTLEERNCSDPGPFVNGYOKITGGPGLI 300
 QY 301 NGRHAKIGTVVSFPCNNSVYLSGNEKRTQONGMSGKOPICIKACREKISDLVRRVYL 360
 DB 301 NGRHAKIGTVVSFPCNNSVYLSGNEKRTQONGMSGKOPICIKACREKISDLVRRVYL 360
 QY 361 PMOVOSRETFPLQVLSAARSXOKLOSAPTKKALPPGDDPMGQYOHHTLOJECISPFPR 420
 DB 361 PMOVOSRETFPLQVLSAARSXOKLOSAPTKKALPPGDDPMGQYOHHTLOJECISPFPR 420
 QY 421 RLGSSRRCTLRGTGKMSGRAPCIPICGIENITAPKTQGLRMPWQAIIRRTSGVHDSGL 480
 DB 421 RLGSSRRCTLRGTGKMSGRAPCIPICGIENITAPKTQGLRMPWQAIIRRTSGVHDSGL 480
 QY 481 HXGAWFLVCSGALVNERTVVAACHCTDGLKXTMTALDKVYLGFYHDDDRDEKTIOS 540
 DB 481 HXGAWFLVCSGALVNERTVVAACHCTDGLKXTMTALDKVYLGFYHDDDRDEKTIOS 540
 QY 541 LQISATILHPNDPILDDADIAIILKLDKARISTRVQPICLAASRDLSFSFQESHITTVAG 600
 DB 541 LQISATILHPNDPILDDADIAIILKLDKARISTRVQPICLAASRDLSFSFQESHITTVAG 600
 QY 601 MNVLADVRSPGFNDTLRSGVSVVDSLCEQHEHDGIPVSVTDNMFCASMEPTAPSDI 660
 DB 601 MNVLADVRSPGFNDTLRSGVSVVDSLCEQHEHDGIPVSVTDNMFCASMEPTAPSDI 660
 QY 661 CTAETGCIAAVSFPGASPEPRHMLGLVSWSYDKTCSHRLSTAFKTVLPFDWIERNNK 720
 DB 661 CTAETGCIAAVSFPGASPEPRHMLGLVSWSYDKTCSHRLSTAFKTVLPFDWIERNNK 720
 RESULT 8
 US-09-989-728-231
 ; Sequence 231, Application US/09989728
 ; Patent No. 7029873
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnovers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerlitsen, Mary E.

APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Kijavini, Ivar J.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 FILE REFERENCE: P2730P1C72
 CURRENT APPLICATION NUMBER: US/09/989,728
 PRIOR FILING DATE: 2001-11-20
 PRIOR APPLICATION NUMBER: 60/049787
 PRIOR FILING DATE: 1997-06-16
 PRIOR APPLICATION NUMBER: 60/062250
 PRIOR FILING DATE: 1997-10-17
 PRIOR APPLICATION NUMBER: 60/065186
 PRIOR FILING DATE: 1997-11-12
 PRIOR APPLICATION NUMBER: 60/065311
 PRIOR FILING DATE: 1997-11-13
 PRIOR APPLICATION NUMBER: 60/066770
 PRIOR FILING DATE: 1997-11-24
 PRIOR APPLICATION NUMBER: 60/075945
 PRIOR FILING DATE: 1998-02-25
 PRIOR APPLICATION NUMBER: 60/078910
 PRIOR FILING DATE: 1998-03-20
 PRIOR APPLICATION NUMBER: 60/083322
 PRIOR FILING DATE: 1998-04-28
 PRIOR APPLICATION NUMBER: 60/084600
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/087106
 PRIOR FILING DATE: 1998-05-28
 PRIOR APPLICATION NUMBER: 60/087607
 PRIOR FILING DATE: 1998-06-02
 PRIOR APPLICATION NUMBER: 60/087609
 PRIOR FILING DATE: 1998-06-02
 PRIOR APPLICATION NUMBER: 60/087759
 PRIOR FILING DATE: 1998-06-02
 PRIOR APPLICATION NUMBER: 60/087827
 PRIOR FILING DATE: 1998-06-03
 PRIOR APPLICATION NUMBER: 60/088021
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088025
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088026
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088028
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088029
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088030
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088033
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088326
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088167
 PRIOR FILING DATE: 1998-06-05
 PRIOR APPLICATION NUMBER: 60/088202
 PRIOR FILING DATE: 1998-06-05
 PRIOR APPLICATION NUMBER: 60/088212
 PRIOR FILING DATE: 1998-06-05
 PRIOR APPLICATION NUMBER: 60/088217
 PRIOR FILING DATE: 1998-06-05
 PRIOR APPLICATION NUMBER: 60/088655

PRIOR FILING DATE: 1998-06-09
 PRIOR APPLICATION NUMBER: 60/088724
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088738
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088742
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088810
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088824
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088826
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088858
 PRIOR FILING DATE: 1998-06-11
 PRIOR APPLICATION NUMBER: 60/088861
 PRIOR FILING DATE: 1998-06-11
 PRIOR APPLICATION NUMBER: 60/088876
 PRIOR FILING DATE: 1998-06-11
 PRIOR APPLICATION NUMBER: 60/089105
 PRIOR FILING DATE: 1998-06-12
 PRIOR APPLICATION NUMBER: 60/089440
 PRIOR FILING DATE: 1998-06-16
 PRIOR APPLICATION NUMBER: 60/089512
 PRIOR FILING DATE: 1998-06-16
 PRIOR APPLICATION NUMBER: 60/089514
 PRIOR FILING DATE: 1998-06-16
 PRIOR APPLICATION NUMBER: 60/089532
 PRIOR FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: 60/089538
 PRIOR FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: 60/089598
 PRIOR FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: 60/089599
 PRIOR FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: 60/089600
 PRIOR FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: 60/089653
 PRIOR FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: 60/089801
 PRIOR FILING DATE: 1998-06-18
 PRIOR APPLICATION NUMBER: 60/089907
 PRIOR FILING DATE: 1998-06-18
 PRIOR APPLICATION NUMBER: 60/089908
 PRIOR FILING DATE: 1998-06-18
 PRIOR APPLICATION NUMBER: 60/089947
 PRIOR FILING DATE: 1998-06-19
 PRIOR APPLICATION NUMBER: 60/089948
 PRIOR FILING DATE: 1998-06-19
 PRIOR APPLICATION NUMBER: 60/089952
 PRIOR FILING DATE: 1998-06-19
 PRIOR APPLICATION NUMBER: 60/090246
 PRIOR FILING DATE: 1998-06-22
 PRIOR APPLICATION NUMBER: 60/090252
 PRIOR FILING DATE: 1998-06-22
 PRIOR APPLICATION NUMBER: 60/090254
 PRIOR FILING DATE: 1998-06-22
 PRIOR APPLICATION NUMBER: 60/090349
 PRIOR FILING DATE: 1998-06-23
 PRIOR APPLICATION NUMBER: 60/090355
 PRIOR FILING DATE: 1998-06-23
 PRIOR APPLICATION NUMBER: 60/090429
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090431
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090435
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090444
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090445
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090472
 PRIOR FILING DATE: 1998-06-24

PRIOR APPLICATION NUMBER: 60/090535
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090540
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090542
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090676
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090678
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090690
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090694
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090695
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090696
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090862
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/090863
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 3945; DB 3; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MELGCMTQGLTFLQLLISLIPREYVINEACPGAEWNIIMCECEYDQIECVCPKRE 60
1 MELGCMTQGLTFLQLLISLIPREYVINEACPGAEWNIIMCECEYDQIECVCPKRE 60
DB 1 MELGCMTQGLTFLQLLISLIPREYVINEACPGAEWNIIMCECEYDQIECVCPKRE 60
QY 61 VGGYITPCCNENECDSCLIPHCCTI FENCKSCRNCSWGGLDDFYVKGFTYCAECRAG 120
61 VGGYITPCCNENECDSCLIPHCCTI FENCKSCRNCSWGGLDDFYVKGFTYCAECRAG 120
DB 61 VGGYITPCCNENECDSCLIPHCCTI FENCKSCRNCSWGGLDDFYVKGFTYCAECRAG 120
QY 121 YGGDCMRCGVLAAPKQIILLESYPLNACGEWTHAAGVYIQRFMLSLEPYMCQYD 180
121 YGGDCMRCGVLAAPKQIILLESYPLNACGEWTHAAGVYIQRFMLSLEPYMCQYD 180
DB 121 YGGDCMRCGVLAAPKQIILLESYPLNACGEWTHAAGVYIQRFMLSLEPYMCQYD 180
QY 181 YVEVRDNDNRDGOIKKVCNERNPAPIOSIGSLAHV FHSDDSGNPFDFHAYEETIACS 240
181 YVEVRDNDNRDGOIKKVCNERNPAPIOSIGSLAHV FHSDDSGNPFDFHAYEETIACS 240
DB 181 YVEVRDNDNRDGOIKKVCNERNPAPIOSIGSLAHV FHSDDSGNPFDFHAYEETIACS 240
QY 241 SSPCFHDTGVLVDKAGSYKACLAGYTGORCENLLEERNCSDPGPNVGYOKITGPGGLI 300
241 SSPCFHDTGVLVDKAGSYKACLAGYTGORCENLLEERNCSDPGPNVGYOKITGPGGLI 300
DB 241 SSPCFHDTGVLVDKAGSYKACLAGYTGORCENLLEERNCSDPGPNVGYOKITGPGGLI 300
QY 301 NGRAKIGTVVSPFCNNSYVLSGNEKRTCOONGMWSKOPICIAKCEPKISDLYRRRVL 360
301 NGRAKIGTVVSPFCNNSYVLSGNEKRTCOONGMWSKOPICIAKCEPKISDLYRRRVL 360
DB 301 NGRAKIGTVVSPFCNNSYVLSGNEKRTCOONGMWSKOPICIAKCEPKISDLYRRRVL 360
QY 361 PMQVSRRTPLHQLYSAFSAFKQKQSAPTKKPALPFGDLPMGYOHLHTQOYECISPFYR 420
361 PMQVSRRTPLHQLYSAFSAFKQKQSAPTKKPALPFGDLPMGYOHLHTQOYECISPFYR 420

DB 361 PMQVSRRTPLHQLYSAFSAFKQKQSAPTKKPALPFGDLPMGYOHLHTQOYECISPFYR 420
QY 421 RUGSSRRRTCLRTGKSGRAPSCIPICGKIENITAPPTQGLRMPQAAITRRISGVHDSL 480
421 RUGSSRRRTCLRTGKSGRAPSCIPICGKIENITAPPTQGLRMPQAAITRRISGVHDSL 480
DB 421 RUGSSRRRTCLRTGKSGRAPSCIPICGKIENITAPPTQGLRMPQAAITRRISGVHDSL 480
QY 481 HIGAMFLVCSGALVNERTVVAHAQCTDYGKTYMTKTADLKVVLGKPYRDDDRDEKTIQS 540
481 HIGAMFLVCSGALVNERTVVAHAQCTDYGKTYMTKTADLKVVLGKPYRDDDRDEKTIQS 540
DB 481 HIGAMFLVCSGALVNERTVVAHAQCTDYGKTYMTKTADLKVVLGKPYRDDDRDEKTIQS 540
QY 541 LQISALIHHPNDPILDDADIALKLLDKARISTRVOPICLAASRDLSTFQESHITTVAG 600
541 LQISALIHHPNDPILDDADIALKLLDKARISTRVOPICLAASRDLSTFQESHITTVAG 600
DB 541 LQISALIHHPNDPILDDADIALKLLDKARISTRVOPICLAASRDLSTFQESHITTVAG 600
QY 601 WNYLADVRSPPGRNDTLRSQVSVVDSLLCEQHEHDIIPVSVTDNMFCAWEPFAPSDI 660
601 WNYLADVRSPPGRNDTLRSQVSVVDSLLCEQHEHDIIPVSVTDNMFCAWEPFAPSDI 660
DB 601 WNYLADVRSPPGRNDTLRSQVSVVDSLLCEQHEHDIIPVSVTDNMFCAWEPFAPSDI 660
QY 661 CTAETGCIAAVSPPGASPEPRWHLMLGVSVDKTCSHRLSTAFKVLPPFQDWIERNNK 720
661 CTAETGCIAAVSPPGASPEPRWHLMLGVSVDKTCSHRLSTAFKVLPPFQDWIERNNK 720
DB 661 CTAETGCIAAVSPPGASPEPRWHLMLGVSVDKTCSHRLSTAFKVLPPFQDWIERNNK 720

RESULT 9
US-09-997-349-231
Sequence 231, Application US/09997349
Patent No. 7034106
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Feriara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltzen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gueney, Austin L.
APPLICANT: Kjaavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PIC37
CURRENT APPLICATION NUMBER: US/09/997,349
PRIOR FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28

;; PRIOR APPLICATION NUMBER: 60/091978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 3945; DB 3; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEIGCTOGLTFLQILLISLPREYTVINEACPGAEMNIMCBCEYDIECVCPKRE 60
DB 1 MEIGCTOGLTFLQILLISLPREYTVINEACPGAEMNIMCBCEYDIECVCPKRE 60
QY 61 VVGVTTPCCNNEECSCLIHPGCTTFENCKSCRNMGCTLDDFVYKFCACRAGW 120
DB 61 VVGVTTPCCNNEECSCLIHPGCTTFENCKSCRNMGCTLDDFVYKFCACRAGW 120
QY 121 YGGDCMRGCVLAPKQIILLESYPLNACEMWTHAKRGFVIOIRFVMSLEFDYMCQYD 180
DB 121 YGGDCMRGCVLAPKQIILLESYPLNACEMWTHAKRGFVIOIRFVMSLEFDYMCQYD 180
QY 121 YGGDCMRGCVLAPKQIILLESYPLNACEMWTHAKRGFVIOIRFVMSLEFDYMCQYD 180
DB 121 YGGDCMRGCVLAPKQIILLESYPLNACEMWTHAKRGFVIOIRFVMSLEFDYMCQYD 180
QY 181 YVEVRDGNRDGQIIRKVCGERPAPIQSIGSSILHVLFSHSDSKNPDGFAIYEITACS 240
DB 181 YVEVRDGNRDGQIIRKVCGERPAPIQSIGSSILHVLFSHSDSKNPDGFAIYEITACS 240
QY 241 SSSCFHDGTVDLAKAGYKCAACLAGYGCRCENILBERNCSDDPGPVNGYQKITGGPGLI 300
DB 241 SSSCFHDGTVDLAKAGYKCAACLAGYGCRCENILBERNCSDDPGPVNGYQKITGGPGLI 300
QY 301 NGRHAKIGTVSFFCNSVYLSGNERKTCQONGEMSGKOPICIKACEPKISDLVRRVL 360
DB 301 NGRHAKIGTVSFFCNSVYLSGNERKTCQONGEMSGKOPICIKACEPKISDLVRRVL 360
QY 361 PMQVOSRETPHLQYLSAFAKQKQSAFTKPKPALPFBDLPMGQHLHTQAYECISPFYR 420
DB 361 PMQVOSRETPHLQYLSAFAKQKQSAFTKPKPALPFBDLPMGQHLHTQAYECISPFYR 420
QY 421 RLSSSRRTCLRTGKWSGRASCPICCKINENTAPKTQGLRMPQOALYRTSGVHDSL 480
DB 421 RLSSSRRTCLRTGKWSGRASCPICCKINENTAPKTQGLRMPQOALYRTSGVHDSL 480
QY 481 HKGAMFLVCSGALVNERTVVAAHCVTDLGVMTIKTADLKVLYGKRYRDDDEKTIQS 540
DB 481 HKGAMFLVCSGALVNERTVVAAHCVTDLGVMTIKTADLKVLYGKRYRDDDEKTIQS 540
QY 541 LQISATILHNPDPILADADIALIKLIDKARISTRVQPICLAASRDLSFQESHITVAG 600
DB 541 LQISATILHNPDPILADADIALIKLIDKARISTRVQPICLAASRDLSFQESHITVAG 600
QY 601 WNVLADVRSGPFGKNDTLRSQVSVVDSLLCEBOHEDHGIPIVSYTDNMFCAWEPABSDI 660
DB 601 WNVLADVRSGPFGKNDTLRSQVSVVDSLLCEBOHEDHGIPIVSYTDNMFCAWEPABSDI 660
QY 661 CTAETGSIASVSPGRASPEPRMIMGLVMSYDKTCSHSLSTAFFTVLAFKWMIEKMK 720
DB 661 CTAETGSIASVSPGRASPEPRMIMGLVMSYDKTCSHSLSTAFFTVLAFKWMIEKMK 720

RESULT 10
US-09-997-653-231

;; Sequence 231, Application US/09997653

;; Patent No. 7034122

;; GENERAL INFORMATION:

;; APPLICANT: Ashkenazi, Avi J.

;; APPLICANT: Baker, Kevin P.

;; APPLICANT: Botstein, David

;; APPLICANT: Desnuyers, Luc

;; APPLICANT: Eaton, Dan L.

;; APPLICANT: Ferrara, Napoleone

;; APPLICANT: Fong, Sherman

;; APPLICANT: Gerber, Hanspeter

;; APPLICANT: Gerltsen, Mary E.
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Grimaldi, J. Christopher
;; APPLICANT: Gujney, Austin L.
;; APPLICANT: Kijavini, Ivar J.
;; APPLICANT: Napier, Mary A.
;; APPLICANT: Pan, James
;; APPLICANT: Paoni, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Watanabe, Colin K.
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
;; APPLICANT: Zhang, Zemin
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE REFERENCE: P2730P1C38
;; CURRENT APPLICATION NUMBER: US/09/997,653
;; CURRENT FILING DATE: 2001-11-15
;; PRIOR APPLICATION NUMBER: 60/049787
;; PRIOR FILING DATE: 1997-06-16
;; PRIOR APPLICATION NUMBER: 60/062250
;; PRIOR FILING DATE: 1997-10-17
;; PRIOR APPLICATION NUMBER: 60/065186
;; PRIOR FILING DATE: 1997-11-12
;; PRIOR APPLICATION NUMBER: 60/065311
;; PRIOR FILING DATE: 1997-11-13
;; PRIOR APPLICATION NUMBER: 60/066770
;; PRIOR FILING DATE: 1997-11-24
;; PRIOR APPLICATION NUMBER: 60/075945
;; PRIOR FILING DATE: 1998-02-25
;; PRIOR APPLICATION NUMBER: 60/078910
;; PRIOR FILING DATE: 1998-03-20
;; PRIOR APPLICATION NUMBER: 60/083322
;; PRIOR FILING DATE: 1998-04-28
;; PRIOR APPLICATION NUMBER: 60/084600
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/087106
;; PRIOR FILING DATE: 1998-05-28
;; PRIOR APPLICATION NUMBER: 60/087607
;; PRIOR FILING DATE: 1998-06-02
;; PRIOR APPLICATION NUMBER: 60/087609
;; PRIOR FILING DATE: 1998-06-02
;; PRIOR APPLICATION NUMBER: 60/087759
;; PRIOR FILING DATE: 1998-06-02
;; PRIOR APPLICATION NUMBER: 60/087827
;; PRIOR FILING DATE: 1998-06-03
;; PRIOR APPLICATION NUMBER: 60/088021
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088025
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088026
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088028
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088029
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088030
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088033
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088326
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088167
;; PRIOR FILING DATE: 1998-06-05
;; PRIOR APPLICATION NUMBER: 60/088202
;; PRIOR FILING DATE: 1998-06-05
;; PRIOR APPLICATION NUMBER: 60/088212
;; PRIOR FILING DATE: 1998-06-05
;; PRIOR APPLICATION NUMBER: 60/088217
;; PRIOR FILING DATE: 1998-06-05

PROR APPLICATION NUMBER: 60/088655
PROR FILING DATE: 1998-06-09
PROR APPLICATION NUMBER: 60/088734
PROR FILING DATE: 1998-06-10
PROR APPLICATION NUMBER: 60/088738
PROR FILING DATE: 1998-06-10
PROR APPLICATION NUMBER: 60/088742
PROR FILING DATE: 1998-06-10
PROR APPLICATION NUMBER: 60/088810
PROR FILING DATE: 1998-06-10
PROR APPLICATION NUMBER: 60/088824
PROR FILING DATE: 1998-06-10
PROR APPLICATION NUMBER: 60/088826
PROR FILING DATE: 1998-06-10
PROR APPLICATION NUMBER: 60/088858
PROR FILING DATE: 1998-06-11
PROR APPLICATION NUMBER: 60/088861
PROR FILING DATE: 1998-06-11
PROR APPLICATION NUMBER: 60/088876
PROR FILING DATE: 1998-06-11
PROR APPLICATION NUMBER: 60/089105
PROR FILING DATE: 1998-06-12
PROR APPLICATION NUMBER: 60/089440
PROR FILING DATE: 1998-06-16
PROR APPLICATION NUMBER: 60/089512
PROR FILING DATE: 1998-06-16
PROR APPLICATION NUMBER: 60/089514
PROR FILING DATE: 1998-06-16
PROR APPLICATION NUMBER: 60/089532
PROR FILING DATE: 1998-06-17
PROR APPLICATION NUMBER: 60/089538
PROR FILING DATE: 1998-06-17
PROR APPLICATION NUMBER: 60/089598
PROR FILING DATE: 1998-06-17
PROR APPLICATION NUMBER: 60/089599
PROR FILING DATE: 1998-06-17
PROR APPLICATION NUMBER: 60/089600
PROR FILING DATE: 1998-06-17
PROR APPLICATION NUMBER: 60/089653
PROR FILING DATE: 1998-06-17
PROR APPLICATION NUMBER: 60/089801
PROR FILING DATE: 1998-06-18
PROR APPLICATION NUMBER: 60/089907
PROR FILING DATE: 1998-06-18
PROR APPLICATION NUMBER: 60/089908
PROR FILING DATE: 1998-06-18
PROR APPLICATION NUMBER: 60/089947
PROR FILING DATE: 1998-06-19
PROR APPLICATION NUMBER: 60/089948
PROR FILING DATE: 1998-06-19
PROR APPLICATION NUMBER: 60/089952
PROR FILING DATE: 1998-06-19
PROR APPLICATION NUMBER: 60/090246
PROR FILING DATE: 1998-06-22
PROR APPLICATION NUMBER: 60/090252
PROR FILING DATE: 1998-06-22
PROR APPLICATION NUMBER: 60/090254
PROR FILING DATE: 1998-06-22
PROR APPLICATION NUMBER: 60/090349
PROR FILING DATE: 1998-06-23
PROR APPLICATION NUMBER: 60/090355
PROR FILING DATE: 1998-06-23
PROR APPLICATION NUMBER: 60/090429
PROR FILING DATE: 1998-06-24
PROR APPLICATION NUMBER: 60/090431
PROR FILING DATE: 1998-06-24
PROR APPLICATION NUMBER: 60/090435
PROR FILING DATE: 1998-06-24
PROR APPLICATION NUMBER: 60/090444
PROR FILING DATE: 1998-06-24
PROR APPLICATION NUMBER: 60/090445
PROR FILING DATE: 1998-06-24
PROR APPLICATION NUMBER: 60/090472

PROR FILING DATE: 1998-06-24
PROR APPLICATION NUMBER: 60/090535
PROR FILING DATE: 1998-06-24
PROR APPLICATION NUMBER: 60/090540
PROR FILING DATE: 1998-06-24
PROR APPLICATION NUMBER: 60/090542
PROR FILING DATE: 1998-06-24
PROR APPLICATION NUMBER: 60/090557
PROR FILING DATE: 1998-06-24
PROR APPLICATION NUMBER: 60/090676
PROR FILING DATE: 1998-06-25
PROR APPLICATION NUMBER: 60/090678
PROR FILING DATE: 1998-06-25
PROR APPLICATION NUMBER: 60/090690
PROR FILING DATE: 1998-06-25
PROR APPLICATION NUMBER: 60/090694
PROR FILING DATE: 1998-06-25
PROR APPLICATION NUMBER: 60/090695
PROR FILING DATE: 1998-06-25
PROR APPLICATION NUMBER: 60/090696
PROR FILING DATE: 1998-06-25
PROR APPLICATION NUMBER: 60/090862
PROR FILING DATE: 1998-06-26
PROR APPLICATION NUMBER: 60/090863
PROR FILING DATE: 1998-06-26
PROR APPLICATION NUMBER: 60/091360
PROR FILING DATE: 1998-07-01
PROR APPLICATION NUMBER: 60/091478
PROR FILING DATE: 1998-07-02
PROR APPLICATION NUMBER: 60/091544
PROR FILING DATE: 1998-07-01
PROR APPLICATION NUMBER: 60/091519
PROR FILING DATE: 1998-07-02
PROR APPLICATION NUMBER: 60/091626
PROR FILING DATE: 1998-07-02
PROR APPLICATION NUMBER: 60/091633
PROR FILING DATE: 1998-07-02
PROR APPLICATION NUMBER: 60/091978
PROR FILING DATE: 1998-07-07
PROR APPLICATION NUMBER: 60/091982
PROR FILING DATE: 1998-07-07
PROR APPLICATION NUMBER: 60/092182
PROR FILING DATE: 1998-07-09

Query Match 100.0%; Score 3945; DB 3; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MELGCTGTLGLTFLQLLLSLSPREYTVINEACPGAEMNIMCRECEYDIECVCPGKRE 60
1 MELGCTGTLGLTFLQLLLSLSPREYTVINEACPGAEMNIMCRECEYDIECVCPGKRE 60

61 VVGTTTCCGNEBNECDSCLIHPGCTTFENCKSCRNCSKCGTIDDPYKGFYCAECRAGW 120
61 VVGTTTCCGNEBNECDSCLIHPGCTTFENCKSCRNCSKCGTIDDPYKGFYCAECRAGW 120

121 YGGDKMRCGQVLPAPKQIILLESYPLNAHCEWTHAKPGFVIOIRFVMLSLEPDYMCQYD 180
121 YGGDKMRCGQVLPAPKQIILLESYPLNAHCEWTHAKPGFVIOIRFVMLSLEPDYMCQYD 180

181 YVEVRDGNDRDGOIIRKVCNERNPAPIOSIGSSLAHYLFHSDGSKNFDGFAIYEBITACS 240
181 YVEVRDGNDRDGOIIRKVCNERNPAPIOSIGSSLAHYLFHSDGSKNFDGFAIYEBITACS 240

241 SSPCFHDGTGTVLDKAGSYKACIAGTYGQRCENULBERNCSDPGCPVNGYQKTTGGGGLI 300
241 SSPCFHDGTGTVLDKAGSYKACIAGTYGQRCENULBERNCSDPGCPVNGYQKTTGGGGLI 300

301 NGRHAKIGTVVSFFCNNSYVLSGNEKRTCOQNGEMSGKOPICIKACEPKISDLYRRRYL 360
301 NGRHAKIGTVVSFFCNNSYVLSGNEKRTCOQNGEMSGKOPICIKACEPKISDLYRRRYL 360

361 PMOVQSRERPLHOLYSAFSGKOKLQSAFTRKPPALPFGLDPMGYOHLHTOLQYECISPFYR 420

Db 361 PMQVGRREFPLHQLYSAARSKQLQGAFTKPKALPFQDLPWGQHLHTQLOQRECIAPFR 420
QY 421 RLSSRRTRCTRTKMGSRAPSCPIPGKIENTIAPTQGLRWQAAITRTISGVHDGSI 480
Db 421 RLSSRRTRCTRTKMGSRAPSCPIPGKIENTIAPTQGLRWQAAITRTISGVHDGSI 480
QY 481 HKGAWFLVSGALWNRVTVAACHCTDGLKVMITADLKVYLGVFYDDDDDEXTIOS 540
Db 481 HKGAWFLVSGALWNRVTVAACHCTDGLKVMITADLKVYLGVFYDDDDDEXTIOS 540
QY 541 LQISAILHPNYDPIILDADIALIKLIDKARISTRVQPICLAARDLSTSFQESHITVAG 600
Db 541 LQISAILHPNYDPIILDADIALIKLIDKARISTRVQPICLAARDLSTSFQESHITVAG 600
QY 601 WNVLADVRSPGFNDLTRSGVSVVDSLLCEQHEHGHIPVSVTDMMFCASMEPTAPSDI 660
Db 601 WNVLADVRSPGFNDLTRSGVSVVDSLLCEQHEHGHIPVSVTDMMFCASMEPTAPSDI 660
QY 661 CTATGTGIAAVSPRGRASPEPRMHLGLVSNVYDKTCSHRLSTAFKKVLPEKDMIRNMK 720
Db 661 CTATGTGIAAVSPRGRASPEPRMHLGLVSNVYDKTCSHRLSTAFKKVLPEKDMIRNMK 720

RESULT 11
US-09-989-293A-231
Sequence 231, Application US/09989293A
Patent No. 7034136
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertlisen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C66
CURRENT APPLICATION NUMBER: US/09/989,293A
PRIOR FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322

PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087609
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087759
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087827
PRIOR FILING DATE: 1998-06-03
PRIOR APPLICATION NUMBER: 60/088021
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088025
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088026
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088028
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088029
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088030
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088033
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088326
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088167
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088202
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088212
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088217
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088655
PRIOR FILING DATE: 1998-06-09
PRIOR APPLICATION NUMBER: 60/088734
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088738
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088742
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088810
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088824
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088826
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088858
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088861
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088876
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/089105
PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/089440
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089512
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089514
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089532
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089538
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089598
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089599
PRIOR FILING DATE: 1998-06-17

PRIOR APPLICATION NUMBER: 60/089600
 PRIOR FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: 60/089653
 PRIOR FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: 60/089801
 PRIOR FILING DATE: 1998-06-18
 PRIOR APPLICATION NUMBER: 60/089907
 PRIOR FILING DATE: 1998-06-18
 PRIOR APPLICATION NUMBER: 60/089908
 PRIOR FILING DATE: 1998-06-18
 PRIOR APPLICATION NUMBER: 60/089947
 PRIOR FILING DATE: 1998-06-19
 PRIOR APPLICATION NUMBER: 60/089948
 PRIOR FILING DATE: 1998-06-19
 PRIOR APPLICATION NUMBER: 60/089952
 PRIOR FILING DATE: 1998-06-19
 PRIOR APPLICATION NUMBER: 60/090246
 PRIOR FILING DATE: 1998-06-22
 PRIOR APPLICATION NUMBER: 60/090252
 PRIOR FILING DATE: 1998-06-22
 PRIOR APPLICATION NUMBER: 60/090254
 PRIOR FILING DATE: 1998-06-22
 PRIOR APPLICATION NUMBER: 60/090349
 PRIOR FILING DATE: 1998-06-23
 PRIOR APPLICATION NUMBER: 60/090355
 PRIOR FILING DATE: 1998-06-23
 PRIOR APPLICATION NUMBER: 60/090429
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090431
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090435
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090444
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090445
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090472
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090535
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090540
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090542
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090557
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090676
 PRIOR FILING DATE: 1998-06-25
 PRIOR APPLICATION NUMBER: 60/090678
 PRIOR FILING DATE: 1998-06-25
 PRIOR APPLICATION NUMBER: 60/090690
 PRIOR FILING DATE: 1998-06-25
 PRIOR APPLICATION NUMBER: 60/090694
 PRIOR FILING DATE: 1998-06-25
 PRIOR APPLICATION NUMBER: 60/090695
 PRIOR FILING DATE: 1998-06-25
 PRIOR APPLICATION NUMBER: 60/090696
 PRIOR FILING DATE: 1998-06-25
 PRIOR APPLICATION NUMBER: 60/090862
 PRIOR FILING DATE: 1998-06-26
 PRIOR APPLICATION NUMBER: 60/090863
 PRIOR FILING DATE: 1998-06-26
 PRIOR APPLICATION NUMBER: 60/091360
 PRIOR FILING DATE: 1998-07-01
 PRIOR APPLICATION NUMBER: 60/091478
 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091544
 PRIOR FILING DATE: 1998-07-01
 PRIOR APPLICATION NUMBER: 60/091519
 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091626
 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091633

PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091978
 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/091982
 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/092182
 PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 3945; DB 3; Length 720;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MELGWTQLGLTFQLQLLSLPREYTVINEACPGAEWIMCECEYDIECCPGKRE 60
 DB 1 MELGWTQLGLTFQLQLLSLPREYTVINEACPGAEWIMCECEYDIECCPGKRE 60
 QY 61 VVGTTIPCCNEBNECDSCIHHGCTTFENCKSCRNKSGWGTLDFFVKGFTCAECRAGW 120
 DB 61 VVGTTIPCCNEBNECDSCIHHGCTTFENCKSCRNKSGWGTLDFFVKGFTCAECRAGW 120
 QY 121 YGGDKMRCGGVLRAPKQIILLESYPLNAGCEWTHAKPGFVQLRFVMLSLEFDYMCQYD 180
 DB 121 YGGDKMRCGGVLRAPKQIILLESYPLNAGCEWTHAKPGFVQLRFVMLSLEFDYMCQYD 180
 QY 181 YVEVRDGNRDQIIRKVCNERNPAPQISGSLHYLFHSDGSKNDFGFAIYEETIACS 240
 DB 181 YVEVRDGNRDQIIRKVCNERNPAPQISGSLHYLFHSDGSKNDFGFAIYEETIACS 240
 QY 241 SSPCFHDGTVDLDKASGYKACLAGTGORCENULLEBRNCSDPGPGVNGYQKITGPGELI 300
 DB 241 SSPCFHDGTVDLDKASGYKACLAGTGORCENULLEBRNCSDPGPGVNGYQKITGPGELI 300
 QY 301 NGRHAKIGTVSFFCNNSVYLSGNEKRTCOQNGEMSGKOPICIKAREPXSILVRRVYL 360
 DB 301 NGRHAKIGTVSFFCNNSVYLSGNEKRTCOQNGEMSGKOPICIKAREPXSILVRRVYL 360
 QY 361 PMQVQSERETPLHQLYSAAFSKQLQSAPTKPPALPMGYQHLHTOLQYCISSPFYR 420
 DB 361 PMQVQSERETPLHQLYSAAFSKQLQSAPTKPPALPMGYQHLHTOLQYCISSPFYR 420
 QY 421 RLGSRRRTCLRTGKWSGRAPSCIPICGKIENITAPYTOGIRMPWQAIIYRRTSGVHDGSL 480
 DB 421 RLGSRRRTCLRTGKWSGRAPSCIPICGKIENITAPYTOGIRMPWQAIIYRRTSGVHDGSL 480
 QY 481 HKGAMFLVCSGALVNEETVVAAHCVTDGKVTMKTADLKVVLGKFRYRDDDEKTIQS 540
 DB 481 HKGAMFLVCSGALVNEETVVAAHCVTDGKVTMKTADLKVVLGKFRYRDDDEKTIQS 540
 QY 541 LQISATILHNPYDPIILDADIALIKLIDKARISTRVQPICLAASRLDSTFQESHITVAG 600
 DB 541 LQISATILHNPYDPIILDADIALIKLIDKARISTRVQPICLAASRLDSTFQESHITVAG 600
 QY 601 WNTLADYRSPGFNDTLRSQVSVVDSLLCEEQHEHDGIPVSYTDNNFCASWEPTAPSDI 660
 DB 601 WNTLADYRSPGFNDTLRSQVSVVDSLLCEEQHEHDGIPVSYTDNNFCASWEPTAPSDI 660
 QY 661 CTABTGIAAVSPFGASPRPRWMLGLVSWSYDKTCSHRLSTAFATKVLFPKDMIRNNK 720
 DB 661 CTABTGIAAVSPFGASPRPRWMLGLVSWSYDKTCSHRLSTAFATKVLFPKDMIRNNK 720

RESULT 12
 US-10-067-422-9
 Sequence 9, Application US/10067422
 Patent No. 6743613
 GENERAL INFORMATION:
 APPLICANT: Ni et al.
 TITLE OF INVENTION: Bone Morphogenic Protein (BMP) Polynucleotides, Polypeptides, and
 FILE REFERENCE: P7004P1
 CURRENT APPLICATION NUMBER: US/10/067,422
 CURRENT FILING DATE: 2002-02-07
 PRIOR APPLICATION NUMBER: 09/685,899

```

; PRIOR FILING DATE: 2000-10-11
; PRIOR APPLICATION NUMBER: PCT/US00/09028
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/152,933
; PRIOR FILING DATE: 1999-09-09
; PRIOR APPLICATION NUMBER: 60/147,020
; PRIOR FILING DATE: 1999-08-03
; PRIOR APPLICATION NUMBER: 60/131,672
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: 60/130,693
; PRIOR FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; LENGTH: 570
; SEQ ID NO 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-067-422-9

```

```

Query Match      74.7%; Score 2946.5; DB 2; Length 570;
Best Local Similarity 96.8%; Pred. No. 8.4e-237;
Matches 552; Conservative 0; Mismatches 1; Indels 17; Gaps 1;

```

```

QY 168 MSLSEFDYMCQYDYVEVRDGDNRDGOIIRKVCNERNPAPIQSIGSLHLVLFHSDGSKNFD 227
DB 1 MSLSEFDYMCQYDYVEVRDGDNRDGOIIRKVCNERNPAPIQSIGSLHLVLFHSDGSKNFD 60
QY 228 GFHAIEYETACSSSPCFHDTGTCVLDAKSGYKCAAGYTGRCENI----- 274
DB 61 GFHAIEYETACSSSPCFHDTGTCVLDAKSGYKCAAGYTGRCENILEAGSKIRASED 120
QY 275 -----LEERNCSDDGPNNGYOKITGPGGLNGRRAKIGTVVSFFCNNSYVLSGNERKTCQ 330
DB 121 SLISVLEERNCSDDGPNNGYOKITGPGGLNGRRAKIGTVVSFFCNNSYVLSGNERKTCQ 180
QY 331 QNEMSGKOPICIKACEPKISDLVRRVLPMOVOSRETPHOLYSAFSGKOLQSAPTK 390
DB 181 QNEMSGKOPICIKACEPKISDLVRRVLPMOVOSRETPHOLYSAFSGKOLQSAPTK 240
QY 391 KPALPGDLPNGYOHHTLOLYECISPFYRRLGSSRRRTCLRTGKWSGRABSCIPICGKIE 450
DB 241 KPALPGDLPNGYOHHTLOLYECISPFYRRLGSSRRRTCLRTGKWSGRABSCIPICGKIE 300
QY 451 NITAPRTQGLRMWMOAIYRTSGVHDSLHKGAMFLVCSGALVNEETVVAAHCTYDLG 510
DB 301 NITAPRTQGLRMWMOAIYRTSGVHDSLHKGAMFLVCSGALVNEETVVAAHCTYDLG 360
QY 511 KVTMIKTADLVKVLGKFRYRDDDEKTIQSLQISAILHPNYDPIILDADIALIKLIDKA 570
DB 361 KVTMIKTADLVKVLGKFRYRDDDEKTIQSLQISAILHPNYDPIILDADIALIKLIDKA 420
QY 571 RISTRVOPICLAASRDLSFQESHITVAGMNVLADVRSPGFKNIDTLRSQVSVVSDLSLC 630
DB 421 RISTRVOPICLAASRDLSFQESHITVAGMNVLADVRSPGFKNIDTLRSQVSVVSDLSLC 480
QY 631 EEEHEDHGIPVSTDMNFCASWEPTASDICTAETGIIAAVSPFGRASPEPRHMLGLVS 690
DB 481 EEEHEDHGIPVSTDMNFCASWEPTASDICTAETGIIAAVSPFGRASPEPRHMLGLVS 540
QY 691 WSYDKTCSHRLSTAFTKVLFPKDIERNMK 720
DB 541 WSYDKTCSHRLSTAFTKVLFPKDIERNMK 570

```

```

RESULT 13
US-10-183-992-4
; Sequence 4, Application US/10183992
; Patent No. 6849426
; GENERAL INFORMATION:
; APPLICANT: Chen, Lin
; APPLICANT: Pepe, Michael
; TITLE OF INVENTION: Methods and Reagents for Detecting Endotoxin
; FILE REFERENCE: 02877.00008

```

```

; CURRENT APPLICATION NUMBER: US/10/183,992
; CURRENT FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US 60/310,125
; PRIOR FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1019
; TYPE: PRT
; ORGANISM: Tachypleudus tridentata
US-10-183-992-4

```

```

Query Match      17.0%; Score 672; DB 2; Length 1019;
Best Local Similarity 25.6%; Pred. No. 5e-47;
Matches 223; Conservative 117; Mismatches 308; Indels 222; Gaps 37;

```

```

QY 34 PGAEWNIM-----CRECEVDQIE---CVCPRGREVVYTIPOCRNEENECDSCLIHPGCT 86
DB 184 PNGWSSFPKPCIKRECAKSSPEHGKVNAPSGNMIEGATL-----RFSCDS-----PYUL 233
QY 87 IFENCKSCR-NSWGGTL----- 103
DB 234 ICGETLTCQNGQWSGOIPQCKKLVFCPDLDPVNAEHQVKGVEQKYGQFPGTEVYTT 293
QY 104 ---DDFYVKGFCACER--AGWYGG--DCMR-----CGQYLR--APKG 137
DB 294 CSGNYFLMGFNTLKCNPDSGWSGSPSCVAVADREYDCSKAVDFLDVGEPRIRHCPAG 353
QY 138 QILLES-----YPLNAHCEWTIHA---KPGFYI----- 163
DB 354 CSTIAGTWTGTAIYHLLSSVCRAIHAIGLPRSGAVHYVNNPYSDFLGSDLNGIKSE 413
QY 164 LRFVMSLEFDYMCQYDYVEVRDGDNRDGOIIRKVCNERNPAPIQSIGSLHLVLFHSDGSKNFD 227
DB 414 LKSLARSPREDYVSSSTAGRSGCPDMFEVEECVYVTSKORAMERAOGCTMAARLAV 473
QY 207 IQS--IGSSLHLVLFHSDG--SKNFDGPH-----AIYEITACSSSPCF 245
DB 474 LDKDLIPSSLTETLRKGLTTWIGHRLDAEKPFVWELMDRSNVVJNLNLTFFWASGEPG 533
QY 246 HDGTCV-LDKAGS---YKACIAGYTGRCENILEERN---CSDPGPNNGYOKITGPG 297
DB 534 NETNVCYLDIRDQLOVWMTKSCFQPSFACMDLSDRKAKCDDPGPLENGHATLHGOS 593
QY 298 GLINGHAKIGTVVSFFCNNSYVLSGNERKTCQONEMSGKOPICIK--ACREPKISDLV 355
DB 594 --IDGFYA--GSSIRASCEVLHLSGTEVYTCYTNCTWGAAPKRCIKVITCQNPVPYSY 649
QY 356 RRRVLPMOVOSRETPHOLYSAFSGKOLQ---SAPTKKALPFGD-----LP 400
DB 650 SVEIKP---PSRNSISRVGSPFLRLPLPLARAKPPKPRSSQSPSTVDLASKVKLP 706
QY 401 MGYOHHTLOLYECISPFYRRLGSSRRRTCLRTGKWSGRABSCIPICGKIENTIAP----- 455
DB 707 BGRYVGSRAIYICBSRYIELLASQGRCDSCNMSGRPASCIPVCGKSDSPSPSPITWNG 766
QY 456 -KTQGLRMWMOAIYRTSGVHDSLHKGAMFLVCSGALVNEETVVAAHCTYDLGKVTM 514
DB 767 NSTEIQGMWMOAGISMLA-----DHMMWFLQGGGSLNEMKVIYTAHCVIYSATAEI 819
QY 515 IKTADLVKVLGKFRYRDDDEKTIQSLQISAILHPNYDPIILDADIALIKLIDKARIST 574
DB 820 IDPSQFKIYLGKRYRDSRDDDDVQVREALEIHVNPNYDPCGNLFDIALIQLTPTVYLT 879
QY 575 RVOPICLAASRDLSFQESHITVAGMNVLADVRSPGFKNIDTLRSQVSVVSDLSLC 630
DB 880 RVOPICLP--DIT--RHLKEGTLAVYTWG---LNENNTYSEMIOQAVLPVVAAS 930
QY 629 LCEBHEHDHGIPVSTDMNFCASWEPTASDICTAETGIIAAVSPFGRASPEPRHMLGL 688
DB 931 TCEBGEYKADLPLTVEENFCAGYK--KGRYDACSGBSG--PLVFADDSRTERRWLLEGI 987
QY 689 VMSYDKTCSH-RLSTAFTKVLFPKDIERN 717

```

Db 988 VSWGSPSGCGKANQYGGFTKVNFLSWIRQ 1017

RESULT 14

US-08-296-014A-4
Sequence 4, Application US/08296014A

Patent No. 5716834

GENERAL INFORMATION:

APPLICANT: Ding, Jeak Ling

APPLICANT: Ho, Bow

TITLE OF INVENTION: The Cloned Factor C cDNA of the

TITLE OF INVENTION: Singapore Horseshoe Crab, Carcinus scurpius

TITLE OF INVENTION: rotundicauda and Purification of Factor C Proenzyme

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Birch, Stewart, Kolaach & Birch

STREET: 8110 Gatehouse Road, Suite 500 East

CITY: Falls Church

STATE: Virginia

COUNTRY: USA

ZIP: 22042

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/296.014A

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Murphy, Jr., Gerald M.

REGISTRATION NUMBER: 28,977

REFERENCE/DOCKET NUMBER: 1781-105P

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 205-8000

TELEFAX: (703) 205-8050

TELEX: 248345

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 1019 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-296-014A-4

Query Match 16.9%; Score 665; DB 1; Length 1019;

Best Local Similarity .25.4%; Pred. No. 1.9e-46;

Matches 222; Conservative 118; Mismatches 304; Indels 230; Gaps 37;

QY 34 PGAEWNIMCRRCCEYDIECYCPGKRE-----VVGVTIPCCRNENEGDSCLIH 82

Db 184 PNGQWSNPPPKICR---ECAMVSSPHGKYNALSGMIEGATL-----RFSDDS--- 229

QY 83 PGCTIFENCKSCR-NGSMGTL-----VVGVTIPCCRNENEGDSCLIH 103

Db 230 PYVILIGETLTCQNGNKGQIPQCKNLVFCRDLDPVNHAKKXIGVEQKYGQPGSTE 289

QY 104 -----DFYVKGFGYCAECR--AGWYGG--DCMR-----CGQVLR-- 133

Db 290 VTYTCSNRYFLMGDTLKCNDPDSMSGSGQFSCVKADREVDSDSKAVDFLDVGEPIRIH 349

QY 134 APKGQILLES-----YPLNHCWETIHA-----KRGFVL----- 162

Db 350 CPACGSLTACTGWTAGTAIYHELISVCRAIHHAGKLPNSGGAHVANNNGPYSDFLSLNGI 409

QY 163 ---QLRFVMLSLFEDYM-----CQYDVEYRD-----GNDROQILKRYCGN--E 202

Db 410 KSEELKSLARSFRDYRBSSTAGKSGCGPDGWFEDVENCVVYTSKRAMERAGVCTNMAA 469

QY 203 RPAPIQS--IGSSLHLVLFHSDG--SKNFDGFI-----ALYEITACSS 241

Db 470 RLAVLDKVIPLNSLTETLRGKGLTTTWIGLHRLDAKPPRIWELMDRSNVVLNDLTFMAS 529

QY 242 SPCEHDGTCVL-----DKAGS-YKCACTAGYTGRCENTLBERN---CSPDGGFVNGYOKI 293

Db 530 GERGETNVCYMDIQDQLOSVMKTKSCFPQSSPACMDLSDRKAKCDDPGLSENGHATL 589

QY 294 TGGPGLINGHAKIGTVSPFCNSYVLISGNEKRTCCQNGEMSGKQIPIC--ACREPKI 351

Db 590 HGQS--IDGFYA--GGSIRYSCVHLHYLSTGETVCTTGTNGTWSAPRRCIKVITQNPV 645

QY 352 SDLVRRRVLPVQVQSETEPLHOLYSAFSGKQLQ---SAPTKRALPFED----- 398

Db 646 PSYGSVEIKP---PSRTNSISRVSGSPFLRLPLRLPLAAAKPPRPRSSQBPSTVLASK 702

QY 399 --LPMGYOHLTQLOECISPFYRRGSSRRRTCLRTGKMSGRAPSCIPICGKIENITAP- 455

Db 703 VKLPBGHYRVSALITCESRYIELLSQGRCDNSGNWSGRASCIPVCGRSDSRSP 762

QY 456 ----KTQGLRWPQALYRRTSGVHDGSLHKGMFLVCSGALVNBRTVVAACVTDLG 510

Db 763 INGNSTEGQWPMQAGISRWLA-----DHNWFLQGGSLNKKMTYTAHCTYLSA 815

QY 511 KTMITADLKVVYGFYRDDDEKTIQSLQISAILHPNDPILLDADIALKLIDRA 570

Db 816 TAEIIDNPQKMYLGYRDSRDDYVQREALETHVNPNDPGLNFDIALIOLKTPV 875

QY 571 RISTRVOPICLASRDLSTSFQESH-----TVAGNNVLADVRSPGKNDLTRSGVSV 624

Db 876 TLTRVOPICLPT--DITT---REHLKEGLAVVTGNG---LNENNTYSETIQOAVLPV 926

QY 625 VDSLCEQHEHDGIPVSYTDNMFCSAWEPTASDICTAETGIAAVSPFGRAPEPRMH 684

Db 927 VAATCEGKYKADLPVTIENMFAGYK-KGRYDACSQSGG--PLVFADSRTERRW 963

QY 685 LMLVKSXYTKCSH-RLSTAFKYLPRKDWIR 717

Db 984 LEGIVSWSPSGCGKANQYGGFTKVNFLSWIRQ 1017

RESULT 15

US-08-596-405-4
Sequence 4, Application US/08596405

Patent No. 5858706

GENERAL INFORMATION:

APPLICANT: Ding, Jeak Ling

APPLICANT: Ho, Bow

TITLE OF INVENTION: The Cloned Factor C cDNA of the

TITLE OF INVENTION: Singapore Horseshoe Crab, Carcinus scurpius

TITLE OF INVENTION: rotundicauda and Purification of Factor C Proenzyme

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Birch, Stewart, Kolaach & Birch

STREET: 8110 Gatehouse Road, Suite 500 East

CITY: Falls Church

STATE: Virginia

COUNTRY: USA

ZIP: 22042

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/596.405

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Murphy, Jr., Gerald M.

REGISTRATION NUMBER: 28,977

REFERENCE/DOCKET NUMBER: 1781-105P

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 205-8000

TELEFAX: (703) 205-8050

TELEX: 248345
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1019 amino acids
 TYPE: amino acid
 TOPOLOGY: 1linear
 MOLECULE TYPE: protein
 US-08-596-405-4

Query Match 16.9%; Score 665; DB 1; Length 1019;
 Best Local Similarity 25.4%; Pred. No. 1.9e-46;
 Matches 222; Conservative 118; Mismatches 304; Indels 230; Gaps 37;

```

QY 34 PGAEWNIMGECCEYQICVCGKRE-----VGYTIPCCRNENECDSCLIH 82
DB 184 PNGQMSNPPKCIK-----ECAMVSPHGKVNALSGDMTEGATL-----RSCDS----- 229
QY 83 PCCTIFENCKSCR-NGSMGTL----- 103
DB 230 PYLLIGQETLTCQNGQNGQIPQCKNLVFCPLDVPVNAHEHKVIGVEQKYQFPQTE 289
QY 104 -----DFTYVKGFCACGR--AGWYG--DCNR-----CGQVLR-- 133
DB 290 VTYTSGNYFLMGFDLKCNDPDSGSGQSPSCVAVADREVDCSKAVDFLDVGEPRVIR 349
QY 134 APKGOILLES-----YPLNHCMTIHA---KPGVI----- 162
DB 350 CPAGCSLTNGTWTGAIYHELSSVCRAALHAGKLPNSGAVHVNNGPYSDFLGSDLNGI 409
QY 163 ---QLRFVNLSEFDYM-----COYDYVEVRD-----GDNRDGQIIRKVCN--E 202
DB 410 KSEELKSLARSPFDYRSTAGKSGCPDGMFEVDENCYVYTSKQAMERAGQVCTNMMA 469
QY 203 RPAPIOS--IGSSLHVLHFSHG--SKNFDGFH-----AIYEITACSS 241
DB 470 RLAVLDKDVIPNSLTETLRGKGLTTWIGLHRLDAEKPFWEIMDRSNVNLNDMLTFMAS 529
QY 242 SPCFHGTCVL-----DKAGS--YKCACTAGTGCRCENLEBRV---CSPDGGPVNGYOKI 293
DB 530 GEPGNETNCVYMDIQDQLOSVMTKSCFPPSSPACMDLSDRNKAKCDDGSLNGHATL 589
QY 294 TGGPGLINGRHAIGTIVSFFCNNSYVLSGNEKRTCOQNGEMSGKOPICIX--ACREPKI 351
DB 590 HGGG--IDGFRYA--GSSIRYSCVHLHLSGETVYTCITNGTWASAPKRCIKVITCQNPV 645
QY 352 SDLVRRRVLPMOVQSEETPLHQLYSAFSKQKIQ--SAPTKKRALPFGD----- 398
DB 646 PSYGSVEIKP---PSRTNSISRVGSPFLRLPLRLPLARAAPPKPPRSQSPSTVDLASK 702
QY 399 --LPMGYOHLHQLOVECLISPFYRLGSSKRTCLRTGKWSGRAPSCIPICGKIENITAP- 455
DB 703 VKLPEGHYRVSRAIYTCESRYELLGSGRRCDNSNGNWSGRPASCIPVCGRSDSPSP 762
QY 456 -----KTQGLRMPWQAIYRRTSGVHDGSLHKGAMFLVCSGALVNERVTYVVAHCVTLG 510
DB 763 INNGNSTELIGQWPMQAGISRWLA-----DHNMFLQCGSLINEXMIVTAHCVITYSA 815
QY 511 KVTMTKTADLKVVLGKFYRDDDRDEKTIQSLQISAILHBNYDPIILDADIALIKLIDRA 570
DB 816 TAEIIPNQFKWYLGKYRDRSDRDYQVREALEIHVNPNYDGNLNFIDIALIQLKTPV 875
QY 571 RISTRVOPICLAASRLSTSFQESH-----TVAGMNLADYRSPGPKNDITLRSQVSY 624
DB 876 TLITRROPICLPT--DITT--REHLKEGLAVVVGW-----LNENNTYSETIQOAVLPV 926
QY 625 VDSLCEQEHEDHGIPIVSVTDNMFCASWEPTAPSDICTAETGIAAVSPGRASPEPRMH 684
DB 927 VAASTCEBGKENDLPLVTYENMFCAGYK--KGRYDACSQDSG--PLVFPADDSRTERRNV 983
QY 685 LMGVSMYSYDKTCSH--RLSTAFTKVLPFKDWIER 717
DB 984 LEGIVSWGSPSGCGKANQYGGFTKVVNFILSMIRQ 1017

```

Search completed: April 4, 2007, 21:57:08
 Job time : 50 secs

THIS PAGE BLANK (USPTO)

GenCore version 6.2
Copyright (c) 1993 - 2007 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 4, 2007, 21:56:36 ; Search time 22 Seconds
(without alignments)
3148.912 Million cell updates/sec

Title: US-10-063-546-38

Perfect score: 3945

Sequence: 1 MEIGCWTQGLTFLOLLIS.....LSNATFKVLPKQWIRNNK 720

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 9621673 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database:

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	949	24.1	181	2 T08805	hypothetical prote
2	672	17.0	1019	2 A38738	coagulation factor
3	482	12.2	699	1 I54763	Ra-reactive factor
4	403.5	10.2	705	1 C1HURB	complement subcomp
5	400.5	10.2	686	1 A59271	Ra-reactive factor
6	378.5	9.6	695	1 S05008	complement subcomp
7	354	9.0	1524	2 J30337	polyprotein - Afri
8	340.5	8.6	694	2 J06554	complement subcomp
9	334	8.5	688	1 C1HUS	complement subcomp
10	331.5	8.4	1019	1 A56318	enteropeptidase (E
11	330.5	8.4	1034	1 A53663	enteropeptidase (E
12	320	8.1	461	1 UX0210	proteol C (activat
13	317.5	8.0	1035	1 A43090	enteropeptidase (E
14	314.5	7.9	855	1 EXCH	coagulation factor
15	313	7.9	855	2 JC7731	membrane-bound arg
16	310.5	7.6	441	1 KKHU	protein C (activat
17	299.5	7.6	441	2 I46932	coagulation factor
18	293.5	7.4	407	1 KFB07	coagulation factor
19	292	7.4	461	1 S18994	protein C (activat
20	285.5	7.2	452	1 A30351	coagulation factor
21	283.5	7.1	482	1 EXRT	coagulation factor
22	282	7.1	456	1 KXBO	protein C (activat
23	281.5	7.1	558	2 J05878	plasma hyaluronan
24	281	7.1	492	1 EXBO	coagulation factor
25	280.5	7.1	264	2 I38136	chymotrypsin-like
26	280	7.1	562	1 UKHUT	t-plasminogen acti
27	278.5	7.1	466	1 KFHU7	coagulation factor
28	278	7.0	488	1 EXHU	coagulation factor
29	278	7.0	1113	2 J60315	low-density lipopr

30	277	7.0	559	1 A29941	t-plasminogen acti
31	277	7.0	559	1 A35029	t-plasminogen acti
32	276.5	7.0	625	1 A46688	hepatocyte growth
33	274.5	7.0	625	1 TBBO	thrombin (EC 3.4.2
34	273	6.9	560	1 JC4795	plasma hyaluronan
35	270	6.8	477	2 J80597	t-plasminogen acti
36	264.5	6.7	431	2 J80599	t-plasminogen acti
37	264.5	6.7	618	2 A35827	thrombin (EC 3.4.2
38	262.5	6.7	461	1 KFHU	coagulation factor
39	262	6.6	477	2 J80598	t-plasminogen acti
40	261.5	6.6	442	1 UKPE	u-plasminogen acti
41	261	6.6	431	1 UKHU	u-plasminogen acti
42	261	6.6	433	1 JN0560	u-plasminogen acti
43	260	6.6	477	1 A34369	t-plasminogen acti
44	259	6.6	244	2 S72219	chymotrypsin B - A
45	259	6.6	416	1 KFB0	coagulation factor
46	258.5	6.6	786	1 A47547	serine proteinase
47	258	6.5	251	2 PC1235	29K serine protein
48	258	6.5	433	1 UKGAY	u-plasminogen acti
49	257.5	6.5	1004	2 T30338	oviductin (EC 3.4.
50	255.5	6.5	763	2 T50807	complement factor
51	254	6.4	617	2 S10511	thrombin (EC 3.4.2
52	253	6.4	1070	2 T31069	collid-BMP-1 like
53	249.5	6.3	400	1 A48050	coagulation factor
54	249.5	6.3	986	1 B58788	procollagen C-endo
55	248.5	6.3	459	2 J00419	coagulation factor
56	248	6.3	263	1 A31299	chymotrypsin (EC 3
57	248	6.3	638	1 KOHUP	plasma kallikrein
58	247.5	6.3	991	2 I49540	procollagen C-endo
59	247	6.3	275	2 A32410	trypsinase (EC 3.4.2
60	247	6.3	764	1 BBHU	complement factor
61	246.5	6.2	347	1 G00006	haploglobin - blac
62	246.5	6.2	622	1 TBHU	thrombin (EC 3.4.2
63	246	6.2	236	2 C42696	plasma (EC 3.4.2
64	246	6.2	812	1 PLBO	thrombin (EC 3.4.2
65	245	6.2	234	2 F42696	plasma kallikrein
66	244	6.1	730	1 KQSPPL	procollagen C-endo
67	242.5	6.1	823	1 A58788	trypsin (EC 3.4.21
68	241.5	6.1	242	2 S49489	haploglobin precu
69	240	6.1	406	1 HPHU2	chymotrypsin (EC 3
70	239.5	6.1	245	1 KYBOA	trypsin (EC 3.4.21
71	239	6.1	237	1 TRCY1	chymotrypsin (EC 3
72	238	6.0	263	2 A21195	haploglobin precu
73	238	6.0	347	1 HPHU1	limulus clotting e
74	238	6.0	810	2 A23689	plasma (EC 3.4.21
75	238	6.0	375	1 A23689	trypsin (EC 3.4.21
76	237.5	6.0	270	2 S56160	trypsin (EC 3.4.21
77	237	6.0	263	1 KYRBA	trypsin (EC 3.4.21
78	236.5	6.0	274	2 JC4171	trypsin (EC 3.4.21
79	236.5	6.0	707	2 UC2218	procollagen C-endo
80	235	6.0	270	2 S56160	mast cell trypsinase
81	235	6.0	345	2 I36941	haploglobin - chim
82	235	6.0	1420	2 A32869	apolipoprotein(a)
83	233.5	5.9	263	2 S47537	chymotrypsin (EC 3
84	232	5.9	416	1 S33777	hepsin (EC 3.4.21
85	232	5.9	638	1 KQRPPL	plasma kallikrein
86	229.5	5.8	329	1 HPDG	haploglobin precu
87	228.5	5.8	235	2 E42696	thrombin (EC 3.4.2
88	228.5	5.8	347	1 HPMS	haploglobin precu
89	228.5	5.8	861	2 A48825	Notch homolog Motc
90	228.5	5.8	2531	2 A46019	notch-1 protein -
91	228	5.8	812	1 PLMS	plasma (EC 3.4.21
92	227.5	5.8	242	2 S31775	trypsin (EC 3.4.21
93	227.5	5.8	349	2 I36944	haploglobin - chim
94	227	5.8	1464	2 S31776	trypsin (EC 3.4.21
95	227	5.8	242	2 S58984	development protei
96	226.5	5.7	238	2 S31779	trypsin (EC 3.4.21
97	226.5	5.7	761	2 JC5759	brain-specific ser
98	226	5.7	394	2 UC5060	t-plasminogen acti
99	226	5.7	625	1 KFHU1	coagulation factor
100	225	5.7	615	1 KFHU12	coagulation factor
101	224.5	5.7	271	1 ELRT2	pancreatic elastas
102	224	5.7	245	1 KYBOB	chymotrypsin (EC 3

103	223.5	5.7	274	2	S35339	trypsin (EC 3.4.21	176	199.5	5.1	2555	2	A40043	notch protein homo
104	223.5	5.7	348	1	HPHUR	haptoglobin-relate	177	198.5	5.0	229	1	TRBOTR	trypsin (EC 3.4.21
105	222.5	5.6	417	1	S00845	hepsin (EC 3.4.21.	178	198.5	5.0	232	1	KOPG	tissue kallikrein
106	222.5	5.6	434	1	A35005	u-plasminogen acti	179	198.5	5.0	237	2	S55378	serine proteinase
107	222.5	5.6	790	1	PLPG	plasmin (EC 3.4.21	180	198	5.0	229	2	S68424	allergen Der f III
108	222	5.6	269	2	A26823	pancreatic elastase	181	198	5.0	270	2	B29334	pancreatic elastase
109	222	5.6	275	2	S18563	trypsin (EC 3.4.2	182	198	5.0	760	1	CMWS	classical-compleme
110	221.5	5.6	2531	2	S18188	notch protease (EC	183	197.5	5.0	250	2	T01779	trypsin (EC 3.4.21
111	221	5.6	231	2	S31778	trypsin (EC 3.4.21	184	197.5	5.0	258	2	I36947	haptoglobin Hpp -
112	220.5	5.6	274	2	A45754	trypsin (EC 3.4.2	185	196.5	5.0	259	2	C26823	pancreatic elastase
113	220.5	5.6	1057	1	A39288	dorsal-ventral pat	186	196.5	5.0	570	2	A48836	fibropellin C prec
114	220	5.6	275	2	A43563	trypsin (EC 3.4.2	187	196.5	5.0	767	2	T30018	hypothetical prote
115	219.5	5.6	235	2	H42696	thrombin (EC 3.4.2	188	196.5	5.0	2524	2	A35844	hypothetical prote
116	219.5	5.6	271	2	A25528	pancreatic elastase	189	196	5.0	3623	2	T08618	intrinsic factor-B
117	219.5	5.6	761	1	BMS5	complement factor	190	195.5	5.0	271	2	I46580	factor IX - pig (f
118	219	5.6	343	1	A57014	proteasins (EC 3.4.	191	195	4.9	432	1	S18932	u-plasminogen acti
119	218	5.5	271	2	S41308	serine proteinase	192	194.5	4.9	246	1	TRRT1	trypsin (EC 3.4.21
120	217.5	5.5	243	2	A56338	venom proteinase (193	194	4.9	261	2	A25606	tissue kallikrein
121	217	5.5	239	2	A27207	tissue kallikrein	194	194	4.9	267	2	S40006	trypsin (EC 3.4.21
122	217	5.5	268	2	S68825	pancreatic elastase	195	193.5	4.9	249	2	A55634	trypsin (EC 3.4.21
123	217	5.5	273	2	A47246	trypsin (EC 3.4.2	196	193.5	4.9	347	1	HPPR	granzyme M (EC 3.4
124	217	5.5	603	2	S28941	coagulation factor	197	193.5	4.9	2471	2	A49128	haptoglobin precur
125	217	5.5	2703	1	A24420	notch protein - fr	198	193	4.9	240	1	CPBOA3	cell fate determin
126	216.5	5.5	236	2	I42696	thrombin (EC 3.4.2	199	193	4.9	246	1	DBHU	procathepsinidase
127	216.5	5.5	346	2	I36942	haptoglobin - chim	200	191.5	4.9	247	1	A25852	complement factor
128	216.5	5.5	2616	2	A57096	ndel protein prec	201	191.5	4.9	281	2	T13596	trypsin (EC 3.4.21
129	216	5.5	810	1	PLHU	plasmin (EC 3.4.21	202	191.5	4.9	830	2	A30359	P-selectin homolog
130	215.5	5.5	247	1	TRDG	trypsin (EC 3.4.21	203	190.5	4.8	579	2	UC7529	P-selectin precurs
131	215.5	5.5	248	2	S55066	trypsin (EC 3.4.21	204	190.5	4.8	768	2	A42755	membrane-type friz
132	215	5.4	241	2	S39048	trypsin (EC 3.4.21	205	190.5	4.8	1064	2	A40136	P-selectin precurs
133	215	5.4	268	2	S68826	trypsin (EC 3.4.21	206	189.5	4.8	266	2	S54146	fibropellin Ia - s
134	214.5	5.4	247	2	S13813	pancreatic elastase	207	189.5	4.8	1737	2	T00209	MEGF8 protein - hu
135	214.5	5.4	366	2	JE0105	trypsin (EC 3.4.21	208	189	4.8	246	2	JQ1472	trypsin (EC 3.4.21
136	214.5	5.4	593	2	S45281	testicular serine	209	189	4.8	247	2	S05494	trypsin (EC 3.4.21
137	214	5.4	275	2	C35863	coagulation factor	210	189	4.8	253	2	A53968	serine proteinase
138	213.5	5.4	235	2	D42696	trypsin (EC 3.4.2	211	189	4.8	258	4	S70439	pancreatic elastase
139	213.5	5.4	2352	2	T30201	Notch homolog prot	212	189	4.8	267	4	A56615	probable pancreati
140	212	5.4	455	2	I56559	neuropilin - mouse	213	189	4.8	646	2	JN0473	P-selectin precurs
141	212	5.4	455	2	A61545	plasmin (EC 3.4.21	214	188.5	4.8	282	2	I84621	coagulation factor
142	211	5.3	237	2	S68702	trypsin (EC 3.4.2	215	188	4.8	253	2	S15586	tissue kallikrein
143	211	5.3	276	2	A38654	mast cell proteinase	216	187.5	4.8	250	2	S55493	serine proteinase
144	210.5	5.3	1220	2	A56136	lagged protein pre	217	187.5	4.8	259	2	I38363	trypsin (EC 3.4.21
145	210	5.3	2437	2	S42612	transmembrane prot	218	187.5	4.8	304	2	S33496	trypsin (EC 3.4.21
146	209	5.3	433	1	UKMS	u-plasminogen acti	219	187	4.7	246	2	JQ1471	trypsin (EC 3.4.21
147	208.5	5.3	258	2	I36945	haptoglobin Hp - C	220	187	4.7	261	2	S45303	tissue kallikrein
148	207.5	5.3	239	2	G42696	thrombin (EC 3.4.2	221	187	4.7	271	2	S29239	chymotrypsin (EC 3
149	207.5	5.3	269	2	B26823	pancreatic elastase	222	186	4.7	1594	2	T30549	hensin - rabbit
150	207	5.2	238	1	TKRVSY	trypsin-like prote	223	185.5	4.7	711	1	A47136	macrophage-stimula
151	206.5	5.2	246	1	TKRT2	trypsin (EC 3.4.21	224	185.5	4.7	927	1	JQ0948	AS antigen precurs
152	206.5	5.2	256	2	T10109	trypsin (EC 3.4.21	225	185	4.7	256	1	NGMSA	7S nerve growth fa
153	206	5.2	430	1	A24702	serine proteinase	226	183.5	4.7	1372	2	T25933	hypothetical prote
154	206	5.2	4548	1	S00657	apoptotrin(a) (EC	227	183	4.6	265	1	KQRTP	tissue kallikrein
155	205.5	5.2	269	2	B2410	mastocytoma protei	228	183	4.6	332	1	A30100	serine proteinase
156	205.5	5.2	460	2	B61545	plasmin (EC 3.4.21	229	182.5	4.6	722	2	JC5092	E-selectin - pig
157	204.5	5.2	367	2	JE0104	testicular serine	230	182.5	4.6	437	2	S18407	DELTA-like 1 - mou
158	204.5	5.2	752	1	CZHU	complement C2 prec	231	182.5	4.6	2531	2	T31070	notch homolog - se
159	204.5	5.2	1203	2	A49175	Motch B protein -	232	182	4.6	261	1	TRMSMS	tissue kallikrein
160	203.5	5.2	247	1	B25852	trypsin (EC 3.4.21	233	181.5	4.6	247	1	PRMSCL	granzyme B (EC 3.4
161	203.5	5.2	263	1	I55608	complement factor	234	181.5	4.6	247	2	S12764	trypsin (EC 3.4.21
162	203.5	5.2	285	2	I48144	coagulation factor	235	181.5	4.6	258	2	A45161	serine proteinase
163	203.5	5.2	309	2	B49878	coagulation factor	236	181.5	4.6	437	2	S18407	acrosin (EC 3.4.21
164	203.5	5.2	3623	2	T09456	intrinsic factor-B	237	181	4.6	261	1	NGMSG	7S nerve growth fa
165	203	5.1	403	2	C82228	probable trypsin-V	238	181	4.6	448	2	A37344	acrosin (EC 3.4.21
166	202	5.1	240	2	S39047	trypsin (EC 3.4.21	239	181	4.6	1291	2	T21694	hypothetical prote
167	202	5.1	2321	2	S78549	notch protein - h	240	180.5	4.6	248	2	S55067	trypsin (EC 3.4.21
168	201.5	5.1	246	2	B25528	trypsin (EC 3.4.21	241	180.5	4.6	275	2	I46712	factor IX - rabbit
169	200.5	5.1	226	1	KCUF	breachypurin (EC 3.4	242	180.5	4.6	436	2	JX0172	acrosin (EC 3.4.21
170	200.5	5.1	231	1	TRPGR	trypsin (EC 3.4.21	243	180	4.6	254	2	S49329	trypsin-like prote
171	200.5	5.1	231	1	B30848	plasmin (EC 3.4.21	244	180	4.6	261	2	S01971	tissue kallikrein
172	199.5	5.1	247	2	A27547	trypsin (EC 3.4.21	245	180	4.6	275	2	S40005	trypsin (EC 3.4.21
173	199.5	5.1	257	2	S33772	tissue kallikrein	246	179.5	4.6	243	2	A35871	trypsin (EC 3.4.21
174	199.5	5.1	258	2	G02959	haptoglobin - rhes	247	179.5	4.6	259	1	WMMS28	complement factor
175	199.5	5.1	275	2	S40007	trypsin (EC 3.4.21	248	179.5	4.6	274	2	I47078	coagulation factor

249	179.5	4.6	728	2	I50719	C-Delta-1 - chicke	322	161.5	4.1	250	2	S31384	trypsin (EC 3.4.21
250	179.5	4.6	1047	2	A55617	pancreatic precurs	323	161.5	4.1	261	2	S40162	cathepsin G (EC 3.
251	179	4.5	256	1	ELRG	pancreatic elastas	324	161.5	4.1	265	2	T15451	hypothetical prote
252	179	4.5	612	2	B42755	B-selectin precurs	325	161.5	4.1	832	2	A31246	neurogenic protein
253	178.5	4.5	402	2	UH0403	procollagen I C-pr	326	161.5	4.1	880	2	S00670	neurogenic repeat
254	177.5	4.5	248	2	A43520	natural killer cel	327	161.5	4.1	1025	1	A43526	complement C3d/Eps
255	177.5	4.5	420	2	A55283	acrosin (EC 3.4.21	328	161	4.1	1827	2	T34288	hypothetical prote
256	177.5	4.5	1964	2	T09059	notch4 - mouse	329	160.5	4.1	661	1	KRNU13	coagulation factor
257	177	4.5	268	2	UQ1473	pancreatic elastas	330	160	4.1	262	1	A31372	granzyme A (EC 3.4
258	177	4.5	473	2	A56175	adhesive plaque pr	331	160	4.1	3002	2	A47221	fibrillin 1 precur
259	177	4.5	747	2	I51579	complement factor	332	159.5	4.0	1722	2	E89753	fibrillin 1 precur
260	176.5	4.5	1091	1	PL0009	complement C3d/Eps	333	159	4.0	244	2	A44284	tissue kallikrein
261	176	4.5	261	2	A29745	tissue kallikrein	334	159	4.0	261	2	A28062	gamma-tenin (EC 3.
262	176	4.5	261	2	A31136	tissue kallikrein	335	159	4.0	2907	2	A57278	fibrillin-2 precur
263	176	4.5	2318	2	S43306	trypsin-like prote	336	158.5	4.0	247	2	S59135	maet cell proteina
264	176	4.5	274	2	S40004	notch 3 protein -	337	158.5	4.0	385	2	S53718	homeotic protein d
265	175.5	4.4	270	2	A29934	trypsin-related pr	338	158.5	4.0	833	2	S19087	gene Delta protein
266	175	4.4	421	1	S11674	pancreatic elastas	339	158	4.0	610	2	T16761	hypothetical prote
267	175	4.4	232	2	S32398	acrosin (EC 3.4.21	340	158	4.0	2918	2	A54105	fibrillin-2 precur
268	174.5	4.4	229	1	TRDGC	serine proteinase	341	157.5	4.0	579	2	A55740	apern-egg recognit
269	174.5	4.4	259	2	A29746	trypsin (EC 3.4.21	342	157.5	4.0	507	2	T27317	hypothetical prote
270	174	4.4	261	1	KQMS1	tissue kallikrein	343	157	4.0	261	2	A35046	tissue kallikrein
271	174	4.4	1295	2	A32901	tissue kallikrein	344	157	4.0	610	2	A35046	B-selectin precurs
272	173.5	4.4	548	2	D82175	glp1 protein precu	345	156.5	4.0	252	2	A36172	procytotoxic T-lym
273	173.5	4.4	229	1	TRDPS	probable trypsin V	346	156.5	4.0	275	2	UC6506	tumor necrosis fac
274	173	4.4	768	2	I53821	trypsin (EC 3.4.21	347	156.5	4.0	1429	2	S06434	homeotic protein 1
275	173	4.4	248	1	PRMSC2	p-selectin - rat	348	156.5	4.0	3635	2	T10053	laminin alpha 5 ch
276	172.5	4.4	277	2	S35340	granzyme C (EC 3.4	349	156	4.0	259	2	A29586	laminin alpha 5 ch
277	172.5	4.4	431	2	S47538	trypsin (EC 3.4.21	350	156	4.0	702	2	T16832	laminin alpha 5 ch
278	172.5	4.4	449	2	A55362	acrosin (EC 3.4.21	351	155.5	3.9	213	2	S17537	tissue kallikrein
279	172.5	4.4	254	2	S65465	procollagen I C-pr	352	155.5	3.9	485	2	S36772	hypothetical prote
280	172	4.4	251	2	A24378	trypsin-like prote	353	155.5	3.9	533	2	UC7985	fibrinolytic prote
281	172	4.4	230	2	A34170	tissue kallikrein	354	155.5	3.9	250	2	S15685	E-selectin - bov
282	172	4.4	230	2	A27802	acrosin (EC 3.4.21	355	155	3.9	2489	2	I73012	brain-specific CUB
283	171.5	4.3	262	1	KQHU	hypodermin C (EC 3	356	155	3.9	652	2	A34877	kallikrein, glandu
284	171.5	4.3	2403	2	A59386	tissue kallikrein	357	154.5	3.9	252	2	S65551	complement C3b/C4b
285	171.5	4.3	257	2	B45061	sanko - human	358	154	3.9	669	2	S65551	C4b-binding protei
286	171	4.3	250	2	A45061	granzyme A (EC 3.4	359	153.5	3.9	251	2	UC2125	factor H - bovine
287	171	4.3	266	1	ELRT1	granzyme A (EC 3.4	360	153.5	3.9	387	2	B49175	chymase (EC 3.4.21
288	171	4.3	273	2	S40003	pancreatic elastas	361	153.5	3.9	551	2	I46709	endothelial leukoc
289	171	4.3	2139	2	A35672	trypsin-related pr	362	153.5	3.9	1786	1	MMMSB1	laminin beta-1 cha
290	171	4.3	248	2	S33756	crumbs protein - f	363	153	3.9	152	2	A53274	complement factor
291	170	4.3	266	2	UC4850	granzyme-like prote	364	153	3.9	254	1	TRWV3Y	trypsin-like prote
292	170	4.3	251	2	T10262	trypsin-like prote	365	153	3.9	2871	2	A55567	fibrillin I - bovi
293	169.5	4.3	261	1	S35711	maet cell serine p	366	152.5	3.9	248	1	S01007	granzyme F (EC 3.4
294	169.5	4.3	421	1	S29599	semenogelase (EC 3	367	152.5	3.9	264	2	S65663	granzyme 3 (EC 3.4
295	169.5	4.3	560	2	T16833	acrosin (EC 3.4.21	368	152.5	3.9	385	2	A54785	predipocyte facto
296	169.5	4.3	214	2	S17680	hypothetical prote	369	152.5	3.9	422	1	KCHUZ2	plasma protein 2 p
297	169	4.3	246	2	S64707	fibrinolytic prote	370	152	3.9	281	1	A61021	granzyme B (EC 3.4
298	169	4.3	259	2	B31136	chymase (EC 3.4.21	371	152	3.9	686	2	UC7569	Delta-4 protein -
299	169	4.3	504	2	S56745	tissue kallikrein	372	151.5	3.8	761	2	A34079	tissue kallikrein
300	169	4.3	248	2	S33755	mucin (clone pGM31	373	151.5	3.8	216	1	A40332	macrophage-stimula
301	168.5	4.3	597	2	S71352	granzyme-like prot	374	151.5	3.8	977	2	I52657	seizure-related pr
302	168	4.3	2014	2	I36936	metalloproteinase	375	151	3.8	249	1	A35842	chymase (EC 3.4.21
303	168	4.3	251	1	A32297	complement recepto	376	151	3.8	261	2	A41020	tissue kallikrein
304	167.5	4.2	383	2	S53716	semenogelase (EC 3	377	151	3.8	1620	2	T27283	hypothetical prote
305	167.5	4.2	247	2	S45113	delta-like homeoti	378	150.5	3.8	248	2	S43259	granzyme-like prote
306	167	4.2	260	2	A37938	granzyme-like prot	379	150.5	3.8	277	2	A41735	hyaluronate-bindin
307	167	4.2	265	2	T10495	tissue kallikrein	380	150.5	3.8	285	2	T35195	probable serine pr
308	166	4.2	2043	2	T18524	chymotrypsin (EC 3	381	150.5	3.8	685	2	UC7570	Delta-4 protein -
309	165	4.2	449	1	NBHJHS	scavenger receptor	382	150.5	3.8	1053	2	S46159	probable complemen
310	164.5	4.2	1231	1	NBHJHS	complement factor	383	150	3.8	263	1	WMVZSP	apolipoprotein H h
311	164.5	4.2	230	2	I48685	complement factor	384	150	3.8	267	1	ELHUL	leukocyte elastase
312	164	4.2	613	2	S15468	maet cell proteina	385	150	3.8	601	1	B36346	fibrillin 1 precuro
313	164	4.2	2871	2	A55624	fibrillin-1 precu	386	150	3.8	770	2	T00203	LDL receptor-relat
314	164	4.2	276	2	T20239	hypothetical prote	387	149.5	3.8	236	1	A32121	snake venom factor
315	163	4.1	276	2	A47290	TSG-6 homolog P84	388	149.5	3.8	239	1	TRSMG	trypsin (EC 3.4.21
316	162.5	4.1	1290	2	A57190	ednetin precursor	389	149.5	3.8	13288	2	T03099	mucin, submaxillar
317	162.5	4.1	2083	2	T42721	CRP-ductin-alpha p	390	149	3.8	216	1	KYVH20	chymotrypsin (EC 3
318	162.5	4.1	261	1	EGMSB	tissue kallikrein	391	149	3.8	683	2	C36346	fibrillin 1 precuro
319	162	4.1	226	2	S69370	duodenase - bovine	392	149	3.8	770	2	T00204	LDL receptor relat
320	161.5	4.1	248	2	S01006	cytotoxic T-lympho	393	149	3.8	1408	2	S16148	gene serrate prote
321	161.5	4.1					394	149	3.8				

395	148	3.8	218	1	KYH2C	chymotrypsin (EC 3	468	134	3.4	3034	2	T14119	seven-pass transme
396	148	3.8	668	2	A46013	coagulation factor	469	133.5	3.4	154	2	S35207	protease 7 - buf
397	148	3.8	1469	2	B36655	alt protein 2 pre	470	133.5	3.4	1687	2	T30176	EGF repeat transme
398	148	3.8	1480	2	A36655	alt protein 1 pre	471	133.5	3.4	3507	2	T34513	hypothetical prote
399	147.5	3.7	244	2	A46721	chymase (EC 3.4.21	472	133	3.4	810	2	T10756	Nel-homolog protei
400	147.5	3.7	244	2	A34910	mast cell proteina	473	132.5	3.4	331	2	T27906	hypothetical prote
401	147.5	3.7	597	1	S53711	C4BP alpha chain p	474	132	3.3	246	2	A38678	mast cell proteina
402	147.5	3.7	1786	1	MMHUB1	laminin beta-1 cha	475	132	3.3	372	2	JC5177	L-selectin precurs
403	147.5	3.7	4391	2	A38096	perlecan precursor	476	132	3.3	558	2	S57953	C4BP protein alpha
404	147	3.7	236	2	A28566	T-cell suppressor	477	132	3.3	2109	1	I50421	aggreccan precursor
405	147	3.7	259	2	D23863	ribase kallikrein	478	132	3.3	3871	2	T22812	hypothetical prote
406	147	3.7	262	1	JC4803	venombin A (EC 3.4	479	131.5	3.3	302	1	WMBB1E	secretory compleme
407	147	3.7	716	1	JC5061	macrophage-stimula	480	131.5	3.3	1268	2	S52781	neurocan - mouse
408	147	3.7	1557	2	T28811	hypothetical prote	481	130.5	3.3	1257	2	S28764	neurocan precursor
409	147	3.7	3084	1	MMMSA	laminin alpha-1 ch	482	130.5	3.3	3672	2	T23433	hypothetical prote
410	146.5	3.7	236	1	B32121	heparan sulfate fac	483	130.5	3.3	3704	2	T37316	probable laminin a
411	146.5	3.7	3707	2	S18252	hypothetical prote	484	129.5	3.3	223	1	JG0169	venombin A (EC 3.4
412	146	3.7	263	2	T28450	hypothetical prote	485	129.5	3.3	376	2	JC4892	L-selectin precurs
413	145	3.7	256	1	TRPF	trypsin-like prote	486	129.5	3.3	381	1	B26359	decay-accelerating
414	145	3.7	263	1	C36838	L-selectin precurs	487	129.5	3.3	440	2	A26359	venombin AB (EC 3.
415	145	3.7	372	1	A32375	tenascin-like prot	488	129	3.3	235	1	S65621	cathepsin G (EC 3.
416	145	3.7	782	1	A61625	mast cell proteina	489	128.5	3.3	255	2	A27122	hypothetical prote
417	144.5	3.7	246	2	B38678	trypsin homolog -	490	128.5	3.3	321	2	T33161	azurocidin - pig
418	144.5	3.7	303	2	T13598	complement control	491	128	3.2	5147	1	TRPGA2	cadherin-related c
419	144.5	3.7	360	2	B71252	B18L protein - var	492	128	3.2	1531	2	T42218	glyc-1 protein hom
420	144	3.7	685	2	S78040	fibulin, splice fo	493	127.5	3.2	258	2	I56220	laminin gamma-1 ch
421	144	3.7	263	2	B71252	chymase (EC 3.4.21	494	127	3.2	1609	1	MMHUB2	laminin alpha-1 ch
422	143.5	3.6	247	2	S23504	laminin alpha-1 ch	495	127	3.2	1751	1	MMHOMH	laminin alpha-2 ch
423	143	3.6	3075	2	S14458	chymase (EC 3.4.21	496	127	3.2	3106	1	S53868	secreted leucine-r
424	142.5	3.6	260	2	S26043	trypsin-like prote	497	127	3.2	1025	2	T42626	serine proteinase
425	142	3.6	272	2	JC4170	metalloproteinase	498	126.5	3.2	265	2	A38894	serine proteinase
426	141.5	3.6	310	2	S41055	L-selectin precurs	499	126	3.2	265	2	J50260	complement factor
427	141.5	3.6	385	1	A34015	probable serine pr	500	126	3.2	265	2	I56100	plasma protein S p
428	141	3.6	225	2	S45356	cytotoxic T-lympho	501	126	3.2	642	2	S53433	chymotrypsin-like
429	141	3.6	246	2	A32692	chymase (EC 3.4.21	502	126	3.2	254	2	S35585	neutrophil elatase
430	140.5	3.6	246	1	A6504	complement factor	503	125.5	3.2	264	2	I48679	C4b-binding protei
431	140.5	3.6	1234	1	NBM5H	od protein - frui	504	125.5	3.2	597	1	NBHUC4	serine proteinase
432	140.5	3.6	2406	2	A54148	tenascin-like prot	505	125.5	3.2	152	2	S35209	complement factor
433	140.5	3.6	2515	2	S47008	plasma protein Z -	506	125	3.2	323	1	S09702	L-selectin precurs
434	140	3.5	396	1	KXBO2	chymotrypsin (EC 3	507	125	3.2	1790	1	MMERB1	laminin beta-1 cha
435	139.5	3.5	258	1	S44184	hypothetical prote	508	125	3.2	248	2	A33412	cytotoxic T-lympho
436	139.5	3.5	288	1	T33224	UVS.2 protein - Af	509	124.5	3.2	548	2	T16642	hypothetical prote
437	139.5	3.5	319	2	I51569	latent transformin	510	124.5	3.1	330	2	T46256	brevican - human (
438	139	3.5	1820	2	A55494	chymase (EC 3.4.21	511	124	3.1	710	1	I51283	hepatoctye growth
439	138.5	3.5	244	2	S26042	fibulin, splice fo	512	124	3.1	883	2	S49126	brevican precursor
440	138.5	3.5	247	1	KYHUC	hypothetical prote	513	124	3.1	1221	2	A49457	MEGF5 protein - ra
441	138.5	3.5	705	2	S34958	complement factor	514	124	3.1	1583	2	T13953	hypothetical prote
442	138.5	3.5	1111	2	T26972	complement factor	515	124	3.1	1584	2	T22674	hypothetical prote
443	137.5	3.5	191	2	S54115	C4BP protein beta	516	124	3.1	2180	2	T29764	proteinase 5 - buf
444	137.5	3.5	808	2	D35069	L-selectin precurs	517	124	3.1	151	2	S35205	chymotrypsin (EC 3
445	137	3.5	258	2	S57960	protein T22A3.8 [l	518	123.5	3.1	370	2	S49129	hypothetical prote
446	137	3.5	372	2	S23936	hypothetical prote	519	123.5	3.1	699	2	T33375	fibulin-2 precurs
447	137	3.5	2823	2	R87908	laminin alpha chain	520	123.5	3.1	1184	2	A55184	chymotrypsin (EC 3
448	137	3.5	2823	2	T33064	mast cell proteina	521	123.5	3.1	248	2	S49323	epidermal growth f
449	137	3.5	3102	2	T43291	cyteine rich prot	522	123.5	3.1	308	2	JC7125	decay-accelerating
450	136.5	3.5	247	1	PRRTG	membrane-bound com	523	123	3.1	340	2	I56234	hypothetical prote
451	136.5	3.5	1274	1	T42012	complement C3b rec	524	123	3.1	798	2	T22793	hypothetical prote
452	136	3.4	360	1	WMBB2E	MEGF6 protein - ra	525	123	3.1	1081	2	S28829	receptor tyrosine
453	136	3.4	676	2	A45900	laminin gamma-1 ch	526	123	3.1	152	2	S35206	serine proteinase
454	136	3.4	1574	2	T13954	myonase (EC 3.4.-	527	123	3.1	198	2	I46002	C4BP beta chain -
455	135.5	3.4	226	2	JE0151	hypothetical prote	528	122.5	3.1	676	1	KXHUS	plasma protein S p
456	135.5	3.4	372	2	T29359	complement factor	529	122	3.1	1810	1	AGCH	tenascin precursor
457	135.5	3.4	452	2	A35068	C4b-binding protei	530	122	3.1	245	2	A48598	agrin precursor -
458	135.5	3.4	465	1	NBMS4	coagulation factor	531	122	3.1	416	2	T20448	kallikrein-like se
459	135.5	3.4	159	2	I84615	apolipoprotein H p	532	122	3.1	630	1	I46001	hypothetical prote
460	135	3.4	343	1	G35070	protein P40E10.4 [533	121.5	3.1	5376	2	T42215	C4b-binding protei
461	135	3.4	345	1	NBHU	hypothetical prote	534	121.5	3.1	1627	2	A43902	tenascin - eastern
462	135	3.4	3051	2	S42373	protein P40E10.4 [535	121.5	3.1	2409	1	A60979	pregnancy-associat
463	135	3.4	601	2	D89711	venombin A (EC 3.4	536	121	3.1				versican precursor
464	134.5	3.4	601	2	T22025		537	121					
465	134.5	3.4	232	1	A54361		538	121					
466	134	3.4	2824	2	T22759		539	121					
467	134	3.4					540	121					

541	120.5	3.1	247	2	S64708	chymase (EC 3.4.21	614	112	2.8	228	1	S35689	venombin A (EC 3.4
542	120.5	3.1	252	2	T46247	hypothetical prote	615	112	2.8	918	2	JC4361	scavenger receptor
543	120.5	3.1	345	1	JN0465	apolipoprotein H p	616	112	2.8	1125	1	S57846	protein-tyrosine k
544	120.5	3.1	497	2	JC2054	complement regulat	617	112	2.8	1253	1	JH0675	restrictin precurs
545	120.5	3.1	666	2	S38819	plasma protein S-to	618	112	2.8	1639	1	MMFEB2	laminin gamma-1 ch
546	120.5	3.1	689	2	T42760	fibulin, splice fo	619	112	2.8	3562	2	A47171	chondroitin sulfat
547	120.5	3.1	712	2	T42990	fibulin 1, splice	620	112	2.8	4307	2	T20721	hypothetical prote
548	120.5	3.1	728	1	A60185	hepatocyte growth	621	111.5	2.8	159	2	S35202	proteinase 2 - buf
549	120.5	3.1	1394	2	A35626	transforming growt	622	111.5	2.8	370	2	JC7592	spinal cord-deriv
550	120.5	3.1	1801	1	MMRTS	laminin beta-2 cha	623	111.5	2.8	651	2	T19477	hypothetical prote
551	120	3.0	257	1	JC2479	venombin B (EC 3.4	624	111.5	2.8	1328	2	T43060	agrin - electric r
552	120	3.0	363	2	B43900	complement C3d/Eps	625	111.5	2.8	1797	2	A55677	laminin beta-2 cha
553	120	3.0	493	2	JC5621	epidermal growth f	626	111.5	2.8	2019	1	JQ1322	tenascin precursor
554	120	3.0	589	2	T43210	fibulin-1D precurs	627	111.5	2.8	2531	2	T16743	hypothetical prote
555	120	3.0	912	2	A54423	brevican precursor	628	111.5	2.8	4351	2	T00252	hypothetical prote
556	120	3.0	1548	2	S34583	serine proteinase	629	111	2.8	231	2	A60468	MEGR1 protein - ra
557	120	3.0	1643	2	T14274	versican precursor	630	111	2.8	915	2	T21773	venombin A (EC 3.4
558	120	3.0	2397	1	A55535	versican precursor	631	110.5	2.8	234	1	S20407	hypothetical prote
559	120	3.0	3381	2	T42389	coagulation factor	632	110.5	2.8	297	1	T21773	venombin A (EC 3.4
560	119.5	3.0	161	2	I48158	complement C3b/C4b	633	110.5	2.8	408	2	T22801	apolipoprotein H p
561	119.5	3.0	482	2	A34924	plasma protein S p	634	110.5	2.8	583	2	A29154	hypothetical prote
562	119.5	3.0	675	1	KCBOS	hel protein - chic	635	110.5	2.8	678	2	B48089	growth arrest-spec
563	119.5	3.0	835	2	JF0076	integumentary muc	636	110.5	2.8	692	2	T32980	chromospondin 4 p
564	119.5	3.0	1247	1	MMHUND	protein apx-1 lim	637	110.5	2.8	961	1	TSHUP4	plexin 1 precursor
565	119.5	3.0	1506	2	T30886	hepatocyte growth	638	110.5	2.8	1217	1	EGMSMG	hypothetical prote
566	119	3.0	258	2	A57290	hepatocyte growth	639	110.5	2.8	1894	2	JC4980	protein-tyrosine k
567	119	3.0	513	2	D88991	venom plasminogen	640	110	2.8	266	2	T12992	plexin 1 precursor
568	118.5	3.0	674	2	I55476	growth potentiati	641	110	2.8	1124	1	I58388	hypothetical prote
569	118.5	3.0	728	1	A35644	hepatocyte growth	642	110	2.8	1905	2	S06176	cytotoxic T-lympho
570	118.5	3.0	133	2	S21114	hepatocyte growth	643	109.5	2.8	198	2	I51553	LR1 protein - mou
571	118	3.0	196	2	T08808	apernadhesin AMN -	644	109.5	2.8	2215	2	T00348	hypothetical prote
572	118	3.0	196	2	T08808	hypothetical prote	645	109	2.8	661	2	T42754	hypothetical prote
573	118	3.0	293	2	B26637	neurogenic repetit	646	109	2.8	1808	2	T15099	hypothetical prote
574	118	3.0	838	2	T20125	hypothetical prote	647	109	2.8	2610	2	T20968	hypothetical prote
575	118	3.0	883	2	S57653	brevican precursor	648	108.5	2.8	236	1	A41456	venombin A (EC 3.4
576	117.5	3.0	188	2	B32340	tissue kallikrein	649	108.5	2.8	2825	2	T14271	Doc4 protein, stre
577	117.5	3.0	259	2	T21011	hypothetical prote	650	108	2.7	251	1	TRHUZ2	azurocidin precurs
578	117.5	3.0	642	2	SS3434	plasma protein S p	651	108	2.7	1450	2	T30273	hypothetical prote
579	117.5	3.0	966	2	JH0237	apolipoprotein E r	652	108	2.7	1700	2	S08167	Baldian ring 3 pr
580	117.5	3.0	1160	2	F88369	protein unc-52 lim	653	108	2.7	2476	2	T34022	zonadhesin - pig
581	117.5	3.0	2295	2	C88369	protein unc-52 lim	654	107.5	2.7	640	2	T19346	hypothetical prote
582	117.5	3.0	3375	2	T19821	hypothetical prote	655	107.5	2.7	670	2	I65967	disintegrin-like m
583	116.5	3.0	256	1	PRHU	proteinase 3 (EC 3	656	107.5	2.7	3566	1	A40701	tenascin-X precurs
584	116.5	3.0	377	2	I54479	membrane cofactor	657	107.5	2.7	4544	1	S02392	alpha-2-macroglobu
585	116.5	3.0	378	2	B59180	Wnt inhibitory fac	658	107	2.7	280	2	G02741	skeletal muscle LI
586	116.5	3.0	384	2	S01896	membrane cofactor	659	107	2.7	497	2	T27827	hypothetical prote
587	116.5	3.0	1170	2	A53612	laminin B1k chain	660	106.5	2.7	192	2	E70414	hypothetical prote
588	116	2.9	1376	2	G00043	osteonidogen - hum	661	106.5	2.7	362	2	JC5194	hypothetical prote
589	115.5	2.9	440	2	A43519	complement recepto	662	106.5	2.7	369	2	JC5138	membrane cofactor
590	115.5	2.9	1474	2	D88550	protein ZC84.6 lim	663	106.5	2.7	616	2	T29234	hypothetical prote
591	115.5	2.9	1680	2	A43434	furin (EC 3.4.21.7	664	106.5	2.7	755	2	A44315	cartilage oligomer
592	115	2.9	279	2	JG0164	lim protein, FHL4	665	106	2.7	417	2	T33376	hypothetical prote
593	115	2.9	1207	1	EGHU	epidermal growth f	666	106	2.7	657	2	T00859	hypothetical prote
594	114.5	2.9	270	2	I37278	complement factor	667	106	2.7	927	2	T21772	hypothetical prote
595	114.5	2.9	349	2	G02913	sperm CD46 - human	668	106	2.7	1133	1	EGRT	epidermal growth f
596	114.5	2.9	369	2	I57998	membrane cofactor	669	106	2.7	1142	2	T30272	hypothetical prote
597	114.5	2.9	1798	2	SS3869	laminin beta-2 cha	670	106	2.7	1532	2	H88380	protein T22F7.3 li
598	114	2.9	255	1	A28169	venombin A (EC 3.4	671	106	2.7	1805	2	T21888	hypothetical prote
599	114	2.9	741	2	T46488	integrin beta chat	672	106	2.7	2195	2	T34264	hypothetical prote
600	114	2.9	846	2	A30889	hypothetical prote	673	105.5	2.7	596	2	T46914	hypothetical prote
601	114	2.9	1069	2	T42681	hypothetical prote	674	105.5	2.7	673	2	A45664	variant-specific s
602	113.5	2.9	293	2	T22919	hypothetical prote	675	105.5	2.7	860	1	A48089	growth arrest-spec
603	113.5	2.9	502	2	T20130	hypothetical prote	676	105	2.7	1107	2	QRHLD	LDL receptor precu
604	113.5	2.9	558	2	T17324	hypothetical prote	677	105	2.7	1746	1	S19694	hypothetical prote
605	113.5	2.9	574	2	B88465	protein B0244.8 li	678	105	2.7	1746	1	S19694	tenascin precursor
606	113.5	2.9	879	1	ORRTUD	LDL receptor precu	679	105	2.7	2201	2	A32160	tenascin-C - human
607	113.5	2.9	1712	2	A38261	masking protein pr	680	104.5	2.6	345	1	NBMS	apolipoprotein H p
608	112.5	2.9	161	2	I62744	pancreatic elasta	681	104.5	2.6	1360	2	T33922	apolipoprotein H p
609	112.5	2.9	264	2	A28942	spinal cord-deriv	682	104	2.6	345	1	NBBO	transcription fact
610	112.5	2.9	370	2	UC7591	troponozole cyatei	683	104	2.6	360	1	A55198	Wnt inhibitory fac
611	112.5	2.9	677	2	C42125	mltimerin, endoth	684	104	2.6	473	2	T32326	hypothetical prote
612	112.5	2.9	1228	2	A57384	hypothetical prote	685	104	2.6	473	2	T32326	hypothetical prote
613	112.5	2.9	1797	2	T21889	hypothetical prote	686	104	2.6	2101	2	S57245	insulin receptor (

687	104	2.6	4135	2	T42629	760	98	2.5	102	2	B55885	chondroitin sulfat
688	103.5	2.6	383	2	T21946	761	98	2.5	357	2	S23403	sperm surface prot
689	103	2.6	331	2	A45292	762	98	2.5	909	1	ORXLL1	LDL receptor 1 pre
690	103	2.6	412	2	S72579	763	98	2.5	937	2	I53282	gene PACE4 protein
691	103	2.6	1296	2	T16859	764	98	2.5	1087	2	T31100	probable potassium
692	103	2.6	2148	2	A56081	765	98	2.5	1748	2	UN0786	integrin beta-4 ch
693	102.5	2.6	153	2	S35204	766	98	2.5	2588	2	T14342	NSD1 protein - mou
694	102.5	2.6	473	2	I49283	767	98	2.5	4660	2	T42737	gp130 protein prec
695	102.5	2.6	565	2	T16408	768	97.5	2.5	577	2	A26501	chromodulin pre
696	102.5	2.6	873	1	ORRBD	769	97.5	2.5	837	1	A29512	LDL receptor precu
697	102	2.6	149	2	S35208	770	97.5	2.5	878	2	B71460	probable outer mem
698	102	2.6	280	2	G01884	771	97.5	2.5	884	2	T18649	hypothetical prote
699	102	2.6	380	2	G01639	772	97.5	2.5	1162	2	T21557	hypothetical prote
700	102	2.6	411	2	D88087	773	97.5	2.5	2946	2	T15840	hypothetical prote
701	102	2.6	718	2	T29448	774	97	2.5	126	2	A23473	chymotrypsin-like
702	102	2.6	863	2	S51789	775	97	2.5	379	2	T27350	hypothetical prote
703	102	2.6	1168	2	I56985	776	97	2.5	429	2	T21113	hypothetical prote
704	102	2.6	1713	2	A55347	777	97	2.5	626	2	T27319	hypothetical prote
705	102	2.6	4006	2	T09070	778	97	2.5	799	1	IUMGFB	fibronectin recept
706	101.5	2.6	379	2	T16213	779	97	2.5	808	2	T23129	hypothetical prote
707	101.5	2.6	1106	2	T18739	780	97	2.5	862	2	S43922	versican - pig-tai
708	101.5	2.6	1959	1	AGRT	781	97	2.5	915	1	A48225	subtilisin-like pr
709	101.5	2.6	2415	1	A39086	782	97	2.5	1138	1	S24066	protein-tyrosine k
710	101	2.6	377	2	C88710	783	97	2.5	1133	2	A44018	laminin B2c chain
711	101	2.6	463	2	T26655	784	97	2.5	1292	2	T09329	galactose binding
712	101	2.6	557	2	A48434	785	96.5	2.4	149	1	KQSM	tissue kallikrein
713	101	2.6	1371	2	A33837	786	96.5	2.4	317	2	D42526	BSR protein - vacc
714	101	2.6	1378	2	A36429	787	96.5	2.4	613	2	A69533	thrombospondin 3 p
715	101	2.6	1875	2	T48751	788	96.5	2.4	966	2	A57121	M130 antigen precu
716	100.5	2.5	417	2	T20199	789	96.5	2.4	1149	2	T38006	hypothetical prote
717	100.5	2.5	670	2	S77463	790	96.5	2.4	1193	2	T21133	proteolipain - se
718	100.5	2.5	802	2	T24293	791	96.5	2.4	1297	2	T30274	hemocytin - silkw
719	100.5	2.5	949	2	T24294	792	96.5	2.4	3133	2	S52093	ACN-3 protein - pi
720	100.5	2.5	956	1	A46016	793	96	2.4	116	2	S17567	spermatidhesin AQN-3
721	100.5	2.5	1252	2	S36016	794	96	2.4	116	2	S39434	crysin-related pr
722	100.5	2.5	1356	2	A45445	795	96	2.4	256	2	A56593	hypothetical prote
723	100	2.5	152	2	S35203	796	96	2.4	332	2	T25213	integrin beta-1* c
724	100	2.5	421	2	T25383	797	96	2.4	798	2	A28193	integrin beta-1* c
725	100	2.5	667	2	A48579	798	96	2.4	886	2	A57132	probable hormone r
726	100	2.5	873	1	A49729	799	96	2.4	4753	1	A47437	LDL-receptor-relat
727	100	2.5	1122	2	I54237	800	96	2.4	177	2	S23505	chymase (EC 3.4.21
728	100	2.5	1123	1	UN0712	801	95.5	2.4	218	2	H70770	probable regulator
729	100	2.5	1125	1	JH0771	802	95.5	2.4	330	2	B82415	probable serine pr
730	100	2.5	1151	2	I38004	803	95.5	2.4	427	2	JC4915	hypothetical prote
731	100	2.5	1156	2	I38005	804	95.5	2.4	561	2	T27318	mucin SMC (clone L
732	100	2.5	1251	2	A57293	805	95.5	2.4	1042	2	A57534	G2-G1 polypeptid
733	100	2.5	1299	2	T13251	806	95.5	2.4	1135	1	QJ0128	hypothetical prote
734	100	2.5	330	2	I55975	807	95.5	2.4	1270	2	T22615	peptidyl prollyl ci
735	99.5	2.5	640	1	A30452	808	95.5	2.4	3191	2	T39621	gastric mucin MUC5
736	99.5	2.5	686	2	S43562	809	95.5	2.4	463	2	T39621	LDL receptor prec
737	99.5	2.5	914	1	S07047	810	95	2.4	850	2	S56015	hypothetical prote
738	99.5	2.5	1280	2	A39117	811	95	2.4	869	2	T01519	mucin MUC5B, trach
739	99.5	2.5	1350	2	S00647	812	95	2.4	1245	1	MMG5ND	spermatidhesin AQN-1
740	99.5	2.5	1766	2	A42125	813	95	2.4	1321	2	JEO352	hypothetical prote
741	99.5	2.5	1847	2	T18308	814	95	2.4	643	2	T25473	LDL receptor precu
742	99.5	2.5	1984	2	T13171	815	95	2.4	736	2	S47645	hypothetical prote
743	99	2.5	589	2	B38128	816	94.5	2.4	862	1	QRM5LD	protein ZC84.1 (im
744	99	2.5	591	2	I48141	817	94.5	2.4	1216	2	T26104	epidermal growth f
745	99	2.5	675	1	KQMS	818	94.5	2.4	1416	1	A45558	insulin-like growt
746	99	2.5	675	1	KQRTS	819	94.5	2.4	258	1	B37252	platelet-derived g
747	99	2.5	805	2	S68441	820	94.5	2.4	370	2	UC7998	hypothetical prote
748	99	2.5	892	2	S68439	821	94.5	2.4	634	2	T02594	neuregulin-3 (limp
749	99	2.5	894	2	S68437	822	94.5	2.4	713	2	T44447	hypothetical prote
750	99	2.5	900	2	S68440	823	94	2.4	736	2	T06757	hypothetical prote
751	99	2.5	1162	2	S68438	824	94	2.4	899	2	G02428	subtilisin-like pr
752	99	2.5	1558	2	A82457	825	94	2.4	915	2	UC6148	subtilisin-like pr
753	99	2.5	2809	2	T30213	826	94	2.4	932	2	I52527	PAC64A - mouse (fr
754	98.5	2.5	317	2	T28605	827	94	2.4	1381	2	T31083	paranodin - rat
755	98.5	2.5	317	2	F72172	828	94	2.4	1385	2	T14158	neurexin IV - mous
756	98.5	2.5	427	2	G36855	829	94	2.4				
757	98.5	2.5	427	2	S74211	830	94	2.4				
758	98.5	2.5	1178	1	A39804	831	94	2.4				
759	98	2.5	82	2	T46510	832	94	2.4				

833	94	2.4	3097	2	T00021	DN-cadherin - fru1	906	89.5	2.3	854	1	ORHVL	LDL receptor precu
834	93.5	2.4	258	2	A45403	insulin-like growt	907	89.5	2.3	1164	2	T01871	RNA-directed DNA p
835	93.5	2.4	317	2	U01789	BRK protein precu	908	89.5	2.3	1258	2	A12155	WD-repeat protein
836	93.5	2.4	449	2	TJ35048	probable ATP/GTP	909	89.5	2.3	1364	2	T00250	MEGF2 protein - hu
837	93.5	2.4	456	2	T31483	hypothetical prote	910	89	2.3	319	2	A53502	folliclestatin - Afr1
838	93.5	2.4	466	2	S49820	PtII protein - Ara	911	89	2.3	354	2	T23274	hypothetical prote
839	93.5	2.4	612	2	JH0799	laminin-related pr	912	89	2.3	369	2	F81178	histone deacetylase
840	93.5	2.4	739	2	B88553	protein K04H4.2b1	913	89	2.3	390	2	C90208	hypothetical prote
841	93.5	2.4	1115	2	S40241	G protein-coupled	914	89	2.3	469	1	NM1V27	exo-alpha-sialidas
842	93.5	2.4	1166	1	S57845	protein-tyrosine k	915	89	2.3	525	2	T21357	hypothetical prote
843	93	2.4	104	2	T19868	hypothetical prote	916	89	2.3	907	2	I50404	p50b/p57 (lyc-10)
844	93	2.4	329	2	A48805	insulin-like growt	917	89	2.3	1110	1	B42544	G2-G1 polyprotein
845	93	2.4	873	1	I48952	VDL receptor prec	918	89	2.3	1170	2	A40558	thrombospondin 1 p
846	93	2.4	995	2	A56599	embryo kinase 5 -	919	88.5	2.2	317	2	T37442	EBV gp42, ps/hr pro
847	93	2.4	2767	1	UIHU	thyroglobulin prec	920	88.5	2.2	356	2	T20656	hypothetical prote
848	93	2.4	4545	1	S25111	alpha-2-macroglobu	921	88.5	2.2	438	2	T40509	lim domain protein
849	92.5	2.3	211	2	A46458	human CRI homolog	922	88.5	2.2	693	2	I37570	zinc finger protei
850	92.5	2.3	736	2	T19366	hypothetical prote	923	88.5	2.2	754	2	T47886	transketolase-like
851	92.5	2.3	756	2	S47656	TMDC II protein -	924	88.5	2.2	905	2	S55059	feritin alpha-I -
852	92.5	2.3	802	1	IUCH3	integrin, band 3 p	925	88.5	2.2	1077	2	T41146	probable cyteine-
853	92.5	2.3	955	2	A45441	thrombospondin 4 -	926	88.5	2.2	1096	2	T16875	hypothetical prote
854	92.5	2.3	1367	1	IGHUR1	insulin-like growt	927	88.5	2.2	1170	1	TSHUP1	thrombospondin 1 p
855	92	2.3	334	2	T23027	hypothetical prote	928	88.5	2.2	1978	2	T07081	acetyl-CoA carboxy
856	92	2.3	650	2	A34498	glycoprotein anti	929	88	2.2	621	2	I38467	low density lipopr
857	92	2.3	719	2	T00266	hypothetical prote	930	88	2.2	656	2	JC2005	integrin beta-5 ch
858	92	2.3	915	2	B48225	hypothetical prote	931	88	2.2	798	2	B27079	fibronectin recept
859	92	2.3	964	2	JC5545	integrin beta-4 pr	932	88	2.2	799	2	A38308	integrin beta-5 ch
860	92	2.3	1097	2	S68685	adenylate cyclase	933	88	2.2	962	2	JC5571	subtilisin-like pr
861	92	2.3	1444	2	T15856	angiogenesis inhib	934	88	2.2	1085	2	C96797	uncommon protein (l
862	92	2.3	1895	2	T15881	hypothetical prote	935	88	2.2	1175	2	S52417	E-selectin ligand
863	92	2.3	2533	2	T28675	alpha-5ID immobili	936	88	2.2	1192	2	S69000	laminin gamma 2 ch
864	92	2.3	3869	2	A48205	All-1 protein +GIR	937	87.5	2.2	554	2	A45818	cytolysin precursor
865	91.5	2.3	237	2	I47031	insulin-like growt	938	87.5	2.2	580	2	A37107	spermatogenesis pr
866	91.5	2.3	250	2	T30124	hypothetical prote	939	87.5	2.2	584	1	C8HUA	complement C8 alph
867	91.5	2.3	303	2	H35068	apolipoprotein H-r	940	87.5	2.2	667	2	T01999	hypothetical prote
868	91.5	2.3	511	2	T17298	hypothetical prote	941	87.5	2.2	914	1	JC6319	iodide peroxidase
869	91.5	2.3	588	2	T33815	hypothetical prote	942	87.5	2.2	1807	2	TJ6319	integrin beta-4 ch
870	91.5	2.3	640	2	S49932	MET30 protein - ye	943	87.5	2.2	1816	1	S68960	laminin alpha-4 ch
871	91.5	2.3	1101	2	T16840	hypothetical prote	944	87	2.2	387	2	I38449	extracellular prote
872	91.5	2.3	1161	2	D83076	type 4 fibrillar bi	945	87	2.2	706	2	S74610	hypothetical prote
873	91.5	2.3	2144	2	S71490	aah1 protein - fru	946	87	2.2	743	2	T40521	hypothetical prote
874	91.5	2.3	2672	2	A48126	translation activa	947	87	2.2	860	2	T16892	hypothetical prote
875	91.5	2.3	2910	2	T42214	otogelin - mouse	948	87	2.2	970	2	T18842	receptor protein-c
876	91	2.3	94	2	PC2013	tissue kallikrein	949	87	2.2	975	2	JC5570	subtilisin-like pr
877	91	2.3	293	2	T09065	transcription fac	950	87	2.2	1042	2	T26644	hypothetical prote
878	91	2.3	319	1	I50370	hypothetical prote	951	87	2.2	1056	2	A53767	mucin MUC5B, crach
879	91	2.3	398	2	E71539	tumor necrosis fac	952	87	2.2	1134	1	JN0711	protein-tyrosine k
880	91	2.3	435	2	S4182	gene Tf52 protein	953	87	2.2	1945	2	T13937	plexin A - fru1 f
881	91	2.3	478	2	S47040	LDL receptor 2 pre	954	87	2.2	2481	2	A43908	trichostax homolog
882	91	2.3	909	1	QRXL2	surface antigen - p	955	87	2.2	3968	2	A44655	hypothetical prote
883	91	2.3	2543	2	T31687	alpha-2-macroglobu	956	86.5	2.2	222	2	S72795	hypothetical prote
884	91	2.3	4543	1	A53102	epidermal growth f	957	86.5	2.2	264	2	T16271	polylferredoxin 4x2
885	90.5	2.3	53	2	S17294	urokinase-type pla	958	86.5	2.2	336	2	D69074	hypothetical prote
886	90.5	2.3	330	1	JN0561	LIM protein kinase	959	86.5	2.2	391	2	T34284	hypothetical prote
887	90.5	2.3	642	1	JPO079	meprin A (EC 3.4.2	960	86.5	2.2	471	2	I79528	alkaline phosphata
888	90.5	2.3	746	1	HYHWA	androgen-regulated	961	86.5	2.2	585	2	I46686	complement compone
889	90.5	2.3	776	2	S28258	gamma-aminobutyric	962	86.5	2.2	632	2	T21602	hypothetical prote
890	90.5	2.3	960	2	JE0356	transcription fac	963	86.5	2.2	638	2	AF3463	flagellar protein
891	90.5	2.3	1104	2	I38869	M polypeptide prec	964	86.5	2.2	641	2	F71810	type III DNA modif
892	90.5	2.3	1148	1	GNVUNE	hypothetical prote	965	86.5	2.2	651	2	T05869	hypothetical prote
893	90.5	2.3	1357	2	T16860	antigen WC1.1 prec	966	86.5	2.2	700	2	A32392	protein kinase C (
894	90.5	2.3	1436	2	A46496	von Willebrand fac	967	86.5	2.2	734	2	C81399	isochlorate dehydro
895	90.5	2.3	2813	1	VWNU	tissue kallikrein	968	86.5	2.2	1172	2	A42387	thrombospondin 2 p
896	90	2.3	156	2	B23863	hypothetical prote	969	86.5	2.2	1376	1	J01534	E2 glycoprotein pr
897	90	2.3	340	2	T34423	p47 protein - pig	970	86.5	2.2	1478	2	D75821	ribonucleoside-dip
898	90	2.3	409	2	T11743	hypothetical prote	971	86.5	2.2	1413	2	A20872	ovostatin precursor
899	90	2.3	417	2	T29864	hypothetical prote	972	86.5	2.2	3712	1	YGCEVC	alpha-aminoadipyl-
900	90	2.3	522	2	T29767	integrin beta-6 ch	973	86.5	2.2	455	2	B82525	conserved hypotet
901	90	2.3	577	2	B37057	nicotinic dehydroge	974	86	2.2	713	2	A35502	major surface-labe
902	90	2.3	814	1	I39627	alpha-5ID-immobili	975	86	2.2	738	2	S40992	hypothetical prote
903	90	2.3	2533	2	T28674	DNA binding protei	976	86	2.2	905	2	T23229	hypothetical prote
904	89.5	2.3	417	2	T39939	endopeptidase 2 (E	977	86	2.2	906	2	A71438	probable resistanc
905	89.5	2.3	748	2	S24134		978	86	2.2				

979	86	2.2	933	1	OPHUT	iodide peroxidase	1052	83.5	2.1	311	2	JC7873	L-rihamose-binding
980	86	2.2	969	1	A39490	subtilisin-like pr	1053	83.5	2.1	344	2	A32141	foliistatin 1 prec
981	86	2.2	1487	1	S48719	phospholipase-A(2)	1054	83.5	2.1	348	2	T28623	hypothetical prote
982	86	2.2	1572	2	T00027	brain-specific ang	1055	83.5	2.1	354	2	G64475	GTP-binding protei
983	86	2.2	1650	2	S53457	dominant autoantig	1056	83.5	2.1	358	1	A55973	transcription fact
984	86	2.2	2233	2	T28659	surface protein 51	1057	83.5	2.1	366	2	I53035	lithorax homolog
985	85.5	2.2	317	2	A38493	ps/hr protein - va	1058	83.5	2.1	491	2	H83770	hypothetical prote
986	85.5	2.2	340	1	B55973	transcription fact	1059	83.5	2.1	579	2	B84192	pyruvate kinase [l
987	85.5	2.2	344	1	A27701	collagenin precur	1060	83.5	2.1	589	2	C38128	epithelin/granulin
988	85.5	2.2	358	2	B64427	carbamoyl-phosphat	1061	83.5	2.1	697	2	H86457	76 kD hypothetical
989	85.5	2.2	463	1	A36479	milk fat globule m	1062	83.5	2.1	873	2	D88482	protein C05D11.8 [
990	85.5	2.2	515	2	T05863	hypothetical prote	1063	83.5	2.1	1106	2	T13938	gene shuttla craft
991	85.5	2.2	638	2	S22491	acetoacetate synth	1064	83.5	2.1	2120	2	T30243	alpha tectorin - c
992	85.5	2.2	663	2	T21010	hypothetical prote	1065	83.5	2.1	2702	2	S09118	G surface protein
993	85.5	2.2	798	2	S01659	integrin beta-1 ch	1066	83.5	2.1	4302	2	A38971	polycystic kidney
994	85.5	2.2	1162	2	PC4184	lactin receptor, O	1067	83.5	2.1	13055	2	T16580	hypothetical prote
995	85.5	2.2	1229	2	H84465	hypothetical RNA p	1068	83	2.1	304	2	A83513	probable transcrip
996	85.5	2.2	2452	1	RN202L	DNA-directed RNA p	1069	83	2.1	351	2	S20078	NOV protein - chic
997	85.5	2.2	2457	2	T18492	hypothetical prote	1070	83	2.1	372	2	T39244	probable phospho-2
998	85	2.2	200	2	T42678	hypothetical prote	1071	83	2.1	451	2	F83747	denosylmethionine-
999	85	2.2	291	2	I38098	C-plasminogen acti	1072	83	2.1	492	2	D35114	anthranilate synth
1000	85	2.2	318	2	H86342	hypothetical prote	1073	83	2.1	593	1	GYHU	granulin precursor
1001	85	2.2	343	2	S55369	foliistatin - chic	1074	83	2.1	770	2	S04847	leukocyte adhesion
1002	85	2.2	359	1	I51734	transcription fact	1075	83	2.1	770	2	D89447	protein F57C12.1 [
1003	85	2.2	413	2	T23098	hypothetical prote	1076	83	2.1	771	2	A45839	leukocyte adhesion
1004	85	2.2	542	2	A84554	hypothetical prote	1077	83	2.1	800	2	S54623	probable mitochond
1005	85	2.2	552	2	F83417	sulfite reductase	1078	83	2.1	806	2	C69493	hypothetical prote
1006	85	2.2	606	2	S43118	finger protein - m	1079	83	2.1	1046	2	F71432	hypothetical prote
1007	85	2.2	638	2	S22490	acetoacetate synth	1080	83	2.1	1066	2	B95037	hyaluronidase [lmp
1008	85	2.2	653	2	G96675	hypothetical prote	1081	83	2.1	1111	2	T00324	hypothetical prote
1009	85	2.2	671	1	UYPV19	noncaspid protein	1082	83	2.1	1373	2	JE0095	gastric mucin MUC5
1010	85	2.2	752	1	T26508	hypothetical prote	1083	83	2.1	2116	1	ZLVNSY	genome polyprotein
1011	85	2.2	794	2	F88508	protein H14A12.6 [1084	83	2.1	3020	2	A43932	mucin 2 precursor,
1012	85	2.2	895	2	S74225	lactin receptor, i	1085	82.5	2.1	328	2	F83599	hypothetical prote
1013	85	2.2	1021	2	S26985	probable DNA-direc	1086	82.5	2.1	429	2	A42972	coagulation factor
1014	85	2.2	1078	2	F97907	hyaluronate lyase	1087	82.5	2.1	466	2	S29302	complement C8 beta
1015	85	2.2	1148	1	J01604	M polyprotein prec	1088	82.5	2.1	591	1	C8HUB	hypothetical prote
1016	85	2.2	1533	1	T00344	glutamate synthase	1089	82.5	2.1	753	2	T19338	ribonucleoside-dip
1017	85	2.2	1538	2	S73296	hypothetical prote	1090	82.5	2.1	761	2	E82223	integrin beta3 - c
1018	85	2.2	2150	2	T32497	OX40 antigen precu	1091	82.5	2.1	984	2	T00326	hypothetical prote
1019	84.5	2.1	271	2	S12783	foliistatin - shue	1092	82.5	2.1	994	2	I57549	adenosine deaminas
1020	84.5	2.1	337	2	I47079	foliistatin - bov1	1093	82.5	2.1	1175	2	T34121	insulin receptor p
1021	84.5	2.1	429	2	I45894	hypothetical prote	1094	82.5	2.1	1372	2	A34157	teratocarcinoma-de
1022	84.5	2.1	494	2	A99683	alkaline phosphata	1095	82	2.1	188	2	A39787	deoxyribonuclease
1023	84.5	2.1	494	2	A99683	H+-transporting tw	1096	82	2.1	235	2	AE0114	chitinase (EC 3.2.
1024	84.5	2.1	505	2	A46570	finger protein (C1	1097	82	2.1	338	2	S65019	foliistatin - mous
1025	84.5	2.1	505	2	A46570	hypothetical prote	1098	82	2.1	343	2	S45321	G2R protein - vari
1026	84.5	2.1	615	2	S06346	GGBF family prote	1099	82	2.1	349	2	D72175	cabon storage regu
1027	84.5	2.1	654	2	T30136	hypothetical prote	1100	82	2.1	432	2	D83904	4-chlorobenzoate-C
1028	84.5	2.1	696	2	A12849	GGBF family prote	1101	82	2.1	528	2	B42560	stereoid/thyroid/re
1029	84.5	2.1	696	2	G97626	hypothetical prote	1102	82	2.1	583	2	T34121	formate-tetrahydro
1030	84.5	2.1	744	2	A43353	acetic acidoglyco	1103	82	2.1	599	2	B82439	hypothetical prote
1031	84.5	2.1	746	2	F87243	isocitrate dehydro	1104	82	2.1	711	2	T27358	D2 protein homolo
1032	84.5	2.1	760	2	A40195	meprin A (EC 3.4.2	1105	82	2.1	868	2	T02635	neurexin I - alpha
1033	84.5	2.1	788	2	A26547	platelet glycoprot	1106	82	2.1	1530	2	I45944	F4482.4 protein -
1034	84.5	2.1	789	2	S28259	androgen-regulated	1107	82	2.1	1609	2	S44821	head-activator bin
1035	84.5	2.1	864	2	T49574	probable carnitine	1108	82	2.1	1661	2	T31330	hypothetical prote
1036	84.5	2.1	917	2	I48950	telencephalin prec	1109	82	2.1	2214	2	T16305	giant protein p619
1037	84.5	2.1	950	2	T28793	diacylglycerol kin	1110	82	2.1	4861	2	S71752	hypothetical prote
1038	84	2.1	278	2	T11718	hypothetical prote	1111	81.5	2.1	209	2	T02394	cysteine-rich prot
1039	84	2.1	335	2	T32657	hypothetical prote	1112	81.5	2.1	251	2	A55035	polyferredoxin 4x2
1040	84	2.1	349	2	D36858	gene G4R protein -	1113	81.5	2.1	349	2	S57453	protein P56B3.2 [l
1041	84	2.1	413	2	T34123	hypothetical prote	1114	81.5	2.1	383	2	D88633	knirps protein - f
1042	84	2.1	471	2	A84741	probable myrosinas	1115	81.5	2.1	429	2	S01919	env polyprotein, r
1043	84	2.1	520	2	G88846	protein T124V.2 [l	1116	81.5	2.1	433	2	A25483	hypothetical prote
1044	84	2.1	567	2	T49942	hypothetical prote	1117	81.5	2.1	442	2	T29147	lysine decarboxyla
1045	84	2.1	972	2	A30363	glycoprotein GP330	1118	81.5	2.1	460	2	S67174	probable finger pr
1046	84	2.1	1034	2	JC5598	mucin - rat	1119	81.5	2.1	482	2	A83655	transketolase (EC
1047	84	2.1	1047	2	T34946	probable isoenlucy	1120	81.5	2.1	496	2	T08674	hemagglutinin - ca
1048	84	2.1	1599	2	T16210	scavenger receptor	1121	81.5	2.1	519	2	S54300	hematopoietic grow
1049	84	2.1	2153	2	T14893	C4b-binding protei	1122	81.5	2.1	604	2	HMWZCD	proto-oncogene - m
1050	83.5	2.1	202	1	A44247	probable pepetidas	1123	81.5	2.1	625	2	S35317	
1051	83.5	2.1	278	2	AH0282		1124	81.5	2.1	626	2	S37622	

1125	81.5	2.1	724	2	A48569	antigen Em100 - B1	1198	80	2.0	644	2	I84634	Tamm-Horsfall prot
1126	81.5	2.1	977	2	S49004	tyrosine kinase Mp	1199	80	2.0	656	1	S59631	endo-1,4-beta-xyla
1127	81.5	2.1	1187	2	T18355	hypothetical prote	1200	80	2.0	680	2	PN0510	integrin beta-3 ch
1128	81.5	2.1	1220	2	D88013	protein K10B4.1 (1	1201	80	2.0	713	2	UC6012	glutamine-fructose
1129	81.5	2.1	1507	2	A40228	neurexin I-alpha p	1202	80	2.0	741	2	G84888	probable transket
1130	81	2.1	180	2	AE1010	conserved hypochet	1203	80	2.0	746	2	G84605	hypothetical prote
1131	81	2.1	266	2	C81906	hypothetical prote	1204	80	2.0	753	2	UC7386	retinovin - chicke
1132	81	2.1	348	2	A56247	natural killer cel	1205	80	2.0	817	2	TP4063	hypothetical prote
1133	81	2.1	428	2	T04472	probable porphobil	1206	80	2.0	902	2	T01127	curly leaf protein
1134	81	2.1	441	2	I40455	penicillin binding	1207	80	2.0	1138	2	TP6406	hypothetical prote
1135	81	2.1	501	2	UC7181	maternal transcrip	1208	80	2.0	1184	2	A96638	hypothetical prote
1136	81	2.1	554	2	A31300	perforin precursor	1209	80	2.0	1342	2	A36223	kinase-related tra
1137	81	2.1	560	2	S25092	jasmonate-induced	1210	80	2.0	1385	2	H88569	protein K03H1.5 (1
1138	81	2.1	732	2	T52588	wall-associated se	1211	80	2.0	1409	2	S41028	hypothetical prote
1139	81	2.1	735	2	G02937	feritin beta - cr	1212	80	2.0	2219	2	T27684	hypothetical prote
1140	81	2.1	755	2	I48101	ADAM 6 protein pre	1213	80	2.0	2229	2	T16199	hypothetical prote
1141	81	2.1	769	1	UC1121	leukocyte adhesion	1214	80	2.0	2643	2	T29149	genome polypeptin
1142	81	2.1	787	2	T49614	related to tol pro	1215	80	2.0	3140	2	S47508	KGD-bearing platel
1143	81	2.1	799	2	UC4126	integrin beta olig	1216	79.5	2.0	71	2	A59412	conserved hypochet
1144	81	2.1	821	1	A39667	brain-derived neur	1217	79.5	2.0	217	2	D90033	insulin-like growt
1145	81	2.1	1166	1	S06142	protein-tyrosine k	1218	79.5	2.0	254	2	I48599	insulin-like growt
1146	81	2.1	1344	2	H84557	hypothetical prote	1219	79.5	2.0	254	2	UC1464	transaldolase (EC
1147	81	2.1	1365	2	T00833	RNA-directed DNA p	1220	79.5	2.0	317	2	D64167	chitinase (EC 3.2.
1148	81	2.1	1438	2	A48216	neurexin III-alpha	1221	79.5	2.0	318	2	S43317	chitinase (EC 3.2.
1149	81	2.1	1471	2	B48218	neurexin III-alpha	1222	79.5	2.0	324	2	S20981	chitinase (EC 3.2.
1150	81	2.1	1578	2	I48216	neurexin III-alpha	1223	79.5	2.0	356	2	A25818	chitinase (EC 3.2.
1151	81	2.1	1895	2	T06609	disease resistance	1224	79.5	2.0	357	2	S49300	chromodulin - B
1152	81	2.1	3898	2	S57437	genome polypeptin	1225	79.5	2.0	491	2	C86464	hypothetical prote
1153	80.5	2.0	371	2	B72461	hypothetical prote	1226	79.5	2.0	474	2	A57480	tubulointerstitial
1154	80.5	2.0	390	2	T27256	hypothetical prote	1227	79.5	2.0	614	2	T40652	hypothetical prote
1155	80.5	2.0	409	2	B87661	conserved hypochet	1228	79.5	2.0	661	2	C85758	hypothetical prote
1156	80.5	2.0	416	2	A37877	hemorrhagic protei	1229	79.5	2.0	661	2	B90861	hypothetical prote
1157	80.5	2.0	421	2	S49821	PR12 protein - Ara	1230	79.5	2.0	694	2	S58083	transketolase (EC
1158	80.5	2.0	434	2	T26654	alkaline phosphata	1231	79.5	2.0	700	1	HYH0MB	meprin A (EC 3.4.2
1159	80.5	2.0	471	1	PAECA	protein F13W7.11 (1232	79.5	2.0	713	2	I65253	disintegrin-like t
1160	80.5	2.0	479	2	D86182	hypothetical prote	1233	79.5	2.0	741	2	T09015	transketolase (EC
1161	80.5	2.0	502	2	T16716	hypothetical prote	1234	79.5	2.0	868	2	G84674	probable selenum-
1162	80.5	2.0	509	2	T22238	hypothetical prote	1235	79.5	2.0	952	2	T28792	diacylglycerol kin
1163	80.5	2.0	516	2	S53007	citrate synthase -	1236	79.5	2.0	1161	1	S31213	nidogen precursor
1164	80.5	2.0	535	2	T21028	hypothetical prote	1237	79.5	2.0	1178	2	S08405	hypothetical prote
1165	80.5	2.0	570	2	T46261	hypothetical prote	1238	79.5	2.0	1260	2	A86323	protein F14D16.3 (
1166	80.5	2.0	604	2	T15796	hypothetical prote	1239	79.5	2.0	1390	2	S51364	sperm tail-specific
1167	80.5	2.0	627	2	T00603	hypothetical prote	1240	79.5	2.0	1402	2	T24664	hypothetical prote
1168	80.5	2.0	656	2	B49423	semaphorin I - fru	1241	79.5	2.0	2261	2	T07084	acetyl-CoA carboxy
1169	80.5	2.0	658	2	A86828	transketolase (EC	1242	79.5	2.0	2499	1	A30788	mannose 6-phosphat
1170	80.5	2.0	673	2	A49878	coagulation factor	1243	79	2.0	171	2	S57894	laminin - Hydrx vu
1171	80.5	2.0	741	2	A48040	meprin A (EC 3.4.2	1244	79	2.0	188	2	A30362	teratocarcinoma-de
1172	80.5	2.0	742	2	B81143	isocitrate dehydro	1245	79	2.0	192	1	B57143	chitosulfate-dithio
1173	80.5	2.0	742	2	I37225	leucocyte antigen	1246	79	2.0	192	2	AC0763	chitosulfate reduct
1174	80.5	2.0	773	2	I46059	beta-1 integrin su	1247	79	2.0	206	2	D97285	ribosomal protein
1175	80.5	2.0	1055	2	T05663	hypothetical prote	1248	79	2.0	360	2	S32695	Wnt-2 protein - Ca
1176	80.5	2.0	1119	2	A88481	protein C16A3.6 (1	1249	79	2.0	364	2	T24153	hypothetical prote
1177	80.5	2.0	1245	1	VHWV82	structural polypro	1250	79	2.0	392	2	T33444	hypothetical prote
1178	80.5	2.0	1376	1	VG1HJ2	E2 glycoprotein pr	1251	79	2.0	393	2	A64036	hypothetical prote
1179	80.5	2.0	1382	2	INHUR	insulin receptor p	1252	79	2.0	415	2	D87020	probable membrane
1180	80.5	2.0	1526	2	T19473	hypothetical prote	1253	79	2.0	417	2	T08724	hypothetical prote
1181	80.5	2.0	1558	2	C89114	protein C37C3.6a (1254	79	2.0	587	2	C85044	hypothetical prote
1182	80.5	2.0	1611	2	G84493	probable retroelem	1255	79	2.0	602	2	B81420	GTP-binding protei
1183	80.5	2.0	2167	2	T34395	hypothetical prote	1256	79	2.0	606	2	T22105	hypothetical prote
1184	80.5	2.0	2262	2	T30890	calcium channel al	1257	79	2.0	630	2	T48369	hypothetical prote
1185	80	2.0	211	1	CYRTB3	beta-crystallin B3	1258	79	2.0	660	2	S71949	hypothetical prote
1186	80	2.0	243	2	T27036	hypothetical prote	1259	79	2.0	687	2	T16352	metalloproteinase
1187	80	2.0	284	2	T25938	hypothetical prote	1260	79	2.0	729	2	A45716	leukemia virus cel
1188	80	2.0	290	2	T46470	hypothetical prote	1261	79	2.0	738	2	T41730	hypothetical prote
1189	80	2.0	335	2	A39743	u-plasminogen acti	1262	79	2.0	753	2	B36268	platelet glycoprot
1190	80	2.0	395	2	S64299	probable membrane	1263	79	2.0	773	2	JEO387	exo-alpha-sialidas
1191	80	2.0	437	1	S24802	polyferredoxin 6x2	1264	79	2.0	778	2	A60798	platelet glycoprot
1192	80	2.0	464	2	S05478	properdin - mouse	1265	79	2.0	788	2	I77349	platelet glycoprot
1193	80	2.0	466	2	H82928	ATP synthase beta	1266	79	2.0	790	2	D81668	phenylalanine-tRNA
1194	80	2.0	500	2	A36388	RNA-directed RNA p	1267	79	2.0	826	2	A60385	monocyte surface a
1195	80	2.0	589	2	I38598	zinc finger protei	1268	79	2.0	871	2	T04667	hypothetical prote
1196	80	2.0	642	2	C89124	protein K07C11.9 (1269	79	2.0	952	2	T18900	disintegrin and me
1197	80	2.0	644	1	A40212	ucromodulin precurs	1270	79	2.0	1023	2	T30257	IgG Fc binding pro

1271	79	2.0	1289	1	RMXR3	mRNA guanylyltrans	1344	78	2.0	4085	2	S28600	hypothetical prote
1272	79	2.0	1391	2	T20406	hypothetical prote	1345	77.5	2.0	46	2	UT0747	epiregulin - rat
1273	79	2.0	1513	2	A54895	myc2, intestina	1346	77.5	2.0	162	2	S68401	epiregulin precurs
1274	79	2.0	1522	2	T00028	brain-specific ang	1347	77.5	2.0	244	2	AB2505	histidine kinase-1
1275	79	2.0	1642	2	T19130	hypothetical prote	1348	77.5	2.0	255	2	H96776	hypothetical prote
1276	79	2.0	1777	2	T00490	nonstructural prot	1349	77.5	2.0	255	2	UC5559	hypothetical prote
1277	79	2.0	1777	2	AC2088	serine/threonine k	1350	77.5	2.0	295	2	UC5559	hypothetical prote
1278	78.5	2.0	116	2	S65875	apernadhesin PSP-I	1351	77.5	2.0	296	2	AS5647	conserved hypochet
1279	78.5	2.0	307	1	S18523	fructokinase (EC 2	1352	77.5	2.0	402	2	S02099	phyllipoid - fruit
1280	78.5	2.0	327	2	A55356	urokinase-type pla	1353	77.5	2.0	407	2	C82428	phosphoribulokinas
1281	78.5	2.0	341	2	I61725	natural killer as8	1354	77.5	2.0	413	4	FOHUE2	glucose-1-phosphat
1282	78.5	2.0	344	2	I57658	foliistatin - rat	1355	77.5	2.0	457	2	B85749	retrovirus-related
1283	78.5	2.0	355	2	C70457	hypothetical prote	1356	77.5	2.0	457	2	B85749	ATP-dependent RNA
1284	78.5	2.0	363	1	C55973	transcription fact	1357	77.5	2.0	457	2	G90869	ATP-dependent RNA
1285	78.5	2.0	376	2	E70361	chaperone DnaJ - A	1358	77.5	2.0	469	2	T36362	probable DNA repai
1286	78.5	2.0	389	2	D75180	hypothetical prote	1359	77.5	2.0	488	2	T21701	hypothetical prote
1287	78.5	2.0	401	2	S65138	glycoprotein antig	1360	77.5	2.0	548	2	B75375	probable amidase -
1288	78.5	2.0	436	2	S06884	viD2 protein - Ag	1361	77.5	2.0	548	2	S38864	Ig epsilon chain C
1289	78.5	2.0	474	2	B38634	tumor necrosis fac	1362	77.5	2.0	559	2	S38864	probable transposo
1290	78.5	2.0	495	2	A57053	germ cell nuclear	1363	77.5	2.0	645	2	S20138	probable protein k
1291	78.5	2.0	507	2	T06452	probable legumin A	1364	77.5	2.0	717	2	B32838	DNA-directed RNA p
1292	78.5	2.0	517	1	FMWMA	legumin A precursor	1365	77.5	2.0	721	2	A39707	erythrocyte membra
1293	78.5	2.0	552	2	C45710	R transactivator h	1366	77.5	2.0	729	2	A69202	conserved hypochet
1294	78.5	2.0	600	2	I49281	fertilin alpha pre	1367	77.5	2.0	767	2	E85079	hypothetical prote
1295	78.5	2.0	658	2	D86477	protein F1504.27 l	1368	77.5	2.0	809	2	A57283	integrin beta chai
1296	78.5	2.0	662	2	F85024	probable GHP-rich	1369	77.5	2.0	845	2	G82773	phage-related prot
1297	78.5	2.0	662	2	I37892	IL12 receptor comp	1370	77.5	2.0	848	2	AF0020	nitrite reductase
1298	78.5	2.0	717	2	T25431	hypothetical prote	1371	77.5	2.0	933	2	A31930	cytoactin - chick
1299	78.5	2.0	748	2	T00732	hypothetical prote	1372	77.5	2.0	1017	2	D75028	h+-transporting AT
1300	78.5	2.0	757	2	T05688	hypothetical prote	1373	77.5	2.0	1079	1	TVFVMI	gag-RmlI-env polyp
1301	78.5	2.0	763	2	I49089	hypothetical prote	1374	77.5	2.0	1142	2	A45031	cysteine-rich fibr
1302	78.5	2.0	842	2	T04555	hypothetical prote	1375	77.5	2.0	1333	2	E88257	protein let-23 lim
1303	78.5	2.0	1119	2	T16720	hypothetical prote	1376	77.5	2.0	1374	2	S70712	protein-tyrosine k
1304	78.5	2.0	1121	2	S57058	probable membrane	1377	77.5	2.0	2895	2	T08437	hyperplastic discs
1305	78.5	2.0	1131	2	T30951	hypothetical prote	1378	77.5	2.0	3085	2	T00327	polyprotein - infe
1306	78.5	2.0	1137	2	T18625	atrial natriuretic	1379	77	2.0	194	2	S70663	lectin heavy chain
1307	78.5	2.0	1188	2	JC4889	phosphatidylinosit	1380	77	2.0	230	2	T31722	hypothetical prote
1308	78.5	2.0	3473	1	A46112	genome polyprotein	1381	77	2.0	230	2	A44074	probable EGF-like
1309	78.5	2.0	3473	2	S27927	polyprotein - rice	1382	77	2.0	279	2	T16201	hypothetical prote
1310	78.5	2.0	3864	2	D87757	protein C44B4.1a l	1383	77	2.0	317	2	T45984	hypothetical prote
1311	78	2.0	247	2	T27778	hypothetical prote	1384	77	2.0	375	2	F70691	hypothetical prote
1312	78	2.0	334	2	T03157	probable capsid as	1385	77	2.0	452	2	H84772	hypothetical prote
1313	78	2.0	360	2	T26037	hypothetical prote	1386	77	2.0	476	2	T19786	probable serine ca
1314	78	2.0	360	2	G82994	glycine-cleavage s	1387	77	2.0	500	2	AE2032	hypothetical prote
1315	78	2.0	372	2	T31060	hypothetical prote	1388	77	2.0	502	2	T41148	hypothetical prote
1316	78	2.0	385	2	A81926	hypothetical prote	1389	77	2.0	535	2	T19706	hypothetical prote
1317	78	2.0	401	2	C89102	protein F25E5.10 l	1390	77	2.0	540	1	OYHUCR	trp-asp repeat con
1318	78	2.0	404	2	T40553	trp-asp repeat pro	1391	77	2.0	591	2	S33542	hypothetical prote
1319	78	2.0	415	2	E83377	probable alcohol d	1392	77	2.0	713	2	T40729	catechol oxidase (
1320	78	2.0	441	2	AH2930	oxidoreductase Atu	1393	77	2.0	729	2	A49120	protein ZC123.1 [l
1321	78	2.0	446	2	F98351	probable oxidoredu	1394	77	2.0	768	2	A87722	brain-derived neur
1322	78	2.0	454	1	GQMS71	tumor necrosis fac	1395	77	2.0	821	1	S06943	neuroal different
1323	78	2.0	468	2	B40228	neurexin I-beta pr	1396	77	2.0	1019	2	UC7538	hypothetical prote
1324	78	2.0	468	2	S26741	T-cell glycoprotei	1397	77	2.0	1302	2	T00038	hypothetical prote
1325	78	2.0	482	2	T17250	transmembrane glyc	1398	77	2.0	1458	2	B97355	DNA segregation AT
1326	78	2.0	522	2	A46103	conserved hypochet	1399	77	2.0	1552	2	G86344	T2211.2 protein -
1327	78	2.0	523	2	C95303	importin alpha - c	1400	77	2.0	1733	2	S58880	receptor DRC-205 -
1328	78	2.0	527	2	T04329	prostaglandin-endo	1401	77	2.0	2165	2	T26859	hypothetical prote
1329	78	2.0	559	2	JH0259	integrin beta-3 ch	1402	77	2.0	2165	2	T21371	hypothetical prote
1330	78	2.0	723	2	PM0509	hypothetical prote	1403	77	2.0	2584	2	T24158	hypothetical prote
1331	78	2.0	725	2	T27148	epidermal growth f	1404	77	2.0	2606	2	T24157	hypothetical prote
1332	78	2.0	843	2	A27131	epidermal growth f	1405	77	2.0	2769	1	UIBO	chryoglobulin prec
1333	78	2.0	957	2	T15976	hypothetical prote	1406	77	2.0	3033	1	GNWV78	genome polyprotein
1334	78	2.0	989	2	T47503	hypothetical prote	1407	77	2.0	3660	1	S02041	dystrophin, muscle
1335	78	2.0	1016	2	G86295	hypothetical prote	1408	77	2.0	4957	2	T03455	ALR protein - huma
1336	78	2.0	1016	2	G86295	hypothetical prote	1409	77	2.0	5262	2	T03454	platelet-aggregati
1337	78	2.0	1131	2	T38744	structural polypro	1410	77	2.0	71	2	A59413	hypothetical prote
1338	78	2.0	1260	1	VHMB	protein-tyrosine k	1411	76.5	1.9	146	2	G95995	platelet aggregati
1339	78	2.0	1330	1	TVRTNU	epidermal growth f	1412	76.5	1.9	216	2	JX0265	phosphoribosylform
1340	78	2.0	1339	2	JC4387	epidermal growth f	1413	76.5	1.9	224	2	AD2115	insulin-like growt
1341	78	2.0	1369	2	S70713	protein-tyrosine k	1414	76.5	1.9	254	2	I48603	hypothetical prote
1342	78	2.0	1658	2	D75489	hypothetical prote	1415	76.5	1.9	264	2	T22380	enoyl-(acyl-carrie
1343	78	2.0	3224	1	S58884	Ran-binding protei	1416	76.5	1.9	272	2	AG2669	

1417	76.5	1.9	272	2	E97451	hypothetical prote
1418	76.5	1.9	279	2	JC6565	four-and-a-half LI
1419	76.5	1.9	302	2	E86267	hypothetical prote
1420	76.5	1.9	322	1	S37344	chitinase (EC 3.2.
1421	76.5	1.9	333	2	T24636	hypothetical prote
1422	76.5	1.9	337	2	AC0156	probable cobalamin
1423	76.5	1.9	359	2	T36050	probable histidino
1424	76.5	1.9	359	2	E83262	hypothetical prote
1425	76.5	1.9	385	2	AH0793	probable lipopolys
1426	76.5	1.9	386	2	TI1257	hypothetical prote
1427	76.5	1.9	388	2	EHMS	Ig epsilon chain C
1428	76.5	1.9	420	2	S74388	gamma-glutamyl pho
1429	76.5	1.9	435	2	T25350	hypothetical prote
1430	76.5	1.9	481	2	A56346	transcription fact
1431	76.5	1.9	483	2	T48328	importin alpha-lik
1432	76.5	1.9	487	2	T21384	hypothetical prote
1433	76.5	1.9	504	2	T33404	hypothetical prote
1434	76.5	1.9	518	2	G88961	protein F59A7.8 [I
1435	76.5	1.9	520	2	C70311	hypothetical prote
1436	76.5	1.9	536	1	A39036	H+-transporting tw
1437	76.5	1.9	545	1	PMBYA	hypothetical prote
1438	76.5	1.9	601	2	T34396	hypothetical prote
1439	76.5	1.9	623	2	S56206	probable membrane
1440	76.5	1.9	658	2	T47960	hypothetical prote
1441	76.5	1.9	707	2	S68858	finger protein - m
1442	76.5	1.9	712	2	T16338	hypothetical prote
1443	76.5	1.9	722	2	S32659	integrin beta 2 ch
1444	76.5	1.9	837	2	A42112	musclin-like peptid
1445	76.5	1.9	849	2	I50617	starch phosphoryla
1446	76.5	1.9	1000	2	S47243	hypothetical prote
1447	76.5	1.9	1004	2	T31665	suppressor protein
1448	76.5	1.9	1056	2	T33167	DNA polymerase III
1449	76.5	1.9	1071	2	T18307	RNA polymerase (be
1450	76.5	1.9	1153	2	T00615	aldehyde-CoA carbox
1451	76.5	1.9	1201	2	AD1107	vitellinogenin vit-6
1452	76.5	1.9	1349	2	T01699	hypothetical prote
1453	76.5	1.9	1561	2	S46200	Munc13-2 - rat
1454	76.5	1.9	1561	2	T18561	alpha tectorin - m
1455	76.5	1.9	1738	2	C84507	protein CTRP - mal
1456	76.5	1.9	1985	2	I61776	protein CTRP - mal
1457	76.5	1.9	2098	2	T18397	alpha tectorin - m
1458	76.5	1.9	2155	2	T30197	surface protein ty
1459	76.5	1.9	2395	1	S50820	xin protein - chic
1460	76.5	1.9	2562	1	T14266	trichoxen protein
1461	76.5	1.9	3828	2	T13857	hypothetical prote
1462	76.5	1.9	4550	2	T18440	herc2 protein - mo
1463	76.5	1.9	4836	2	T14346	tissue kallikrein
1464	76.5	1.9	96	2	A05308	sperm motility inh
1465	76.5	1.9	136	2	S72508	teratocarcinoma-de
1466	76.5	1.9	171	2	I49612	hypothetical prote
1467	76.5	1.9	233	2	T22396	rRNA methylase, YS
1468	76.5	1.9	261	2	G97190	paired box transcr
1469	76.5	1.9	269	2	S36166	conserved hypochet
1470	76.5	1.9	287	2	A11072	hypothetical prote
1471	76.5	1.9	333	2	T15257	transcription fact
1472	76.5	1.9	349	1	I51739	membrane-associate
1473	76.5	1.9	374	2	A42264	hypothetical prote
1474	76.5	1.9	415	2	T32467	hypothetical prote
1475	76.5	1.9	418	2	T24350	oxidoreductase - D
1476	76.5	1.9	454	2	D75446	probable ADA-like
1477	76.5	1.9	490	2	T35948	putr bi-functional
1478	76.5	1.9	512	1	DTBSRH	hypothetical prote
1479	76.5	1.9	531	2	T22021	2-aminobenzoyl-Co
1480	76.5	1.9	603	3	S22402	metallopeptidase
1481	76.5	1.9	605	2	S71630	MD-repeat protein
1482	76.5	1.9	612	2	T39666	probable RNA-dirac
1483	76.5	1.9	616	2	RRVOWA	hypothetical prote
1484	76.5	1.9	626	1	T09345	probable DEAD box
1485	76.5	1.9	634	2	AG0252	transketolase (imp
1486	76.5	1.9	670	2	A12223	furin (EC 3.4.21.7
1487	76.5	1.9	837	2	S43656	EBB kinase activa
1488	76.5	1.9	860	2	JC5702	hypothetical prote
1489	76.5	1.9	897	2	S67283	

1490	76	1.9	908	2	T27117	hypothetical prote
1491	76	1.9	925	2	T37475	lipoprotein recept
1492	76	1.9	926	1	OPPGIT	iodide peroxidase
1493	76	1.9	934	1	A34372	complement C6 prec
1494	76	1.9	967	2	T48210	hypothetical prote
1495	76	1.9	1001	2	AG1979	hypothetical prote
1496	76	1.9	1084	2	T18292	nicotinamide nucle
1497	76	1.9	1097	2	S17308	leukemia inhibitor
1498	76	1.9	1206	2	T18557	probable hydrogena
1499	76	1.9	1245	1	VHWVB2	structural polypro
1500	76	1.9	1385	2	S34230	156k protein - Pla

ALIGNMENTS

RESULT 1
 T08805
 hypothetical protein DKFZps56H2123.1 - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
 C/Accession: T08805
 R/Annotator: W. J. Mewes, H. W. Gassenhuber, J. Wiemann, S.
 submitted to the Protein Sequence Database, May 1999
 A/Reference number: Z16472
 A/Accession: T08805
 A/Molecule type: mRNA
 A/Residues: 1-181 <MUT>
 A/Cross-references: UNIPROT:Q9Y432; UNIPARC:UPI0000070151; EMBL:AL050214
 A/Experimental source: adult uterus; clone DKFZps56H2123
 C/Genetics:
 A/Note: DKFZps56H2123.1

Query Match 24.1%; Score 949; DB 2; Length 181;
 Best Local Similarity 99.4%; Pred. No. 6, 8e-57;
 Matches 180; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY	540	SLQISAIILHPNYPDILLDDADILKLDKARISTRVQPICLAASFDLSTSFQESHITVA	599
DB	1	SLRISAIILHPNYPDILLDDADILKLDKARISTRVQPICLAASFDLSTSFQESHITVA	60
QY	600	GMNVLDVSPGPKNDLTSGVSVVDSILCEQHDHGPVSTNMFCASWEPTAPSD	659
DB	61	GMNVLDVSPGPKNDLTSGVSVVDSILCEQHDHGPVSTNMFCASWEPTAPSD	120
QY	660	ICTAETGTGIAAASFPPRASPEPRMHLGLVMSYDTCSHRLSTATTXYLPFQWTERNM	719
DB	121	ICTAETGTGIAAASFPPRASPEPRMHLGLVMSYDTCSHRLSTATTXYLPFQWTERNM	180
QY	720	K 720	
DB	181	K 181	

RESULT 2

A38738
 coagulation factor C precursor - horseshoe crab (Tachypleus tridentatus)
 N/Continue names: coagulation-complement factor C; Limulus factor C
 C/Species: Tachypleus tridentatus
 C/Date: 04-Oct-1991 #sequence_revision 04-Oct-1991 #text_change 09-Jul-2004
 C/Accession: A38738; B38738; S00105
 R/Muta: T.; Miyata, T.; Mismura, Y.; Tokunaga, F.; Nakamura, T.; Toh, Y.; Ikehara, Y.; I.
 J. Biol. Chem. 266, 6554-6561, 1991
 A/Title: Limulus factor C. An endotoxin-sensitive serine protease zymogen with a mosaic
 A/Reference number: A38738; MIMD:91177916; PMID:2007602
 A/Accession: A38738
 A/Molecule type: mRNA
 A/Residues: 1-1019 <MUT>
 A/Cross-references: UNIPROT:P28175; UNIPARC:UPI000012E5D2; GB:D90271; NID:g217396; PID:
 A/Molecule type: mRNA
 A/Residues: 1-466, 616, 'DN', 619-620, 'A', 622 <MUT>

A:Cross-references: UNIPARC:UPI0000179B67; GB:D90272
 R:Tokunaga, F.; Miyata, T.; Nakamura, T.; Morita, T.; Kuma, K.I.; Miyata, T.; Iwanaga, S
 Eur. J. Biochem. 167, 405-416, 1987
 A:Title: Lipopolysaccharide-sensitive serine-protease zymogen (factor C) of horseshoe cr
 is a novel type of serine protease.
 A:Reference number: S00105; MUID:88004461; PMID:3308457
 A:Accession: S00105
 A:Molecule type: Protein
 A:Residues: 'S', 27-39, 'S', 41, 'T', 43-54, 'E', 691-782, 950-977 <NOK>
 A:Cross-references: UNIPARC:UPI0000179B66; UNIPARC:UPI0000179B69; UNIPARC:UPI0000179B6A
 C:Superfamily: coagulation factor C; C-type lectin homology; complement factor H repeat
 C:Keywords: alternative splicing; glycoprotein; hemolymph coagulation; hydrolase; serine
 F:1-25/Domain: signal sequence #status predicted <SIG>
 F:136-690/Product: coagulation factor C heavy chain #status experimental <HCH>
 F:136-195/Domain: complement factor H repeat homology <FH01>
 F:139-254/Domain: complement factor H repeat homology <FH02>
 F:260-321/Domain: complement factor H repeat homology <FH03>
 F:436-564/Domain: C-type lectin homology <LCH>
 F:576-634/Domain: complement factor H repeat homology <FH04>
 F:685-747/Domain: complement factor H repeat homology #status experimental <PPA>
 F:763-1019/Product: coagulation factor C light chain peptide B #status experimental <PPE>
 F:763-1015/Domain: trypsin homology <TRY>
 F:523,534,624,912/Binding site: carbonyl (Asn) (covalent) #status predicted
 F:767/Binding site: carbonyl (Asn) (covalent) #status experimental
 F:809,865,966/Active site: His, Asp, Ser #status predicted

Query Match 17.0%; Score 672; DB 2; Length 1019;

Best Local Similarity 25.6%; Pred. No. 2e-37; Matches 223; Conservative 117; Mismatches 308; Indels 222; Gaps 37;

34 PGAEWNIM---CRECEYDQIE---CVCPRKEVNGYTPCCNNEECDSLIHGCT 86
 184 PNGQMSFPKPCIRECAKVSPEHGKXNAPSGNNIEGATL---RFSDDS---PYIL 233
 87 IFENKSCR-NGSWGTL----- 103
 234 IGETTLTCOGNGGSGQIPCKKLVFCPDDLPVNAHEHQVIGVEKKYGGPQTEVYTT 293
 104 --DDFYKGFYCAECR--AGWYGG--DCMR-----CCGYLR--APKG 137
 294 CSGNYFLMGFTLKCNDPDSGSGQPCVKADREVDSCSKAVDFLDVGGSPVRIHCPAG 353
 138 QILLES-----YPLNACEFTIHA---KPGFVI-----Q 163
 354 CSLAGVWGTATYHELSVGRATIHAGKLPNSGAAHVAVNGYSPFLSDGLNGITSEE 413
 164 LRFVMSLEPDY-----CQDYVEYVD-----GDNRDQIIRKVCN--ERPAP 206
 414 LKSLARFPRDYVSSSTAGSGCCPDGFEVEBENCYVYTSKQRAWERAQGVCTNMAALAV 473
 207 IQS--ISSLHLVHSDG--SKNPFDPH-----AIYEETTASSSPCF 245
 474 LDKLILSSSLTETIRGKGLTITMIGLHRLDAEKFPFWEMLDRSNVNLNDLTFWASGPG 533
 246 HDGTCV-LDRKGS-----YKCACLAGYTGQRCENLEERN---CSDPGPVNGYKITGCP 297
 534 NETGCVLLIDIDQLOPFWKTSQCFOPSSFACMLSLDRNKKKCDPGLBEGHATLNGQS 593
 298 GLNGRIAKTGVVSPFCNNSYVLISGNEKRTCOONGEMSGKOPICR--ACREPKISDLV 355
 594 --IDGFVA--GSSIRYCEVLAHYISGTEVYCTTNGTMSAPKPCIKYITQNPVPSYG 649
 356 RRRVLPMQVOSRETFPLHQLVSAASKQLQ---SAPTKKVLPPGD-----LP 400
 650 SVEIKP---PRTNISISVSGPRLPLPLPLAARAPPKPPSSQSPSTVDLASKVYLP 706
 401 MGYOHLTOLQYECISPFYRLLGSSRRCTRTGKMSGRAFPICIGKIENTAP-----455
 707 EGHARVGSRAIYTESRKYELLGSGQRCDNGKMSGRPASCTFVCGSDBSPRPFTWNG 766
 456 -KTQGLRPMQOAIYRTSGVHDSGLKGANFLVCSGALVNERTVVVAACHCVTDLGRVTM 514

Db 767 NSTEIGQMPQWQAGISRMLA-----DNNMFLQCGSGLINEKIVTAACHVTSATAEI 819
 515 IKTADLKVYLGRKRRDDDEKTIQSLQISAILLHNPYDILLADALITLKIDKARISF 574
 820 IDPSQFTYIGKTKRDSRDDYVREALEHVNPNYDGNLNFIDALIQLTPTVTLTT 879
 575 RVOPICLAASRDLSFQESH-----TVAGNVLADVRSPPGKNDLRSGVSVDSL 628
 880 RVQPICLPT--DITL---RHLLEGLAVVTGNG-----LNENNTYSBMIGQAVLPVVAAS 930
 629 LCSEQHEDHCIPVSVTDNFCASWEPTASPDCTAETGTAIVSFGKASPEPRHMLGL 668
 931 TCSEGYKEDLPVTVENNEFCAGYK--KGRYDACSQSGG--PLVFADDSKTERRRVYLEG 987
 689 VSMYSYKTCGSH-RLSTAFKVLPLFPKQWTER 717
 988 VSMGSPSGCGKANQYGGFTKVNPLSMIRO 1017

RESULT 3

154763
 Ra-reactive factor (EC 3.4.21.-) 1 precursor - human

N:Alternate names: mannos binding protein-associated serine proteinase 1 (MASP-1)

C:Species: Homo sapiens (man)

C:Date: 19-May-2000 #sequence_rev19-May-2000 #text_change 09-Jul-2004

C:Accession: 154763; JN0883

R:Sato, T.; Endo, Y.; Matsushita, M.; Fujita, T.

Int. Immunol. 6, 665-669, 1994

A:Title: Molecular characterization of a novel serine protease involved in activation o

A:Reference number: 154763; MUID:94289349; PMID:8018603

A:Accession: 154763

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-699 <SNT>

A:Cross-references: UNIPROT:P48740; UNIPARC:UPI000016AD0B; GB:D28553; NID:G790963; PIDN

R:Ikeda, F.; Takayama, Y.; Hattsuue, H.; Kawakami, M.

Biochem. Biophys. Res. Commun. 196, 1003-1009, 1993

A:Title: A new member of the C1s family of complement proteins found in a bactericidal

A:Reference number: JN0883; MUID:94059062; PMID:8240317

A:Accession: JN0883

A:Molecule type: mRNA

A:Residues: 1-234, 'E', 226-284, 'G', 286-498, 'K', 500-542, 'K', 544-642, 'S', 644-699 <TAK>

A:Cross-references: UNIPARC:UPI000016AF63; DBJ:D17525; NID:G439712; PIDN:BA004477.1; P

A:Experimental source: liver

C:Comment: This is a serum bactericidal factor that activates complement C4 and C2 comp

C:Genetic: GDB:MASP1; GDB:CRANP; CRANF1; PNSS5; MASP

A:Gene: GDB:MASP1; GDB:CRANP; CRANF1; PNSS5; MASP

A:Cross-references: GDB:361104; GDB:330954; OMIM:600521

A:Map position: 3q27-3q28

C:Superfamily: complement-activating serine proteases C1r/C1s/MASP; C1r/C1s repeat homo

C:Keywords: beta-hydroxyasparagine; complement pathway; duplication; glycoprotein; hydr

F:1-17/Domain: signal sequence #status predicted <SIG>

F:18-48,449-699/Product: Ra-reactive factor #status predicted <MAT>

F:110-145/Domain: C1r/C1s repeat homology <C1R1>

F:143-181/Domain: EGF homology <EGF>

F:185-294/Domain: C1r/C1s repeat homology <C1R2>

F:301-362/Domain: complement factor H repeat homology <FH1>

F:367-432/Domain: complement factor H repeat homology <FH2>

F:449-691/Domain: trypsin homology <TRY>

F:49,178,407/Binding site: carbonyl (Asn) (covalent) #status predicted

F:77-91,143-157,153-166,168-181,185-212,242-260,301-349,329-362,367-414,397-432,436-572

F:159/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted

F:448-449/leavage site: Arg-Ile (autolytic) #status predicted

F:430,552,646/Active site: His, Asp, Ser #status predicted

Query Match 12.2%; Score 482; DB 1; Length 699;

Best Local Similarity 24.9%; Pred. No. 8.2e-25;

Matches 178; Conservative 99; Mismatches 215; Indels 228; Gaps 39;

69 CRNEENECDSLIHPCCTIRENCKSCNNGSGTLDPFYKGYCAECRAGWY---GCD 124

Db 143 CKREDEBELSCDHY-----CHN-----YIGGYCS-CRFGYILHTDNR 180


```

Db      127 TIMPKFSLAYQAVIDDECSRSKSGEEDPOCOHLCHNYVGGYFCS--CRPEYBLQED 185
      121 ---YGDGCMRCGQILAPKGOI--LLE---SYPLNAHCWTHAPRGVIOGRFVMSLEEF 173
      186 RHCQAEAC--SSELYTEASGISLSLEYPRSPDPDRCNYSIRVRGGLTLHKFE---PF 240
      174 D-----YMCQDYVEVRADGNRDGOIIRKVCGERPAPLOSISLSLHVLPHSDGSKNFD 227
      241 DIDHQVHCYDQLQI---YANGKNIGFCGKQRPRDLDTSSNAVLDLFTBESGDSR 296
      228 GFHAIIY--EETACSSSPCFHDTGCVLDKAGSYKCAACLAGYQRCENLLEBRNCSDPGCP 286
      297 GWKLRYYTEIICCPQKTLDEFTIIONLOPOYQ---FRDYFIATCK----- 339
      287 VNGYQKITGPGQLNGRAKIGTVVSPFCNNSYVLSGNEKRTCCQNGEWSGKPIIC--IKA 345
      340 -QGQILBGNQVL-----HSPF-----AVCDDGTHMRAMPKCKIKD 375
      346 CREPKISDLVRRRVLPQVQSRRETPHLQLYSAFSAFKQLQSAPTKPKPALPGDL----PM 401
      376 CGQPR-----NLPRGDFRYTTTM 393
      402 GYQHILHTOLOECISPFYR--RLGSSRR---TCLRTGKWSG---RAPSCIPICGK 448
      394 GVNTYKARIQYQYCHEPYYKMQTRAGSRESEGVYTCQGIWKNEQKKEKIPRLCLPVCGK 453
      449 IEN-----ITAPKQGLMMPQOAIYRRTSGVHDGSLHKGMFLVCSGLVNERIVV 500
      454 PVNVEQORRIIGQKAMGNFMQV---FTNHHG---RG-----GGALLGDRMTL 498
      501 VAAHCVTDLGKVTMIKTADLKVVLGKFFYRDDDEKTIQSLQ-----ISAIIILHPNY-- 552
      499 TAAHTLPKHEBAQ--SNASLDVFLG-----HTNVEBELMKGNPIHRAVSHHPDVRQ 548
      553 -DPIILLADDAIILKLDKARISTRVQPICLAASRDLSFQESH--TVAGNNVLAD---- 606
      549 DESYNFSGDIALLELSVTLGPMLPLCLP---DNDFYDLGLMGVYSGGVWEKIAH 605
      607 ---VRSRPGFNDTLRSGVSVVSDSLCEBQHEHDGIVSVSTDMFPCASWEPAPSDICT 662
      606 DLRRVLRP-----VANPQACENMLRGKRMNDVFSQNNFPCAG--HPSLKQDPCQ 651
      663 AETGIAAVSPGRASPEPRMHLGLVSWSYDKTCSHRLSTAFKVLPRFKDMIRNNK 720
      652 GDSCGVFAVRDPN---TDRKVVATGIYSWGI--CS--RGYGFYTKVLYNVDMIKENB 702

RESULT 5
A59271
Ra-reactive factor (EC 3.4.21.-) 2 precursor - human
N:Alternate names: mannose binding protein-associated serine proteinase 2 (MASP-2)
C:Species: Homo sapiens (man)
C>Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
C:Accession: A59271
R:Title1, S.: Vorup-Jensen, T.; Stover, C.M.; Schmaeble, W.J.; Laursen, S.B.; Poulsen, K.
Nature 386, 506-510, 1997
A:Title: A second serine protease associated with mannan-binding lectin that activates c
A:Reference number: A59271; MUID:97242412; PMID:9087411
A:Accession: A59271
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-686 <JEN>
A:Cross-references: UNIPROT:O00187; UNIPARC:UPI0000047562; GB:Y09926; NID:94007626; PIDK
A:Experimental source: tissue liver
A:Note: submitted to Genbank, December 1996
C:Genetic8:
A:Gene: GDB:MASP2
A:Cross-references: GDB:6071500
A:Map position: 1p36.2-1p36.3
C:Superfamily: complement-activating serine proteases C1r/C1s/MASP; C1r/C1s repeat homo]
C:Keywords: beta-hydroxyasparagine; complement pathway; duplication; hydrolase; serine p
```

```

F:1-15/Domain: signal sequence #status predicted <SIG>
F:16-44/445-686/Product: Ra-reactive factor 2 #status predicted <MAT>
F:19-134/Domain: C1r/C1s repeat homology <C1R1>
F:142-180/Domain: EGF homology <EGF>
F:184-293/Domain: C1r/C1s repeat homology <C1R2>
F:300-361/Domain: complement factor H repeat homology <FH1>
F:445-679/Domain: complement factor H repeat homology <FH2>
F:72-90,142-156,152-165,167-180,184-211,241-259,300-348,328-361,366-412,396-430,434-552,
F:158/Modified site: erythro-beta-hydroxyasparagine (asn) #status predicted
F:444-445/Cleavage site: Arg-116 (autolytic) #status predicted
F:483,532,633/Active site: His, Asp, Ser #status predicted

Query Match      10.2%; Score 400.5; DB 1; Length 686;
Best Local Similarity 22.7%; Pred. No. 2,5e-19;
Matches 173; Conservative 78; Mismatches 245; Indels 267; Gaps 34;

      128 CGQYLK--APK-----GQILLESYP-----LNAHCWTHAKPGVYIQLRPMLSLEFDY 175
      11  CGSVATPLGPKWPEVPVGRSLASPGFPEYANDGERRTWLTAPPGVRLRLYFTHDELISH 70
      176 MCQDYVEVRADGNRDGOIIRKVCNE--RAP-----IQSGSSLHVLPHSDG--KN 225
      71  LCEYDFVKLSG---AKVIALTCQESTDTERAPKQTFYSLGSSLDITFRSDYSNEKP 126
      226 FDGFHAIIY--EETACSSP-----CFHDTGCVLDKAGSYKCAACLAGYTCOR-----CENL 274
      127 FTFGEAFYAADIDDECVAAGEAPTCDH--CHNHLGGFYCCSRAGYVLRKRKTCAL 183
      275 -----LEE----- 277
      184 CSGQVFTQSGELSPPEYPRPYPKLSCTYSISLEGFVYILDFVESFVETHPETLCPY 243
      278 -----RNCSDP 283
      244 DFLKIQTDRREHGFCCGKTLPHRIETKSNVTITPTVDESGDHTGWKIHYSSTAHAQPYR 303
      284 GGPVNGYQKITGGGGLNGRAK--IGTVVSPFCNNSY--VLSSG-----NEKRTCCQNGEW 335
      304 MAPRNGH-----VSPQAKYILKDSIFICETGYELLOGLHLPLKASTAVCQKDGSH 354
      336 SGKQPIIC--IKACREPKISDLVRRRVLPQVQSRRETPHLQLYSAFSAFKQLQSAPTKPKAL 394
      355 DRPWPACSIYDCGP--DPLPSGRV-----EYITGP----- 383
      395 PFGDLPMGYQHILHTOLOECISPFY--RLGSSRRRTCLRTKNSG-----RAPSCIPICGK 448
      384 -----GVTTYKAVIYQSCBETFTYMKVNDGKYVCEADGFWTSKGEKSLPVCEPVCGL 436
      449 IENTAPKQGLR-----WPMQAIYRRTSGVHDGSLHKGMFLVCSGLVNERIVVVA 502
      437 SARTTGRIYGGQAKAGDPFMQVLLIGTT-----NAGMLLTDNNVTLTA 481
      503 AHCVTDLGKVTMIKTADLKVVLGKFFYRDDDEKTIQSLQ-----ISAIIILHPNY--DP 554
      482 AHAAYE---QKIDASALDIRG-----TLKRSLPHYQAMSEAVPIHEGTHD 526
      555 ILDDDAIILKLDKARISTRVQPICLAASRDLSFQESHITVAGNNVLADVRPFGFN 614
      527 AGFNDIALIKLNKKVININITPICLPKREASFMKRTDIGFASGWSG---LTORGFLA 582
      615 DTLRSGVSVVSDSLCEBQHEHDGIP--VSTDMFPCASWEPAPSDICTAETGIAAVSF 673
      583 RNLMYVDIPIVDHOKCTAAVEKPPYRGASTANMLCGLG--SGCKDSCRDGGG--ALVF 639
      674 PGRASPEPRMHLGLVSWSYDKTCSHRLSTAFKVLPRFKDMIR 716
      640 --LDSETERMVFQGIYSWGMNCGEAGQYVYTKVINIYIMIE 680

RESULT 6
S05008
complement subcomponent C1s (EC 3.4.21.42) precursor [similarity] - golden hamster
```


C:Species: *Mesocricetus auratus* (golden hamster)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: S05008
R:Kinoshita, H.; Sakiyama, H.; Tokunaga, K.; Imajob-Ohmi, S.; Hamada, Y.; Isono, K.; Sak
EBBS Lett. 250, 411-415, 1989
A:Title: Complete primary structure of a calcium-dependent serine proteinase capable of
A:Reference number: S05008; MUID:89325606; PMID:2753140
A:Accession: S05008
A:Molecule type: mRNA
A:Residues: 1-695 <KIN>
A:Cross-references: UNIPROT:P15156; UNIPARC:UP1000012700B; EMBL:X16160; NID:949621; PIDN
A:Note: part of this sequence, including the amino ends of both the heavy and light chain
C:Superfamily: complement-activating serine proteinases Clr/Cls/MASP; Clr/Cls repeat homol
C:Keywords: beta-hydroxyaspartine; calcium binding; duplication; glycoprotein; hydrolas
F:1-21/Domain: signal sequence #status predicted <SIG>
F:17-133/Domain: Clr/Cls repeat homology <Clr1>
F:22-444/Product: serine proteinase heavy chain #status experimental <HCH>
F:141-177/Domain: EGF homology <EGF>
F:181-293/Domain: Clr/Cls repeat homology <Clr2>
F:300-360/Domain: complement factor H repeat homology <FHL>
F:365-428/Domain: complement factor H repeat homology <FHZ>
F:445-682/Domain: trypsin homology <TRY>
F:466-695/Product: serine proteinase light chain #status experimental <LCH>
F:71-89, 141-153, 149-162, 164-177, 181-208, 240-257, 300-347, 327-360, 365-410, 392-428, 432-556,
F:155/Modified site: erythro-beta-hydroxyaspartine (asn) #status predicted
F:180, 413/Binding site: carboxylate (Asn) (covalent) #status predicted
F:482, 536, 638/Active site: His, Asp, Ser #status predicted

Query Match	9.6%;	Score 378.5;	DB 1,	Length 695;
Best Local Similarity	21.8%;	Pred. No. 7.6e-18;		
Matches 168; Conservative	81;	Mismatches 227;	Indels 293;	Gaps 35;

[illegible]

Db 542 LKQPVKMGPTVSPICLPGT---SSEYEPSESGDIGLISGWERTERRIVIGLR-----590
Qy 617 LRSGVSVVDL-----LCEQGHEDHGI PVSVDTNFNCASWEPTAPSDICTAETGGIAAV 671
Db 591 ---GAKLPVTSLEKCRQVKEENKPARADYVFPVSNMICAGEKV---DSCQGSQGAFAAL 644
Qy 672 SFPGRASPEPRMHLMGLVSVSYDKTCSHRLSTAFTKVLPEPKWIERBNRK 720
Db 645 PVPR-VRDPKFYVAGLVSMG--KKCG--TYGIYTKVKNYKDWILDTMQ 687

RESULT 7 .
T30337
polyprotein - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C:Accession: T30337
R:Yang, J. C.; Lindsay, L. L.; Hedrick, J. L.
submitted to the EMBL data library, March 1998
A:Description: cDNA cloning of ovochymase, a chymotrypsin-like protease released from X.
A:Reference numbers: Z20829
A:Accession: T30337
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1524 <YAN>
A:Cross-references: UNIPROT:Q91674; UNIPARC:UP1000000PBA76; EMBL:U081290; NID:G2981640; P
;superfamily: tyrosin related polypeptide; tyrosin homology

Query Match	9.0%	Score 354	DB 2	Length 1524
Best Local Similarity	22.3%	Pred. No. 8e-16		
Matches 166	Conservative 101	Mismatches 260	Indels 216	Gaps 39

```

0Y 55 CPGRREVVG-----TTPCCRNENEDCQLIHRGCIIFENCKSCNNGSLTDLDFEYK 109
Db 214 CHAVLEPIGHPVLDDITMLCAGPEPGGMDACQDSGGPFV--CRR-RSGVW-----FLA 263
0Y 110 GFYCAE-----CRAGW-----YGGDMRCGQVLRAP 135
Db 264 G--CVSMGLCCGSMWAKQIIRSQSGPALFSRVSVSLDPLRPXLTGCGSSKGRITTK 321
0Y 136 KGOI---LLESYPLNAHCWTTHAKRGEVILQLPFVMSLEFDYWCQYDYVEVBDGNDRG 192
Db 322 NGTVRYPLSNYNAINSVCWMMLAVQKAKTIEIFLOLIDIEDHATCTFDYLSFTVNE---- 377
0Y 193 QILKRVCGNRBPAPICQISSLSHLVLFPHSDSKNPFDDGHAIVEBITACSSPFCCHDGCVL 252
Db 378 KMRKVCGSTIPBPVLVRSNKVTVTFPSSDTEFTGRGEFIOFLAIPYWAAC--GSAKIL 435
0Y 253 DKAGSYKACIAGYQRCENLLEERNCSDP-----GAPVNGYKITGPGPOLN 301
Db 436 KKKG-----MYSNYPDPYRLKTCSMIILAPENHLYKLFPEDPNVE 478
0Y 302 GRHAKIGTVVSPFCNNSYVLSGNEKRTCOQNGEMSGKOPICAKREPKISLDVLR---R 358
Db 479 YGHGCIYDAVE---VYDGAEBK-----QILARLCGY 506
0Y 359 VLPWQVQSR-----TFLHOLYSAAFSKQKLQSAPTKPP-ALPRGLPMGYOHLHQ 409
Db 507 TLPPLPSSPPTNMLIREKTIMENSYPG--FKVFSFVPFKKQPSLPDDPPT-ISMHPR 563
0Y 410 ---LQYESICPFYRRLDSSRRTCLRTGKMSGRAPSCIP-ICGIENTITAPKTQGLRMPWQ 465
Db 564 AIALDVCGMAMPM-----TPKM-----MLPRIVGGE--ASPNNS---WPMQ 538
0Y 466 AAI-YRRTSGVHDSLHKGAMFLVCSGALVNERTVVAACHVTDLGKVTMIKTAD---LK 521
Db 599 VQIPFLKT-----FH-----CEGAIISPMILTAHC-----IRAABPYWT 635
0Y 522 VVLGKFPRDDR--DEKTIQSLQISAILHPNTDPIILDADIMILKLLDKARISTRVQPI 579
Db 636 VIAD-----DHNRMMLNESTEQIRINIKTIRIHNNNSSETYDDIMLALYEBPLDLNDFRPV 691

```


137 QUITL-----ESYPLNAHCWTHAKPGFVIOIAFLFVWLSLEFDYMCQDYDVEVADGDRDQ 192

Db 21 GELSPNTPQATPSEVKEKMDIEVEPGYGHLYFTHLIDIEISEKCAVDSVOIIGSDTREG 80

Qy 193 QIKKVCNGNERPAPI-----QSIGSSLAHVFHSDGS--KNFDGFHAIY--EEITACS---S 241

Db 81 RLCCGRSSNNPSPFIIEEFQVPYNNKLOVIFKSDFSNEERFTGFAPAYVATINECTDVED 140

Qy 242 SPCFHDGTCVLDKAGSYKCAACLAGY----- 266

Db 141 VPCSHFCNNFI-----GGYFCSCPEPEYFLHDDMKNGVNCSDGVFTALI,GEIASPNYPKPEYP 197

Qy 267 TGQRENTLL-----EERNCS-----PGSPVNGYQKIT 294

Db 198 ENSKREIYQIRLEKGFQVYVTLTRREDPEVAADSAGNCLDSLVFAVGRQRFQFYGCH----- 253

Qy 295 GGPGLIN-----GRHX--I 307

Db 254 GEPGLINLETGKNALDIIFQTDLTGQKKGWKLAYHODPMCPKEDTPNSVEMPAKAYVF 313

Qy 308 GTVVSFFPCNNSY-VLSG-----NEKRTCOQNGEMSGK---QPICTACREPKISDLVR 357

Db 314 RDVVOITCIDGEEVVEGVRGATSFYSTCGNGKMSNKLKQPV---DCGIP----- 362

Qy 358 RVLPMQVQSRERFPHQLYAASFQKQLQSAFPTKPP-ALPFGDLEPMGYQHLTQLOYESCIS 416

Db 363 -----ESIENGKVEDPESTLFGSV-----IRYTCBE 388

Qy 417 PEY--RLIGSSRRTCLRTGKMSGRA-----PSCIPIGKXIENTIAPKQTGRLMPQQAIIY 469

Db 389 PLYYENGGGGEGYHCNGNSWNVNLELPELPKCVPGV-----VP-----REPFEK-- 435

Qy 470 RRTSGVHDGSLHKGAFLV-----CSGALVNERTVVAALCVTDLGKVTMIKTADLKVYL 524

Db 436 QRIIGSDPADIKNFMQVFEEDNPAGALINETYVTLAAHVVEGNREPT-----YV 487

Qy 525 GKFTYDDDDDEKTIQSLQISAILIHPNYDPII-----DADIALKLKLDKARISTRVQ 577

Db 488 GSTSVQTSRLAKS-KMLTPEHVFHPGWKLEVEPGRTNFDNDIALVRLKDPVXMGPTVS 546

Qy 578 PICTLAASRLDSTFSQESHITVAGMNVLADVRSGQFKN-----TLRSVVSVVSDSLICEBOH 634

Db 547 PICTGETSSDYNLMGDGLGISG-----RTE--KDRVRLYLAARLPAVPLRCKCEYK 599

Qy 635 EDHGIPVS-----VTDNMFCAQSWEPAPSDICTAETGGLIAAASFPGPRASEDEPRWHLNGL 688

Db 600 VEK--PTAAEAAYVFFPNMICAQE--KGMDSCKGDSGGAFAVQDP--NDKTKFYAAGL 652

Qy 689 VWSYSDKTCSHRLSTAFTKVLFPKDWIERNNK 720

Db 653 VSMG--PQCG--TYGLYTRKYNVYDWIMKTQ 680

RESULT 10

A56318

enteropeptidase (EC 3.4.21.9) precursor [validated] - human

N:Alternate names: enterokinase

C:Species: Homo sapiens (man)

C:date: 19-May-1995 #sequence_revision 09-Aug-1996 #text_change 09-Jul-2004

C:Accession: A56318; B43090

R:Kitemoto, Y.; Veille, R.A.; Donis-Keller, H.; Sadlier, J.E.

Biochemistry 34, 4562-4568, 1995

A:Title: cDNA sequence and chromosomal localization of human enterokinase, the proteolytic

A:Reference number: A56318, MIMD:95234679, PMID:7718557

A:Accession: A56318

A:molecule type: mRNA

A:Residues: 1-1019 (K17>

A:Cross-references: UNIPROT:P98073; UNIPARC:UPI000003FE65; GB:U09860; NID:9746412; PIDN

R:Kitemoto, Y.; Yuan, X.; Wu, Q.; McCourt, D.W.; Sadlier, J.E.

Proc. Natl. Acad. Sci. U.S.A. 91, 7588-7592, 1994

A:Title: Enterokinase, the initiator of intestinal digestion, is a mosaic protease compo

A:Reference number: A43090, MIMD:94329561, PMID:8052624

A:Accession: B43090

A:Status: nucleic acid sequence not shown

F:199-236/Domain: LDL receptor ligand-binding repeat homology <LDL1>
F:358-520/Domain: MAM homology <MAM>
F:542-647/Domain: C1r/C1s repeat homology <C1r>
F:659-693/Domain: LDL receptor ligand-binding repeat homology <LDL2>
F:694-799/Domain: scavenger receptor cysteine-rich domain homology <SRC>
F:801-1035/Domain: enterepoptidase light chain #status predicted <LCH>
F:801-1030/Domain: trypsin homology <TRY>
F:116,147,170,194,233,263,264,404,456,486,519,550,646,698,722,741,762,864,903,965/Bindin
F:788-912,826-993,957-972,983-1011/Disulfide bonds: #status predicted
F:841,892,987/Active site: His, Asp, Ser #status predicted

Query Match 8.0%; Score 317.5; DB 1; Length 1035;
Best Local Similarity 24.6%; Pred. No. 1.5e-13;
Matches 146; Conservative 80; Mismatches 225; Indels 143; Gaps 30;

143 SYPLNACEHTIHAHKGPIQLRFLVMLSLEFDYMCQDYDVEVRDGDNRDGIIRKVGNE 202
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
561 SYPLNACEHTIHAHKGPIQLRFLVMLSLEFDYMCQDYDVEVRDGDNRDGIIRKVGNE 614
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
203 RPAPITQISGS---LHVLPHSDGSKNPDGFHAIYEITACS-SSPCFHDG-TCVLIDKAS 257
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
615 -PGVNVDFSTNTMTVLFIITDNLAKGFKANFTTGVGLIPEPCEDNFQC---KDG- 669
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
258 YKCAAGLYGQRCENLLEERNCGDPGSPVNGYQKITGPGELINGRHAIGTIVVSPCNN 317
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
670 -ECIPLVNL---CDGPHCKDGDSEACVFLFNGTTDSGLVQFRIQSIWHV----- 717
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
318 SYVLGNKERTCOONGEMSKQPCICAKREPKISDLVRRVRLVMQVSRRTPLHOLYSA 377
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
718 -----ACAEN---WT-----TQISDDVCQL----- 735
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
378 AFSKQKQSAFTKKRALPFGLPMGYOHLTOLQYECISPRYRLGSSRRTCLRTGKMSG 437
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
736 ---GLGTGNSVPTSTGGP---YVNLNT-----APRGSLIRPSQGLE----- 775
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
438 RARPCIP-----CGK--IENITAPKTQ-----LRPWQAIIYRRTSGVHDGSLHK 483
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
776 --DBLILQCNKYGCKGLVYQEVSPKIVGSGDSREGAMPVVALY-----FDDQ--- 823
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
484 AMFLVCGSALVNERTVVAACHCVTDLGKVTMIKTADLKVLVKGKPYRDDDRDKTIQSIQ 543
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
824 ---OVCGASLVSRLVSAHCV---YGR--NMSPSKMAVLG-LHMASNLTSPOIETRLI 875
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
544 SAIIHPYDPIILDADIAILKLDKARISTRVOPICLAASRDLSFQESH-I-TVAGWN 602
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
876 DQYINPYNKRRKNDIAMHLEMKVNTYDIQICLRENOV---FPPRIGISIAWG 932
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
603 VLADVRSGFKNDTLRSGVSVVDLSLCEQHEHGHIFSVYTDNNFCASWEPTAPSDICT 662
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
933 ALI---YQGSTADVLQADVPRLNSKCCQCMPEY---NITENNVACAGYE-AGGVDSQC 984
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
663 AETGIAVSPFGASPERRWLHGLVMSYDKTCSHRLTAFTKVLFPKXWIE 716
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
985 GDSGG-----PLMCGENRMLLAGVTSFGYQCALPNR-PGVYARVPRFTWIO 1031
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
DB

RESULT 14

EXCH

coagulation factor Xa (EC 3.4.21.6) precursor - chicken
N:Alternate names: virus-activating proteinase
C:Species: Gallus gallus (chicken)
C:Date: 12-Feb-1993 #sequence revision 07-Feb-1997 #text_change 09-Jul-2004
C:Accession: S15838; S20380; S20381
R:Suzuki, H.; Harada, A.; Hayashi, Y.; Wada, K.; Asaka, J.; Gotoh, B.; Ogasawara, T.; Na
FEBS Lett. 283, 281-285, 1991

A:Title: Primary structure of the virus activating protease from chick embryo. Its ident
A:Reference number: S15838; MUID:91257322; PMID:2044767
A:Accession: S15838
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-475 <SUZ>
A:Cross-references: UNIPROT:P25155; UNIPARC:UPI000012A408; DBJ:D00844; NID:9222869; PIR
R:Gotoh, B.; Yamuchi, F.; Ogasawara, T.; Nagai, Y.

FEBS Lett. 296, 274-278, 1992
A:Title: Isolation of factor Xa from chick embryo as the amniotic endoprotease responsi
A:Reference number: S20380; MUID:92164779; PMID:1537403
A:Accession: S20380
A:Molecule type: protein
A:Residues: 41-55 <G02>
A:Cross-references: UNIPARC:UPI00000FCE9E
A:Accession: S20381
A:Molecule type: protein
A:Residues: 241-246, 'X', 248-251, 'X', 253-261 <G0T>
A:Cross-references: UNIPARC:UPI00000FCE9E
A:Function:
A:Description: catalyzes the proteolytic activation of prothrombin to thrombin in the p
A:Pathway: blood coagulation
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglut
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-40/Domain: propeptide #status predicted <PRO>
F:41-185/Product: coagulation factor X light chain #status experimental <LCH>
F:90-121/Domain: EGF homology <EG1>
F:129-167/Domain: EGF homology <EG2>
F:166-475/Product: coagulation factor X heavy chain #status predicted <HC>
F:166-240/Domain: activation peptide #status predicted <APT>
F:241-475/Product: coagulation factor Xa heavy chain #status experimental <HC>
F:241-468/Domain: trypsin homology <TRY>
F:46,47,54,56,59,60,65,66,69,72,75,79/Modified site: gamma-carboxylglutamic acid (Glu) #
F:57-62,90-101,95-110,112-121,129-140,136-152,154-167,175-348,247-252,267-283,396-410,4
F:103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted
F:196,207,228,285/Binding site: carbohydrate (asn) (covalent) #status predicted
F:282,328,425/Active site: His, Asp, Ser #status predicted

Query Match 8.0%; Score 314.5; DB 1; Length 475;
Best Local Similarity 22.2%; Pred. No. 1e-13;
Matches 129; Conservative 79; Mismatches 177; Indels 195; Gaps 25;

183 EVRDGDNRRDQIIRKVGNERPAPISGSLHLPHSDGSKNPDGFHAIYEITACSSS 242
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
47 EMKQGN-----IERENBERGSKBEARE-----FEDNEKT-EEFWMNIVYDGDCCSN 93
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
243 PCHHDGTVLDKAGSYKACLAGYTGQRCENLLEERNCGDPGSPVNGYQKITGPGELING 302
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
94 PCHYGQC-KDGGASYCCLDYGQKCFVLPK-----YCKINNGD----- 135
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
303 RHAIGTVSPFCNNSVVLGNKERTQNGGMS--GKOPICIKAREPKISDLVR--- 357
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
136 -----CGQFSIKSKVQKDVVCTSGYELAEDEKQ--CVSKVYPCGKVLKRIKR 185
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
358 -RVLPQVQSRRTPLHOLYSAFS-KQKLSAFTKKRALPFGLPMGYOHLTOLQYECI 415
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
186 SVLPTSNMNTATSDQVPTNGSILEEVPPTTSTPTP----- 225
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
416 SPFPRIGSSRRITCLRTGKSGAPSCIPICGIENITAPKTGL-----RWPQ 465
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
226 ---PRNGSS-----ITDPNVDTRIYVGDECRPGCEPMQ 255
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
466 AAIYRRTSGVHDGSLHKAMFLVCSGALVNERTVVAACHCVTDLGKVTMIKTADLKVL 525
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
256 AVLIN-----EKGEF--CGGTLLEDETLTAACIN-----QSKIKVVG 295
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
526 KFYRDDDRDKTIQSLQISAIILHPYDPIILDADIAILKLDKARISTRVOPICLAASR 585
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
296 EVDREKEHSHETHTA--KLPFSKIATYNDIALILTKPKIQSEVYVACLPQA- 352
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
586 DLSTFOESHITVAGMNVLDVRSPGKNDTL---RSGVVS----- 623
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
353 -----DFANEVLNMQSGVSGRGEFEAGRLSKRLKYLE 387
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
624 --VYDLSLCEQHEHGHIFSVYTDNNFCASWEPTAPSDICTATGCIAAVSPRABEP 681
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
388 VPYVDSTCKOSTN---FATENMFCAGYE-TEQKDAQGDSGG-----PHVTRYKD 435
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
682 RWHLMGLVMSYDKTCSHR-LSTAFTKVLFPKMIERNMK 720
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
DB

Db 436 TFFVTGIVSWG--EGCARKKYGVYTKLSRFLRWVTVNR 473

RESULT 15

JC7731

membrane-bound arginine-specific serine proteinase precursor - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004

C:Accession: J07731, J07775

R:Kishi, K.; Yamazaki, K.; Yasuda, I.; Yahagi, N.; Ichinose, M.; Tsuchiya, Y.; Athauda, J. Biochem. 130, 425-430, 2001

A:Title: Characterization of a membrane-bound arginine-specific serine protease from rat

A:Reference number: J07731, NCID:21421307; PMID:11530019

A:Accession: J07731

A:Molecule type: mRNA

A:Residues: 1-855 <RTS>

A:Cross-references: UNIPROT:Q9JUT7; UNIPARC:UPI000008BAC0; DDBJ:AB049189

A:Experimental source: strain Male, 7-week-old

R:Satom, S.; Yamazaki, Y.; Tazuki, Y.; Hitomi, Y.; Iwanaga, T.; Fushiki, T. Biochem. Biophys. Res. Commun. 287, 995-1002, 2001

A:Title: A role for membrane-type serine protease (MT-SPI) in intestinal epithelial turn

A:Reference number: J07775; PMID:11573963

A:Contents: Small intestine

A:Accession: J07775

A:Molecule type: mRNA

A:Residues: 1-855 <SAT>

A:Cross-references: UNIPARC:UPI000008BAC0; DDBJ:AB037898

C:Comment: This enzyme, an epithelial-derived, type II integral membrane serine protease of specific proteins or peptides on the brushborder membranes. It also participates in

lial migration and/or cell loss.

C:Genetics:

A:Gene: mt-spi

A:Map position: basolateral cell surface

C:Superfamily: membrane-bound arginine-specific serine proteinase

C:Keywords: protein digestion

Query Match

Best Local Similarity 7.9%; Score 313; DB 2; Length 855;

Matches 151; Conservative 78; Mismatches 227; Indels 250; Gaps 33;

QY 82 HPG--CTIFENCKSCNNGSWGTLDDPFYVGFCAECBAGWGGDDCGQVLRAPKQI 139
 DB 324 HPGFATFQLPKM---SSCGILSF--AQGTSSP---YPG----- 358
 QY 140 LIESYPLNHCENTHAKEGFIQLRFVMSLEFDYM---CQDYEVARDGNDQI 195
 DB 359 ---HYPPINICTWNIKVPNNRNVKVFPLFLVDPNIPVGSCTKDYVEING----- 406
 QY 196 KRYCGNERAPLOSISLSHLVLFHSDGSKNFDGFHAIYEITACSSSPC---FHDGTC 250
 DB 407 EKFCGERSQFVSSNSKIVHSHSDSYDTGFLAEY--LSYDSNDPCGFMCKTGRC 464
 QY 251 VL---DKAGSYKACLAGY---TGRCENL-----EERNS 281
 DB 465 IRKDLACDGAADCPDYSDEHCRCAITHQPCKNQFCKPLFWCDVNDGDSDEGCS 524
 QY 282 DPGGPVNGYQKITGPGGLNGRHAIGTVVSPFCNNSYVL---SGNEKRTCOQNEBWSG 337
 DB 525 CPAG-----SFKCSNGKCLPQSQCGNKDDCCGSDSEAS 558
 QY 338 KQDICTKACREPKISLVLRRLVPMOVQSRHPLHQLYSAFSKQKIQSAPTKKPALPFG 397
 DB 559 CDNVNAVSC----- 567
 QY 398 DLPNGYQHLYTOLQYECISPFYRLGSSRRTCLRTGWSGRAPSCIPICGIENITAPKT 457
 DB 568 ---TKYTRC-----QNGCLCNKGN---PEC---DGKDCSDGSDE 599
 QY 458 Q---GLR-----WPMQAIYRRTSGVHDSLHKAMFLVCSGALVN 495
 DB 600 KNCDCGLRSFTKQARVVVGTTNADGEWPMQVSLHALGQS-----H-----LCGASLIS 647

QY 496 ERTVVAAHCVTDLGKVTWIKTAD---LKVLGKFYRDDRDDEKTIQSLSAIIILHPNY 552
 DB 648 PMVLVSAHCFOD---ETIFKISDHTMTAFIG-LIDGSKASAGVQEHKRIITHPSF 703
 QY 553 DPLLDADIATILKLDKARISTRVOPICLAASRDLSFQESHITVAGNNVLADVRSPGF 612
 DB 704 NDFTFDYDIALLEKBPAYSTVVRPCLPDNTHVFPAKGA--IWTGW---GHTKEGCT 758
 QY 613 KNDTLRSGVSVVDSLLCEQHEDHGIPVSVTDNNFPCASWEPTAFSDICTAETG-IAAV 671
 DB 759 GALILQKEIRIVINQTCBEL-----LPQILPRMKCVGF-LSGGVDSQGDSPGLSSV 812
 QY 672 SPPGRASPEPRNHLMLGVSVDYDXTCSHRLST-AFTKVLPRDWIE 716
 DB 813 EKDGLI-----FOAGVSWG--EGCAQNNKPGVYTRLPVARDWIK 850

Search completed: April 4, 2007, 21:57:44
 Job time : 50 secs

THIS PAGE BLANK (USPTO)

OM protein - protein search, using sw model
Run on: April 4, 2007, 21:58:01 ; Search time 221 Seconds
(without alignments)
1594.208 Million cell updates/sec

Title: US-10-063-546-38
Perfect score: 3945
Sequence: 1 MEIGCTWQLGTFPLQLLIS.....LSTAFKVLPEKQWIRNNK 720
Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5
2782304 segs, 48933398 residues
Total number of hits satisfying Chosen parameters: 2782304
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database :
1: geneseq_200701.*
A: geneseq_1980s.*
2: geneseqp1990s.*
3: geneseqp2000s.*
4: geneseqp2001s.*
5: geneseqp2002s.*
6: geneseqp2003as.*
7: geneseqp2003bs.*
8: geneseqp2004s.*
11: geneseqp2007s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of SUMMARIES

No.	Score	Match	Length	DB	ID	Description
RESULT 1						
ID	AAV6695	standard;	protein;	720	AA.	
DE	Membrane-bound protein					PRO1344.
PN	WO963088-A2.					
PD	09-DEC-1999.					
PA	(GETH) GENENTECH INC.					
Query Match		100.0%;	Score 3945;	DB 3;	Length 720;	
Best Local Similarity		100.0%;	Pred. No. 1.9e-204;			
RESULT 2						
ID	AAU29108	standard;	protein;	720	AA.	
DE	Human PRO polypeptide sequence					#85.
PN	WO200168848-A2.					
PD	20-SEP-2001.					
PA	(GETH) GENENTECH INC.					
Query Match		100.0%;	Score 3945;	DB 4;	Length 720;	
Best Local Similarity		100.0%;	Pred. No. 1.9e-204;			
RESULT 3						
ID	AA87544	standard;	protein;	720	AA.	
DE	Human PRO1344.					
PN	WO200116318-A2.					
PD	08-MAR-2001.					
PA	(GETH) GENENTECH INC.					
Query Match		100.0%;	Score 3945;	DB 4;	Length 720;	
Best Local Similarity		100.0%;	Pred. No. 1.9e-204;			
RESULT 4						
ID	AA865218	standard;	protein;	720	AA.	
DE	Human PRO1344 (UNQ699) protein sequence					SEQ ID NO:231.
PN	WO200073454-A1.					
PD	07-DEC-2000.					
PA	(GETH) GENENTECH INC.					
Query Match		100.0%;	Score 3945;	DB 4;	Length 720;	
Best Local Similarity		100.0%;	Pred. No. 1.9e-204;			
RESULT 5						
ID	ABG95869	standard;	protein;	720	AA.	
DE	Human secreted/transmembrane protein					PRO1344.
PN	US2002119130-A1.					
PD	28-AUG-2002.					
PA	(GETH) GENENTECH INC.					
Query Match		100.0%;	Score 3945;	DB 5;	Length 720;	
Best Local Similarity		100.0%;	Pred. No. 1.9e-204;			
RESULT 6						
ID	ABUS8484	standard;	protein;	720	AA.	

DE	Human PRO polypeptide	#85.			
PN	US2003027272-A1.				
PD	06-FEB-2003.				
Query Match		100.0%;	Score 3945;	DB 6;	Length 720;
Best Local Similarity		100.0%;	Pred. No. 1.9e-204;		
RESULT 7					
ID	ABU86032	standard;	protein;	720	AA.
DE	Novel human secreted and transmembrane protein				PRO1344.
PN	US2003032127-A1.				
PD	13-FEB-2003.				
Query Match		100.0%;	Score 3945;	DB 6;	Length 720;
Best Local Similarity		100.0%;	Pred. No. 1.9e-204;		
RESULT 8					
ID	ABU84347	standard;	protein;	720	AA.
DE	Human secreted/transmembrane protein (PRO)				#85.
PN	US2003032112-A1.				
PD	13-FEB-2003.				
Query Match		100.0%;	Score 3945;	DB 6;	Length 720;
Best Local Similarity		100.0%;	Pred. No. 1.9e-204;		
RESULT 9					
ID	ABR66221	standard;	protein;	720	AA.
DE	Human secreted polypeptide				PRO1344, SEQ ID NO:170.
PN	US2003027278-A1.				
PD	06-FEB-2003.				
Query Match		100.0%;	Score 3945;	DB 6;	Length 720;
Best Local Similarity		100.0%;	Pred. No. 1.9e-204;		
RESULT 10					
ID	ABR65611	standard;	protein;	720	AA.
DE	Human secreted polypeptide				PRO1344, SEQ ID NO:170.
PN	US2003036159-A1.				
PD	20-FEB-2003.				
Query Match		100.0%;	Score 3945;	DB 6;	Length 720;
Best Local Similarity		100.0%;	Pred. No. 1.9e-204;		
RESULT 11					
ID	ABU99551	standard;	protein;	720	AA.
DE	Human secreted/transmembrane protein (PRO)				#85.
PN	US2003040070-A1.				
PD	27-FEB-2003.				
Query Match		100.0%;	Score 3945;	DB 6;	Length 720;
Best Local Similarity		100.0%;	Pred. No. 1.9e-204;		
RESULT 12					
ID	ABUS8033	standard;	protein;	720	AA.
DE	Human PRO polypeptide				#65.
PN	US2003027163-A1.				
PD	06-FEB-2003.				
Query Match		100.0%;	Score 3945;	DB 6;	Length 720;
Best Local Similarity		100.0%;	Pred. No. 1.9e-204;		
RESULT 13					
ID	ABU59111	standard;	protein;	720	AA.
DE	Novel human secreted or transmembrane protein				PRO1344.
PN	US2002132252-A1.				
PD	19-SEP-2002.				
PA	(GETH) GENENTECH INC.				
Query Match		100.0%;	Score 3945;	DB 6;	Length 720;
Best Local Similarity		100.0%;	Pred. No. 1.9e-204;		
RESULT 14					
ID	ABU82623	standard;	protein;	720	AA.
DE	Human secreted/transmembrane protein				PRO1344.
PN	US2003032023-A1.				
PD	13-FEB-2003.				
Query Match		100.0%;	Score 3945;	DB 6;	Length 720;
Best Local Similarity		100.0%;	Pred. No. 1.9e-204;		
RESULT 15					
ID	ABU82790	standard;	protein;	720	AA.
DE	Human PRO polypeptide				#85.
PN	US2003032113-A1.				
PD	13-FEB-2003.				
Query Match		100.0%;	Score 3945;	DB 6;	Length 720;
Best Local Similarity		100.0%;	Pred. No. 1.9e-204;		
RESULT 16					
ID	ABU89911	standard;	protein;	720	AA.
DE	Novel human secreted and transmembrane protein				PRO1344.
PN	US2003036147-A1.				

PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 17
ID ABR68160 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003027264-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 18
ID ABU60542 standard; protein; 720 AA.
DE Human secreted/transmembrane protein, #94.
PN US2002160384-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 19
ID ABU96213 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003036144-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 20
ID ABU92644 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036149-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 21
ID ABO08721 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003044923-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 22
ID ABO02773 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003040062-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 23
ID ABR74927 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040056-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 24
ID ABR94689 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003044926-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 25
ID ABU13924 standard; protein; 720 AA.
DE Human PRO1344 polypeptide.
PN US2002103125-A1.
PD 01-AUG-2002.
PA (GETH) GENENTECH LTD.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 26
ID ABU85662 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003036140-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 27
ID ABU98822 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003013153-A1.
PD 16-JAN-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 28
ID ABU98037 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003017544-A1.
PD 23-JUN-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 29
ID ABU91743 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003027277-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 30
ID ABU89436 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003036141-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 31
ID ABU86277 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036146-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 32
ID ABU67490 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036162-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 33
ID ABU80518 standard; protein; 720 AA.
DE Human PRO protein #85.
PN US2003036137-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 34
ID ABU72509 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003003531-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 35
ID ABU90894 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003018173-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 36
ID ABO33953 standard; protein; 720 AA.

DE Human secreted/transmembrane protein PRO1344.
PN US2003009013-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 37
ID ABR99436 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040063-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 38
ID ABR98826 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040064-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 39
ID ABO16349 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003027267-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 40
ID ABR92249 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003036160-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 41
ID ABO18890 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003044925-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 42
ID ABR78311 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054474-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 43
ID ABR71970 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003018183-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 44
ID ABR85047 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003033114-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 45
ID ABO00186 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003032101-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 46
ID ABO11518 standard; protein; 720 AA.

DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036124-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 47
ID ABO02163 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003040054-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 48
ID ABR8737 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003036133-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 49
ID ABR83432 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036134-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 50
ID ABO06233 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003022294-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 51
ID ABR59269 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003027275-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 52
ID ABO09331 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003027324-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 53
ID ABO19195 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003036118-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 54
ID ABO11213 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036123-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 55
ID ABR6831 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003036148-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 56
ID ABO16044 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003040060-A1.

PD 27-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 57
ID ABO13750 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003044916-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 58
ID ABU71524 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344.
PN US2003013855-A1.
PD 16-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 59
ID ABU65653 standard; protein; 720 AA.
DE Human secreted/transmembrane protein, SEQ ID 170.
PN US2003036156-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 60
ID ABO07501 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003032117-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 61
ID ABO03688 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036128-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 62
ID ABR67136 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003027266-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 63
ID ABO15739 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 64
ID ABUS6020 standard; protein; 720 AA.
DE Human secreted/transmembrane protein, PRO1344.
PN US2003022398-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 65
ID ABU72305 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2002182638-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 66
ID ABU65348 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003032102-A1.

PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 67
ID ABU95293 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003036117-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 68
ID ABU71196 standard; protein; 720 AA.
DE Human PRO1344 protein.
PN US2003036143-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 69
ID ABO07806 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003032130-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 70
ID ABR70047 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003032138-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 71
ID ABR69380 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003036132-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 72
ID ABO01521 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US200308353-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 73
ID ABU81323 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003017542-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 74
ID ABR60120 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003032137-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 75
ID ABU90978 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003018168-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 76
ID ABR67855 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003027269-A1.

PD 06-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 77
ID ABR65243 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003027268-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 78
ID ABR6465 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003027274-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 79
ID ABR7187 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003032135-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 80
ID ABUS9258 standard; protein; 720 AA.
DE Human secreted/transmembrane protein, #94.
PN US2003027162-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 81
ID ABUS357 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003022295-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 82
ID ABUS9047 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003022297-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 83
ID ABUS3127 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003032105-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 84
ID ABUS9483 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003032123-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 85
ID ABUS90531 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003032108-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 86
ID ABUS4042 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003032111-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 87
ID ABUS9693 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003032119-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 88
ID ABO2595 standard; protein; 720 AA.
DE Human PRO1344 polypeptide.
PN US2002127576-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 89
ID ABR64938 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003027263-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 90
ID ABO27299 standard; protein; 720 AA.
DE Human secreted/transmembrane polypeptide PRO1344.
PN US2003009012-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 91
ID ABR68770 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003027271-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 92
ID ABO06586 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036125-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 93
ID ABR99131 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040068-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 94
ID ABUS7015 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003027280-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 95
ID ABUS967 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003022300-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 96
ID ABUS2254 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003036136-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;

Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 97
ID ABU87265 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003036138-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 98
ID ABU83737 standard; protein; 720 AA.
DE Human secreted/cranmembrane protein (PRO) #85.
PN US2003032109-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 99
ID AB008111 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003040066-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 100
ID ABU92494 standard; protein; 720 AA.
DE Human secreted/cranmembrane protein PRO1344.
PN US2003045684-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 101
ID ABU81822 standard; protein; 720 AA.
DE Novel human secreted and cranmembrane protein PRO1344.
PN US2003032104-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 102
ID ABU65986 standard; protein; 720 AA.
DE Novel human secreted and cranmembrane protein PRO1344.
PN US2003036157-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 103
ID ABU81164 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344.
PN US2003027212-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 104
ID ABR59815 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003032120-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 105
ID ABU94003 standard; protein; 720 AA.
DE Novel human secreted and cranmembrane protein PRO1344.
PN US2003036155-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 106
ID ABU99856 standard; protein; 720 AA.
DE Novel human secreted and cranmembrane protein PRO1344.
PN US2003022296-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;

RESULT 107
ID ABR65526 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003027281-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 108
ID ABR90944 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040058-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 109
ID ABO53779 standard; protein; 720 AA.
DE Novel human secreted and cranmembrane protein PRO1344.
PN US2003027986-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 110
ID ABU58964 standard; protein; 720 AA.
DE Human secreted/cranmembrane protein, #94.
PN US2002142961-A1.
PD 03-OCT-2002.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 111
ID ABU94371 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003017540-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 112
ID ABU79253 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003032106-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 113
ID ABU86582 standard; protein; 720 AA.
DE Human secreted/cranmembrane protein (PRO) #85.
PN US2003032129-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 114
ID ABU8687 standard; protein; 720 AA.
DE Novel human secreted and cranmembrane protein PRO1344.
PN US2003032131-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 115
ID ABU94676 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003032103-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 116
ID ABO04603 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003032107-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;

RESULT 117
ID ABR70352 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003032139-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 118
ID ABU92342 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003022187-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 119
ID ABU98517 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003022301-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 120
ID ABR65916 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003036165-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 121
ID ABR64633 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003027262-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 122
ID ABU59407 standard; protein; 720 AA.
DE Novel human secreted or transmembrane protein PRO1109.
PN US2003027985-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 123
ID ABU79558 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003032110-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 124
ID ABU92949 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036142-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 125
ID ABU95908 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003036145-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 126
ID ABU91128 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003036154-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 127
ID ABU90221 standard; protein; 720 AA.
DE Human PRO protein #85.

DE Novel human secreted and transmembrane protein PRO1344.
PN US2003036153-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 128
ID ABO09636 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003044931-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 129
ID ABO10908 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036150-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 130
ID ABR70962 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040069-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 131
ID ABU98281 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2002183493-A1.
PD 05-DEC-2002.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 132
ID ABU87570 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003022293-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 133
ID ABU91438 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003032128-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 134
ID ABU89286 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003036634-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 135
ID ABU84652 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003032116-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 136
ID ABR69742 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003032122-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 137
ID ABU80119 standard; protein; 720 AA.
DE Human PRO protein #85.

PN US2003036139-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 138
ID ABR82493 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2002183494-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 139
ID ABR92173 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003017476-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 140
ID ABR93388 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003017541-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 141
ID ABO09941 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003017543-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 142
ID ABO09026 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036152-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 143
ID ABR96457 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003027993-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 144
ID ABR10879 standard; protein; 720 AA.
DE Human PRO polypeptide #65.
PN US2002123463-A1.
PD 05-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 145
ID ABR10594 standard; protein; 720 AA.
DE Human secreted/transmembrane protein #85.
PN US2002127584-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 146
ID ABR81631 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2002171764-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 147

ID ABR72127 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003023042-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 148
ID ABR95603 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003032115-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 149
ID ABR96812 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003032140-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 150
ID ABR70657 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040076-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 151
ID ABO05008 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003008352-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 152
ID ABO08416 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003044922-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 153
ID ABR88570 standard; protein; 720 AA.
DE Human secreted and transmembrane polypeptide PRO1344.
PN US2002197615-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 154
ID ABO34084 standard; protein; 720 AA.
DE Human PRO1344 polypeptide.
PN US2003017981-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 155
ID ABO05623 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003032118-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 156
ID ABR74012 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003036135-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;

RESULT 157
ID ABR95604 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054455-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 158
ID ABR8901 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049741-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 159
ID ABR81206 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049743-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 160
ID ABM00902 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049769-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 161
ID ABR8504 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068743-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 162
ID ABM77325 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068743-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 163
ID ABO28609 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068685-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 164
ID ABO31554 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068725-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 165
ID ABM07971 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068752-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 166
ID ABO40451 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068682-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 167
ID ABO35876 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003068701-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 168
ID ABO44015 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003068755-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 169
ID ADA77922 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003073180-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 170
ID ABM24810 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104539-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 171
ID ABO03078 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036131-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 172
ID ABR90334 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040075-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 173
ID ABM17248 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054459-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 174
ID ABR94994 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003044930-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 175
ID ABR95299 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040071-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.

```
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 176
ID ADB17095 standard; protein: 720 AA.
DE Human transmembrane PRO polypeptide (SeqID 38).
PN US2003050462-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 177
ID ABO21537 standard; protein: 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003054471-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 178
ID ABR97801 standard; protein: 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064452-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 179
ID ABR87589 standard; protein: 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068705-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 180
ID ABR77630 standard; protein: 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054473-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 181
ID ABR27860 standard; protein: 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064440-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 182
ID ABM06141 standard; protein: 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068704-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 183
ID ABM03647 standard; protein: 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068722-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 184
ID ABR35098 standard; protein: 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073183-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 185
ID ABM26335 standard; protein: 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104549-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 186
ID ABO48117 standard; protein: 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003045749-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 187
ID ABR92859 standard; protein: 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064462-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 188
ID ABO24620 standard; protein: 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003065159-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 189
ID ADA37742 standard; protein: 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US200308297-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 190
ID ABM11631 standard; protein: 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064447-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 191
ID ABM02732 standard; protein: 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073184-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 192
ID ABM16028 standard; protein: 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064463-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 193
ID ABO27589 standard; protein: 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003064451-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 194
```

ID AEM29080 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068721-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 195
ID AEM07056 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068699-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 196
ID AEM21150 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068707-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 197
ID AEM09496 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073175-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 198
ID ABO41366 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068695-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 199
ID ABO36181 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003068703-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 200
ID ABO43710 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003068732-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 201
ID AEM76410 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003082717-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 202
ID AEM76106 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104548-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 203
ID AEM25725 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104542-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 204
ID AEM26030 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104543-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 205
ID ADA21428 standard; protein; 720 AA.
DE Human secreted/transmembrane polypeptide PRO1344.
PN US2003054404-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 206
ID ABO03383 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036127-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 207
ID ABO02468 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003040061-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 208
ID ABO44257 standard; protein; 720 AA.
DE Human secreted/transmembrane polypeptide PRO 1344.
PN US2003018172-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 209
ID ABR90639 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003036130-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 210
ID ABR73707 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054468-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 211
ID ABO16959 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003054470-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 212
ID ABR94384 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003044917-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 213
ID ABR75891 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.

```
PN US2003044929-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
RESULT 214
ID ABR71267 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003059880-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
RESULT 215
ID ABR93164 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064465-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
RESULT 216
ID ABR93469 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054478-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
RESULT 217
ID ADL10215 standard; protein; 720 AA.
DE Human secreted/transmembrane protein, PRO1344.
PN US2003059831-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
RESULT 218
ID ABR87894 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068718-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
RESULT 219
ID ABO27894 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003064454-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
RESULT 220
ID ABO30029 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003064461-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
RESULT 221
ID ABO3338 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003068724-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
RESULT 222
ID ABO4926 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068727-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
RESULT 223
ID ABO08886 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068772-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
RESULT 224
ID ABO36486 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068714-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
RESULT 225
ID ABO35571 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003068758-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
RESULT 226
ID ABO39536 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068776-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
RESULT 227
ID ABO10411 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003069407-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
RESULT 228
ID ABO11936 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104555-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
RESULT 229
ID ABO52082 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003049768-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
RESULT 230
ID ABO52387 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003049771-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
RESULT 231
ID ADL19900 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003069394-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
```

```
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 232
ID ABO23705 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003032134-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
RESULT 233
ID ADB17283 standard; protein; 720 AA.
DE Human transmembrane PRO polypeptide (SeqID 38).
PN US2003050465-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
RESULT 234
ID ADA17759 standard; protein; 720 AA.
DE Human PRO1344 polypeptide.
PN US2003054987-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
RESULT 235
ID ABR97191 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054481-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
RESULT 236
ID ABR86979 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049778-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
RESULT 237
ID AAM11021 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049782-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
RESULT 238
ID AAM28165 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054476-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
RESULT 239
ID ABO32164 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068733-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
RESULT 240
ID AAM15291 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068692-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
RESULT 241
ID ABO6446 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068709-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
RESULT 242
ID ABO4257 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068716-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
RESULT 243
ID ABO22370 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068740-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
RESULT 244
ID ABO7666 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068751-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
RESULT 245
ID ABO40756 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068684-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
RESULT 246
ID ABO35403 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073179-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
RESULT 247
ID ABO33166 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003087374-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
RESULT 248
ID ABO52692 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003049773-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
RESULT 249
ID ABO50252 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049777-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
RESULT 250
ID ABO9246 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003040055-A1.
```


Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 270
ID ABO2427 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US200305886-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 271
ID ABR86369 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049758-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 272
ID ABR86674 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049772-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 273
ID ABM1638 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064448-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 274
ID ABM29690 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064456-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 275
ID ABO29114 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068693-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 276
ID ABM2895 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068735-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 277
ID ABM2385 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068753-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 278
ID ABM23065 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068742-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 279
ID ABO22147 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003054477-A1.
PD 20-MAR-2003.

RESULT 279
ID ABO27706 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068756-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 280
ID ABM28470 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003082715-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 281
ID ABM28775 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003082716-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 282
ID ABM66419 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068737-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 283
ID ABM75801 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104547-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 284
ID ABM34081 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003096359-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 285
ID ABM34386 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003100061-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 286
ID ABO20317 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003032125-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 287
ID ABO21232 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003054454-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 288
ID ABO22147 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003054477-A1.
PD 20-MAR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 289
ID ADA20072 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003055222-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 290
ID ABO34185 standard; protein; 720 AA.
DE Human secreted/transmembrane polypeptide PRO 1344.
PN US2003060601-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 291
ID ABR96581 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054460-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 292
ID ADA94447 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US2003059832-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 293
ID ABR85759 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049753-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 294
ID ABR99741 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049763-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 295
ID ABM00597 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073172-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 296
ID ABM00292 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073172-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 297
ID ABO29724 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068700-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 298
ID ABM23590 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068736-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 299
ID ABM29385 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US200306879-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 300
ID ABO38316 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068767-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 301
ID ABO45616 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003073182-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 302
ID ABM20540 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104557-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 303
ID ADA81441 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003092121-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 304
ID ABO16654 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003027276-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 305
ID ABO18280 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003044920-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 306
ID ABO22707 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003027265-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 307
ID ABO23012 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003054461-A1.
PD 20-MAR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 308
ID ABR92554 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US200306446-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 309
ID ABR81511 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049744-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 310
ID ABR77935 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049783-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 311
ID ABR89724 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073171-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 312
ID ABR26640 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003032121-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 313
ID ABR13766 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064458-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 314
ID ABR28504 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003064460-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 315
ID ABO30334 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003064464-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 316
ID ABR07361 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068702-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 317
ID ABR03952 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068734-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 318
ID ABO37096 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068719-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 319
ID ABO41671 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068729-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 320
ID ABO35266 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003068738-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 321
ID ABR25115 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104540-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 322
ID ABO47507 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049742-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 323
ID ABO47812 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049747-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 324
ID ABO48422 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049750-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 325
ID ABO51472 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003049786-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 326
ID ABO51777 standard; protein; 720 AA.

DE Human PRO polypeptide #85.
PN US2003049767-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
PD 03-APR-2003.
ID ABO50557 standard; protein; 720 AA.
DE Human secreted/cranemembrane protein (PRO) #85.
PN US2003049779-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
PD 27-FEB-2003.
ID ABR79681 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040059-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
PD 27-FEB-2003.
ID ABR16943 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040078-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
PD 27-FEB-2003.
ID ABO0927 standard; protein; 720 AA.
DE Human secreted/cranemembrane protein (PRO) #85.
PN US2003044918-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
PD 13-FEB-2003.
ID ABR9686 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054462-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
PD 27-MAR-2003.
ID ADA38672 standard; protein; 720 AA.
DE Human secreted/cranemembrane protein PRO1344.
PN US2003059780-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
PD 27-MAR-2003.
ID ABR12241 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064445-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
PD 03-APR-2003.
ID ABR16333 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064449-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
PD 03-APR-2003.

Best Local Similarity 100.0%; Pred. No. 1.9e-204;
ID ABR24200 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064441-A1.
PD 03-APR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
PD 03-APR-2003.
ID ABR14681 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068696-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
PD 10-APR-2003.
ID ABR04562 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068712-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
PD 10-APR-2003.
ID ABR06751 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068730-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
PD 10-APR-2003.
ID ABR09191 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073174-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
PD 17-APR-2003.
ID ABO39231 standard; protein; 720 AA.
DE Human secreted/cranemembrane protein (PRO) #85.
PN US2003068775-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
PD 10-APR-2003.
ID ABR75496 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104545-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
PD 05-JUN-2003.
ID ABR25420 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104541-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
PD 05-JUN-2003.
ID ABR19930 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104554-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
PD 05-JUN-2003.
ID ABO4636 standard; protein; 720 AA.
DE Human PRO polypeptide #85.

PN US2003049762-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 346
ID ABO47141 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003049765-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 347
ID ADA83239 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049752-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 348
ID ABR71572 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003032133-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 349
ID ABR72182 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003032136-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 350
ID ABR98521 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003036129-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 351
ID ABO06891 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003040053-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 352
ID ABR84844 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040057-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 353
ID ABR73402 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054467-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 354
ID ABR76496 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003044932-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 355
ID ABR73097 standard; protein; 720 AA.

DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003027270-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 356
ID ABM18163 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054469-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 357
ID ABO20622 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003032126-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 358
ID ABO25365 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003054463-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 359
ID ABO25670 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003054466-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 360
ID ABR94079 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003059879-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 361
ID ADA92793 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US2003060407-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 362
ID ABR79986 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049738-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 363
ID ABM13326 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064469-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 364
ID ABO32933 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003064453-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;

Best Local Similarity	100.0%;	Pred. No.1.9e-204;	
RESULT 365			
ID ABOJ0639 standard; protein; 720 AA.			
DE Human secreted/cransmembrane protein (PRO) #85.			
PN US2003064466-A1.			
PD 03-APR-2003.			
PA (GETH) GENENTECH INC.			
Query Match	100.0%;	Score 3945; DB 6;	Length 720;
Best Local Similarity	100.0%;	Pred. No.1.9e-204;	
RESULT 366			
ID ABOJ0944 standard; protein; 720 AA.			
DE Human secreted/cransmembrane protein (PRO) #85.			
PN US2003064468-A1.			
PD 03-APR-2003.			
PA (GETH) GENENTECH INC.			
Query Match	100.0%;	Score 3945; DB 6;	Length 720;
Best Local Similarity	100.0%;	Pred. No.1.9e-204;	
RESULT 367			
ID ABM7250 standard; protein; 720 AA.			
DE Human secreted polypeptide PRO1344, SEQ ID NO:1170.			
PN US2003068760-A1.			
PD 10-APR-2003.			
PA (GETH) GENENTECH INC.			
Query Match	100.0%;	Score 3945; DB 6;	Length 720;
Best Local Similarity	100.0%;	Pred. No.1.9e-204;	
RESULT 368			
ID ABM5995 standard; protein; 720 AA.			
DE Human secreted polypeptide PRO1344, SEQ ID NO:1170.			
PN US2003068769-A1.			
PD 10-APR-2003.			
PA (GETH) GENENTECH INC.			
Query Match	100.0%;	Score 3945; DB 6;	Length 720;
Best Local Similarity	100.0%;	Pred. No.1.9e-204;	
RESULT 369			
ID ABM05531 standard; protein; 720 AA.			
DE Human secreted polypeptide PRO1344, SEQ ID NO:1170.			
PN US2003045700-A1.			
PD 06-MAR-2003.			
PA (GETH) GENENTECH INC.			
Query Match	100.0%;	Score 3945; DB 6;	Length 720;
Best Local Similarity	100.0%;	Pred. No.1.9e-204;	
RESULT 370			
ID ABM15596 standard; protein; 720 AA.			
DE Human secreted polypeptide PRO1344, SEQ ID NO:1170.			
PN US2003068698-A1.			
PD 10-APR-2003.			
PA (GETH) GENENTECH INC.			
Query Match	100.0%;	Score 3945; DB 6;	Length 720;
Best Local Similarity	100.0%;	Pred. No.1.9e-204;	
RESULT 371			
ID ABM08581 standard; protein; 720 AA.			
DE Human secreted polypeptide PRO1344, SEQ ID NO:1170.			
PN US2003068759-A1.			
PD 10-APR-2003.			
PA (GETH) GENENTECH INC.			
Query Match	100.0%;	Score 3945; DB 6;	Length 720;
Best Local Similarity	100.0%;	Pred. No.1.9e-204;	
RESULT 372			
ID ABO42281 standard; protein; 720 AA.			
DE Human secreted/cransmembrane protein (PRO) #85.			
PN US2003049748-A1.			
PD 13-MAR-2003.			
PA (GETH) GENENTECH INC.			
Query Match	100.0%;	Score 3945; DB 6;	Length 720;
Best Local Similarity	100.0%;	Pred. No.1.9e-204;	
RESULT 373			
ID ABO3801 standard; protein; 720 AA.			
DE Human secreted/cransmembrane protein (PRO) #85.			
PN US2003068765-A1.			
PD 10-APR-2003.			
PA (GETH) GENENTECH INC.			
Query Match	100.0%;	Score 3945; DB 6;	Length 720;
Best Local Similarity	100.0%;	Pred. No.1.9e-204;	
Query Match	100.0%;	Score 3945; DB 6;	Length 720;
Best Local Similarity	100.0%;	Pred. No.1.9e-204;	

RESULT 374	ID	ABO45921	standard; protein; 720 AA.
DE	Human	PRO polypeptide #85.	
PN	US2003049754-A1.		
PD	13-MAR-2003.		
PA	(GETH) GENENTECH INC.		
Query Match		100.0%;	Score 3945; DB 6; Length 720;
Best Local Similarity		100.0%;	Pred. No. 1.9e-204;
RESULT 375	ID	ABM6724	standard; protein; 720 AA.
DE	Human	secreted polypeptide PRO1344, SEQ ID NO:170.	
PN	US2003068688-A1.		
PD	10-APR-2003.		
PA	(GETH) GENENTECH INC.		
Query Match		100.0%;	Score 3945; DB 6; Length 720;
Best Local Similarity		100.0%;	Pred. No. 1.9e-204;
RESULT 376	ID	ADH20282	standard; protein; 720 AA.
DE	Human	secreted/transmembrane protein (PRO) #85.	
PN	US2003082767-A1.		
PD	01-MAY-2003.		
PA	(GETH) GENENTECH INC.		
Query Match		100.0%;	Score 3945; DB 6; Length 720;
Best Local Similarity		100.0%;	Pred. No. 1.9e-204;
RESULT 377	ID	ABM19625	standard; protein; 720 AA.
DE	Human	secreted polypeptide PRO1344, SEQ ID NO:170.	
PN	US2003104552-A1.		
PD	05-JUN-2003.		
PA	(GETH) GENENTECH INC.		
Query Match		100.0%;	Score 3945; DB 6; Length 720;
Best Local Similarity		100.0%;	Pred. No. 1.9e-204;
RESULT 378	ID	ABO49337	standard; protein; 720 AA.
DE	Human	secreted/transmembrane protein (PRO) #85.	
PN	US2003049774-A1.		
PD	13-MAR-2003.		
PA	(GETH) GENENTECH INC.		
Query Match		100.0%;	Score 3945; DB 6; Length 720;
Best Local Similarity		100.0%;	Pred. No. 1.9e-204;
RESULT 379	ID	ABO49642	standard; protein; 720 AA.
DE	Human	secreted/transmembrane protein (PRO) #85.	
PN	US2003049775-A1.		
PD	13-MAR-2003.		
PA	(GETH) GENENTECH INC.		
Query Match		100.0%;	Score 3945; DB 6; Length 720;
Best Local Similarity		100.0%;	Pred. No. 1.9e-204;
RESULT 380	ID	ADA78534	standard; protein; 720 AA.
DE	Human	secreted/transmembrane protein (PRO) #85.	
PN	US2003073181-A1.		
PD	17-APR-2003.		
PA	(GETH) GENENTECH INC.		
Query Match		100.0%;	Score 3945; DB 6; Length 720;
Best Local Similarity		100.0%;	Pred. No. 1.9e-204;
RESULT 381	ID	ABR88199	standard; protein; 720 AA.
DE	Human	secreted polypeptide PRO1344, SEQ ID NO:170.	
PN	US2003068720-A1.		
PD	10-APR-2003.		
PA	(GETH) GENENTECH INC.		
Query Match		100.0%;	Score 3945; DB 6; Length 720;
Best Local Similarity		100.0%;	Pred. No. 1.9e-204;
RESULT 382	ID	ADA00369	standard; protein; 720 AA.
DE	Human	secreted/transmembrane polypeptide PRO 1344.	
PN	US2003073992-A1.		
PD	06-FEB-2003.		
PA	(GETH) GENENTECH INC.		
Query Match		100.0%;	Score 3945; DB 6; Length 720;
Best Local Similarity		100.0%;	Pred. No. 1.9e-204;
RESULT 383	ID	ABM26945	standard; protein; 720 AA.

DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068739-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
ID AM03342 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068763-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
ID ABO39841 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068689-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
ID ABO49947 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049776-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
ID ABO50862 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003048780-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
ID ABO05318 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036126-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
ID ABR74622 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003044924-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
ID ABR77101 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003044927-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
ID ABM17858 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040072-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
ID ABR95909 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040073-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
ID ABR86064 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049759-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
ID ABR86064 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049759-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
ID ABM10716 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064455-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
ID ABM76715 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054455-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
ID ABR89419 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073170-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
ID ABM12546 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073176-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
ID ABM05836 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068717-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
ID ABO34961 standard; protein; 720 AA.
DE Human PRO polypeptide #85.

PN US2003068728-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 403
ID ABR03037 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068764-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 404
ID ABR19015 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104550-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 405
ID ABR19320 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104551-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 406
ID ABR046531 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003049761-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 407
ID ABR049032 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049757-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 408
ID ABR69075 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003027273-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 409
ID ABR89114 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003036119-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 410
ID ABR72487 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003036120-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 411
ID ABR74317 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003036161-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;

Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 412
ID ABR19585 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003044921-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 413
ID ABR80291 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049739-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 414
ID ABR01512 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003059882-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 415
ID ABR02122 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003059884-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 416
ID ABR87284 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068687-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 417
ID ABR12851 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073186-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 418
ID ABR30605 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064443-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 419
ID ABR24505 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064444-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 420
ID ABR029419 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068697-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 421

ID	ABO31149 standard; protein; 720 AA.
DE	Human secreted/transmembrane protein (PRO) #85.
FN	US2003068710-A1.
PD	10-APR-2003.
PA	(GETH) GENENTECH INC.
Query Match	100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity	100.0%; Pred. No. 1.9e-204;
RESULT 422	
ID	ABM414376 standard; protein; 720 AA.
DE	Human secreted polypeptide PRO1344, SEQ ID NO:170.
FN	US2003068686-A1.
PD	10-APR-2003.
PA	(GETH) GENENTECH INC.
Query Match	100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity	100.0%; Pred. No. 1.9e-204;
RESULT 423	
ID	ABM09801 standard; protein; 720 AA.
DE	Human secreted polypeptide PRO1344, SEQ ID NO:170.
FN	US2003073178-A1.
PD	17-APR-2003.
PA	(GETH) GENENTECH INC.
Query Match	100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity	100.0%; Pred. No. 1.9e-204;
RESULT 424	
ID	ABO38926 standard; protein; 720 AA.
DE	Human secreted/transmembrane protein (PRO) #85.
FN	US2003068774-A1.
PD	10-APR-2003.
PA	(GETH) GENENTECH INC.
Query Match	100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity	100.0%; Pred. No. 1.9e-204;
RESULT 425	
ID	ABM34691 standard; protein; 720 AA.
DE	Human secreted polypeptide PRO1344, SEQ ID NO:170.
FN	US2003104538-A1.
PD	05-JUN-2003.
Query Match	100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity	100.0%; Pred. No. 1.9e-204;
RESULT 426	
ID	ABO51167 standard; protein; 720 AA.
DE	Human secreted/transmembrane protein (PRO) #85.
FN	US2003049781-A1.
PD	13-MAR-2003.
PA	(GETH) GENENTECH INC.
Query Match	100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity	100.0%; Pred. No. 1.9e-204;
RESULT 427	
ID	ABO03993 standard; protein; 720 AA.
DE	Human secreted/transmembrane protein (PRO) #85.
FN	US2003036158-A1.
PD	20-FEB-2003.
Query Match	100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity	100.0%; Pred. No. 1.9e-204;
RESULT 428	
ID	ABO10463 standard; protein; 720 AA.
DE	Human PRO polypeptide #85.
FN	US2003036151-A1.
PD	20-FEB-2003.
Query Match	100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity	100.0%; Pred. No. 1.9e-204;
RESULT 429	
ID	ABO53170 standard; protein; 720 AA.
DE	Human secreted/transmembrane protein PRO1344.
FN	US2003044806-A1.
PD	06-MAR-2003.
Query Match	100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity	100.0%; Pred. No. 1.9e-204;
RESULT 430	
ID	ABR77706 standard; protein; 720 AA.
DE	Human secreted polypeptide PRO1344, SEQ ID NO:170.
FN	US2003040067-A1.
PD	27-FEB-2003.
Query Match	100.0%; Score 3945; DB 7; Length 720;

Best Local Similarity	100.0%;	Pred. No. 1.9e-204;	
RESULT 431			
ID ABR78916 standard; protein; 720 AA.			
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.			
PN US2003054456-A1.			
PD 20-MAR-2003.			
Query Match	100.0%;	Score 3945; DB 7;	Length 720;
Best Local Similarity	100.0%;	Pred. No. 1.9e-204;	
RESULT 432			
ID ABO24010 standard; protein; 720 AA.			
DE Human secreted/transmembrane protein (PRO) #85.			
PN US2003054482-A1.			
PD 20-MAR-2003.			
PA (GETH) GENENTECH INC.			
Query Match	100.0%;	Score 3945; DB 7;	Length 720;
Best Local Similarity	100.0%;	Pred. No. 1.9e-204;	
RESULT 433			
ID ABR33774 standard; protein; 720 AA.			
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.			
PN US2003054457-A1.			
PD 20-MAR-2003.			
PA (GETH) GENENTECH INC.			
Query Match	100.0%;	Score 3945; DB 7;	Length 720;
Best Local Similarity	100.0%;	Pred. No. 1.9e-204;	
RESULT 434			
ID ABO1817 standard; protein; 720 AA.			
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.			
PN US2003059883-A1.			
PD 27-MAR-2003.			
PA (GETH) GENENTECH INC.			
Query Match	100.0%;	Score 3945; DB 7;	Length 720;
Best Local Similarity	100.0%;	Pred. No. 1.9e-204;	
RESULT 435			
ID ABR78240 standard; protein; 720 AA.			
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.			
PN US2003049764-A1.			
PD 13-MAR-2003.			
PA (GETH) GENENTECH INC.			
Query Match	100.0%;	Score 3945; DB 7;	Length 720;
Best Local Similarity	100.0%;	Pred. No. 1.9e-204;	
RESULT 436			
ID ABR30029 standard; protein; 720 AA.			
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.			
PN US2003073177-A1.			
PD 17-APR-2003.			
PA (GETH) GENENTECH INC.			
Query Match	100.0%;	Score 3945; DB 7;	Length 720;
Best Local Similarity	100.0%;	Pred. No. 1.9e-204;	
RESULT 437			
ID ADA2354 standard; protein; 720 AA.			
DE Human secreted/transmembrane polypeptide PRO1344.			
PN US2003040473-A1.			
PD 27-FEB-2003.			
Query Match	100.0%;	Score 3945; DB 7;	Length 720;
Best Local Similarity	100.0%;	Pred. No. 1.9e-204;	
RESULT 438			
ID ABR7555 standard; protein; 720 AA.			
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.			
PN US2003064442-A1.			
PD 03-APR-2003.			
PA (GETH) GENENTECH INC.			
Query Match	100.0%;	Score 3945; DB 7;	Length 720;
Best Local Similarity	100.0%;	Pred. No. 1.9e-204;	
RESULT 439			
ID ABR3156 standard; protein; 720 AA.			
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.			
PN US2003064450-A1.			
PD 03-APR-2003.			
PA (GETH) GENENTECH INC.			
Query Match	100.0%;	Score 3945; DB 7;	Length 720;
Best Local Similarity	100.0%;	Pred. No. 1.9e-204;	
RESULT 440			
ID ABO31859 standard; protein; 720 AA.			

DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068731-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 441
ID ABL14071 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068683-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 442
ID ABL08276 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068754-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 443
ID ABL040146 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068681-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 444
ID ABL74581 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003096351-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 445
ID ABL33776 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003096358-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 446
ID ABL20235 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104556-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 447
ID ABL048727 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049756-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 448
ID ABL022540 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US2003017982-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 449
ID ABL72792 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003036122-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;

Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 450
ID ABL05434 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036121-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 451
ID ABL85149 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040065-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 452
ID ABL05129 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003044919-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 453
ID ABL017264 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003040077-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 454
ID ABL17553 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003044928-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 455
ID ABL06520 standard; protein; 720 AA.
DE Human secreted/transmembrane PRO polypeptide #65.
PN US2003049638-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 456
ID ABL39213 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US2003059782-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 457
ID ABL85454 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049746-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 458
ID ABL77020 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054464-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 459
ID ABL028199 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003064459-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.

Query Match	100.0%;	Score 3945;	DB 7;	Length 720;
Best Local Similarity	100.0%;	Pred. No. 1.9e-204;		
RESULT 460				
ID	ABM22980 standard; protein; 720 AA.			
DE	Human secreted polypeptide PRO1344, SEQ ID NO:170.			
FN	US2003068757-A1.			
PD	10-APR-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	100.0%;	Score 3945;	DB 7;	Length 720;
Best Local Similarity	100.0%;	Pred. No. 1.9e-204;		
RESULT 461				
ID	ABM30300 standard; protein; 720 AA.			
DE	Human secreted polypeptide PRO1344, SEQ ID NO:170.			
FN	US2003068723-A1.			
PD	10-APR-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	100.0%;	Score 3945;	DB 7;	Length 720;
Best Local Similarity	100.0%;	Pred. No. 1.9e-204;		
RESULT 462				
ID	ABM21760 standard; protein; 720 AA.			
DE	Human secreted polypeptide PRO1344, SEQ ID NO:170.			
FN	US2003068741-A1.			
PD	10-APR-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	100.0%;	Score 3945;	DB 7;	Length 720;
Best Local Similarity	100.0%;	Pred. No. 1.9e-204;		
RESULT 463				
ID	ABM21455 standard; protein; 720 AA.			
DE	Human secreted polypeptide PRO1344, SEQ ID NO:170.			
FN	US2003068744-A1.			
PD	10-APR-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	100.0%;	Score 3945;	DB 7;	Length 720;
Best Local Similarity	100.0%;	Pred. No. 1.9e-204;		
RESULT 464				
ID	ABM14986 standard; protein; 720 AA.			
DE	Human secreted polypeptide PRO1344, SEQ ID NO:170.			
FN	US2003068766-A1.			
PD	10-APR-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	100.0%;	Score 3945;	DB 7;	Length 720;
Best Local Similarity	100.0%;	Pred. No. 1.9e-204;		
RESULT 465				
ID	ABO41061 standard; protein; 720 AA.			
DE	Human secreted/citransembrane protein (PRO) #85.			
FN	US2003068694-A1.			
PD	10-APR-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	100.0%;	Score 3945;	DB 7;	Length 720;
Best Local Similarity	100.0%;	Pred. No. 1.9e-204;		
RESULT 466				
ID	ABO36791 standard; protein; 720 AA.			
DE	Human secreted/citransembrane protein (PRO) #85.			
FN	US2003068715-A1.			
PD	10-APR-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	100.0%;	Score 3945;	DB 7;	Length 720;
Best Local Similarity	100.0%;	Pred. No. 1.9e-204;		
RESULT 467				
ID	ABO37401 standard; protein; 720 AA.			
DE	Human secreted/citransembrane protein (PRO) #85.			
FN	US2003068726-A1.			
PD	10-APR-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	100.0%;	Score 3945;	DB 7;	Length 720;
Best Local Similarity	100.0%;	Pred. No. 1.9e-204;		
RESULT 468				
ID	ABM75191 standard; protein; 720 AA.			
DE	Human secreted polypeptide PRO1344, SEQ ID NO:170.			
FN	US2003104544-A1.			
PD	05-JUN-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	100.0%;	Score 3945;	DB 7;	Length 720;
Best Local Similarity	100.0%;	Pred. No. 1.9e-204;		
RESULT 469				
ID	ABM75191 standard; protein; 720 AA.			
DE	Human secreted polypeptide PRO1344, SEQ ID NO:170.			
FN	US2003104544-A1.			
PD	05-JUN-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	100.0%;	Score 3945;	DB 7;	Length 720;

Best Local Similarity	100.0%;	Pred. No.1.9e-204;	
RESULT 469			
ID ABM33471 standard; protein; 720 AA.			
DE Human secreted polypeptide PRO1344, SEQ ID NO:1170.			
PN US2003096357-A1.			
PD 22-MAY-2003.			
PA (GETH) GENENTECH INC.			
Query Match	100.0%;	Score 3945; DB 7;	Length 720;
Best Local Similarity	100.0%;	Pred. No.1.9e-204;	
RESULT 470			
ID ABO46226 standard; protein; 720 AA.			
DE Human PRO polypeptide #85.			
PN US2003049760-A1.			
PD 13-MAR-2003.			
PA (GETH) GENENTECH INC.			
Query Match	100.0%;	Score 3945; DB 7;	Length 720;
Best Local Similarity	100.0%;	Pred. No.1.9e-204;	
RESULT 471			
ID ADA82605 standard; protein; 720 AA.			
DE Human secreted/transmembrane protein (PRO) #85.			
PN US2003049755-A1.			
PD 13-MAR-2003.			
PA (GETH) GENENTECH INC.			
Query Match	100.0%;	Score 3945; DB 7;	Length 720;
Best Local Similarity	100.0%;	Pred. No.1.9e-204;	
RESULT 472			
ID ADH85611 standard; protein; 720 AA.			
DE Novel human secreted and transmembrane protein PRO1344.			
PN US2003049735-A1.			
PD 13-MAR-2003.			
PA (GETH) GENENTECH INC.			
Query Match	100.0%;	Score 3945; DB 7;	Length 720;
Best Local Similarity	100.0%;	Pred. No.1.9e-204;	
RESULT 473			
ID ADH96239 standard; protein; 720 AA.			
DE Human PRO polypeptide #65.			
PN US2003054403-A1.			
PD 20-MAR-2003.			
Query Match	100.0%;	Score 3945; DB 7;	Length 720;
Best Local Similarity	100.0%;	Pred. No.1.9e-204;	
RESULT 474			
ID ABM31825 standard; protein; 720 AA.			
DE Human secreted polypeptide PRO1344, SEQ ID NO:1170.			
PN US2003068680-A1.			
PD 10-APR-2003.			
Query Match	100.0%;	Score 3945; DB 7;	Length 720;
Best Local Similarity	100.0%;	Pred. No.1.9e-204;	
RESULT 475			
ID ABM31215 standard; protein; 720 AA.			
DE Human secreted polypeptide PRO1344, SEQ ID NO:1170.			
PN US2003068762-A1.			
PD 10-APR-2003.			
PA (GETH) GENENTECH INC.			
Query Match	100.0%;	Score 3945; DB 7;	Length 720;
Best Local Similarity	100.0%;	Pred. No.1.9e-204;	
RESULT 476			
ID ADH85913 standard; protein; 720 AA.			
DE Human secreted/transmembrane protein (PRO) #85.			
PN US2003054472-A1.			
PD 20-MAR-2003.			
PA (GETH) GENENTECH INC.			
Query Match	100.0%;	Score 3945; DB 7;	Length 720;
Best Local Similarity	100.0%;	Pred. No.1.9e-204;	
RESULT 477			
ID ABM32130 standard; protein; 720 AA.			
DE Human secreted polypeptide PRO1344, SEQ ID NO:1170.			
PN US2003068708-A1.			
PD 10-APR-2003.			
PA (GETH) GENENTECH INC.			
Query Match	100.0%;	Score 3945; DB 7;	Length 720;
Best Local Similarity	100.0%;	Pred. No.1.9e-204;	
RESULT 478			
ID ABM32435 standard; protein; 720 AA.			

DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068713-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 479
ID ADB68290 standard; protein; 720 AA.
DE Human PRO1344 protein.
PN US2003065161-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 480
ID ADB68097 standard; protein; 720 AA.
DE Human PRO1344 protein.
PN US2003060600-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 481
ID ADB31520 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068761-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 482
ID ADB30910 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068771-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 483
ID ADB90914 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003083473-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 484
ID ADC57711 standard; protein; 720 AA.
DE Human PRO polypeptide #65.
PN US2003027754-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 485
ID ADC55075 standard; protein; 720 AA.
DE Human PRO polypeptide #65.
PN US2003045463-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 486
ID ADC11942 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US2003049681-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 487
ID ADC06994 standard; protein; 720 AA.
DE Human PRO1344 protein.
PN US2003060602-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 488
ID ADC56364 standard; protein; 720 AA.
DE Human PRO polypeptide #65.
PN US2003064375-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 489
ID ADC17173 standard; protein; 720 AA.
DE Mammalian PRO polypeptide (Segid 38).
PN US2003065143-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 490
ID ADC07419 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US2003068647-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 491
ID ADC11409 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US2003069403-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 492
ID ADC14871 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003073208-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 493
ID ADC52366 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003138882-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 494
ID ADC14531 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003082546-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 495
ID ADD09063 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003068623-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 496
ID ADC81888 standard; protein; 720 AA.
DE Human PRO polypeptide #65.
PN US2003083461-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 497
ID ADD07530 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2002193299-A1.
PD 19-DEC-2002.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 498
ID ADC82421 standard; protein; 720 AA.
DE Human PRO polypeptide #65.
PN US2003059833-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 499
ID ADD05643 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003087376-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 500
ID ADD08601 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003073090-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 501
ID ADD06850 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2002193300-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 502
ID ADC83097 standard; protein; 720 AA.
DE Human PRO polypeptide #65.
PN US2003059783-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 503
ID ADD55204 standard; protein; 720 AA.
DE Human PRO polypeptide #65.
PN US2003077593-A1.
PD 24-APR-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 504
ID ADD36042 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003105298-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 505
ID ADD56162 standard; protein; 720 AA.
DE Human PRO polypeptide #65.
PN US2003077594-A1.
PD 24-APR-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 506
ID ADD54600 standard; protein; 720 AA.
DE Human PRO polypeptide #65.
PN US2002133253-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 507
ID ADE26754 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003087305-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 508
ID ADE26221 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003087305-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 509
ID ADF67158 standard; protein; 720 AA.
DE Human PRO1344 amino acid sequence SEQ ID NO:231.
PN US2002198148-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 510
ID ADG01043 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003078387-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 511
ID ADG08596 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180793-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 512
ID ADG02638 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003207397-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 513
ID ADG01345 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003207399-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 514
ID ADF95520 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003207398-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 515
ID ADF95217 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180795-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 516
ID ADG1335 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003207392-A1.
PD 06-NOV-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;

Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 517
ID ADH24070 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180918-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 518
ID ADH34096 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180858-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 519
ID ADH29929 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180859-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 520
ID ADH23900 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180919-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 521
ID ADH08995 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003207395-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 522
ID ADG85304 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180904-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 523
ID ADH24580 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180907-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 524
ID ADH37436 standard; protein; 720 AA.
DE Human secreted and transmembrane protein PRO1344 CDNA.
PN US2003181646-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 525
ID ADH02025 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003180837-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 526
ID ADH37606 standard; protein; 720 AA.
DE Human secreted and transmembrane protein PRO1344 CDNA.
PN US2003181648-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 527
ID ADG85644 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180905-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 528
ID ADH24240 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180914-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 529
ID ADH38534 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181643-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 530
ID ADG83655 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003180794-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 531
ID ADH29463 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180860-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 532
ID ADH27579 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180906-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 533
ID ADH37776 standard; protein; 720 AA.
DE Human secreted and transmembrane protein PRO1344 CDNA.
PN US2003181647-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 534
ID ADH37953 standard; protein; 720 AA.
DE Human secreted and transmembrane protein PRO1344 CDNA.
PN US2003181649-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 535

ID ADH57373 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180920-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 536
ID ADH53515 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181636-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 537
ID ADH53685 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181641-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 538
ID ADH52021 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181638-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 539
ID ADH49676 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181639-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 540
ID ADI25386 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181696-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 541
ID ADH90179 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181698-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 542
ID ADI25556 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181669-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 543
ID ADH97730 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181672-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 544
ID ADI35412 standard; protein; 720 AA.
DE Human PRO polypeptide #55.
PN US2003050457-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 545
ID ADI03578 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181656-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 546
ID ADI11935 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003181686-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 547
ID ADH90009 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181697-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 548
ID ADH99904 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003049682-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 549
ID ADH99410 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181707-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 550
ID ADI11085 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003181682-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 551
ID ADI11595 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003181684-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 552
ID ADH96240 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181709-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 553
ID ADH96580 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181708-A1.
PD 25-SEP-2003.

[illegible]

Query Match	100.0%;	Score 3945;	DB 7;	Length 720;
Best Local Similarity	100.0%;	Pred. No. 1.9e-204;		
RESULT 563				
ID ADH97900 standard; protein; 720 AA.				
DE Novel human secreted and transmembrane protein PRO1344.				
PN US2003181652-AA1.				
PD 25-SEP-2003.				
PA (GETH) GENENTECH INC.				
Query Match	100.0%;	Score 3945;	DB 7;	Length 720;
Best Local Similarity	100.0%;	Pred. No. 1.9e-204;		
RESULT 564				
ID ADI01285 standard; protein; 720 AA.				
DE Novel human secreted and transmembrane protein PRO1344.				
PN US2003190669-AA1.				
PD 09-OCT-2003.				
PA (GETH) GENENTECH INC.				
Query Match	100.0%;	Score 3945;	DB 7;	Length 720;
Best Local Similarity	100.0%;	Pred. No. 1.9e-204;		
RESULT 565				
ID ADI01980 standard; protein; 720 AA.				
DE Novel human secreted and transmembrane protein PRO1344.				
PN US2003181652-AA1.				
PD 25-SEP-2003.				
PA (GETH) GENENTECH INC.				
Query Match	100.0%;	Score 3945;	DB 7;	Length 720;
Best Local Similarity	100.0%;	Pred. No. 1.9e-204;		
RESULT 566				
ID ADI03238 standard; protein; 720 AA.				
DE Novel human secreted and transmembrane protein PRO1344.				
PN US2003181655-AA1.				
PD 25-SEP-2003.				
PA (GETH) GENENTECH INC.				
Query Match	100.0%;	Score 3945;	DB 7;	Length 720;
Best Local Similarity	100.0%;	Pred. No. 1.9e-204;		
RESULT 567				
ID ADI11425 standard; protein; 720 AA.				
DE Human PRO polypeptide #19.				
PN US2003181681-AA1.				
PD 25-SEP-2003.				
PA (GETH) GENENTECH INC.				
Query Match	100.0%;	Score 3945;	DB 7;	Length 720;
Best Local Similarity	100.0%;	Pred. No. 1.9e-204;		
RESULT 568				
ID ADI02327 standard; protein; 720 AA.				
DE Novel human secreted and transmembrane protein PRO1344.				
PN US2003181650-AA1.				
PD 25-SEP-2003.				
PA (GETH) GENENTECH INC.				
Query Match	100.0%;	Score 3945;	DB 7;	Length 720;
Best Local Similarity	100.0%;	Pred. No. 1.9e-204;		
RESULT 569				
ID ADI11765 standard; protein; 720 AA.				
DE Human PRO polypeptide #19.				
PN US2003181685-AA1.				
PD 25-SEP-2003.				
PA (GETH) GENENTECH INC.				
Query Match	100.0%;	Score 3945;	DB 7;	Length 720;
Best Local Similarity	100.0%;	Pred. No. 1.9e-204;		
RESULT 570				
ID ADI05402 standard; protein; 720 AA.				
DE Novel human secreted and transmembrane protein PRO1344.				
PN US2003190716-AA1.				
PD 09-OCT-2003.				
PA (GETH) GENENTECH INC.				
Query Match	100.0%;	Score 3945;	DB 7;	Length 720;
Best Local Similarity	100.0%;	Pred. No. 1.9e-204;		
RESULT 571				
ID ADH79474 standard; protein; 720 AA.				
DE Novel human secreted and transmembrane protein PRO1344.				
PN US2003191290-AA1.				
PD 09-OCT-2003.				
PA (GETH) GENENTECH INC.				
Query Match	100.0%;	Score 3945;	DB 7;	Length 720;
Best Local Similarity	100.0%;	Pred. No. 1.9e-204;		
RESULT 572				
ID ADH79474 standard; protein; 720 AA.				
DE Novel human secreted and transmembrane protein PRO1344.				
PN US2003191290-AA1.				
PD 09-OCT-2003.				
PA (GETH) GENENTECH INC.				
Query Match	100.0%;	Score 3945;	DB 7;	Length 720;
Best Local Similarity	100.0%;	Pred. No. 1.9e-204;		
RESULT 573				
ID ADH79474 standard; protein; 720 AA.				
DE Novel human secreted and transmembrane protein PRO1344.				
PN US2003191290-AA1.				
PD 09-OCT-2003.				
PA (GETH) GENENTECH INC.				
Query Match	100.0%;	Score 3945;	DB 7;	Length 720;
Best Local Similarity	100.0%;	Pred. No. 1.9e-204;		
RESULT 574				
ID ADH79474 standard; protein; 720 AA.				
DE Novel human secreted and transmembrane protein PRO1344.				
PN US2003191290-AA1.				
PD 09-OCT-2003.				
PA (GETH) GENENTECH INC.				
Query Match	100.0%;	Score 3945;	DB 7;	Length 720;
Best Local Similarity	100.0%;	Pred. No. 1.9e-204;		
RESULT 575				
ID ADH79474 standard; protein; 720 AA.				
DE Novel human secreted and transmembrane protein PRO1344.				
PN US2003191290-AA1.				

Best Local Similarity	100.0%;	Pred. No. 1.9e-204;
RESULT 572		
ID ADI19431 standard; protein; 720 AA.		
DE Novel human secreted and transmembrane protein PRO1344.		
PN US2003181675-A1.		
PD 25-SEP-2003.		
PA (GETH) GENENTECH INC.		
Query Match	100.0%;	Score 3945; DB 7; Length 720;
Best Local Similarity	100.0%;	Pred. No. 1.9e-204;
RESULT 573		
ID ADI05232 standard; protein; 720 AA.		
DE Novel human secreted and transmembrane protein PRO1344.		
PN US2003181677-A1.		
PD 25-SEP-2003.		
PA (GETH) GENENTECH INC.		
Query Match	100.0%;	Score 3945; DB 7; Length 720;
Best Local Similarity	100.0%;	Pred. No. 1.9e-204;
RESULT 574		
ID ADH79644 standard; protein; 720 AA.		
DE Novel human secreted and transmembrane protein PRO1344.		
PN US2003191288-A1.		
PD 09-OCT-2003.		
PA (GETH) GENENTECH INC.		
Query Match	100.0%;	Score 3945; DB 7; Length 720;
Best Local Similarity	100.0%;	Pred. No. 1.9e-204;
RESULT 575		
ID ADI01470 standard; protein; 720 AA.		
DE Novel human secreted and transmembrane protein PRO1344.		
PN US2003181678-A1.		
PD 25-SEP-2003.		
PA (GETH) GENENTECH INC.		
Query Match	100.0%;	Score 3945; DB 7; Length 720;
Best Local Similarity	100.0%;	Pred. No. 1.9e-204;
RESULT 576		
ID ADI01640 standard; protein; 720 AA.		
DE Novel human secreted and transmembrane protein PRO1344.		
PN US2003181679-A1.		
PD 25-SEP-2003.		
PA (GETH) GENENTECH INC.		
Query Match	100.0%;	Score 3945; DB 7; Length 720;
Best Local Similarity	100.0%;	Pred. No. 1.9e-204;
RESULT 577		
ID ADI01810 standard; protein; 720 AA.		
DE Novel human secreted and transmembrane protein PRO1344.		
PN US2003181680-A1.		
PD 25-SEP-2003.		
PA (GETH) GENENTECH INC.		
Query Match	100.0%;	Score 3945; DB 7; Length 720;
Best Local Similarity	100.0%;	Pred. No. 1.9e-204;
RESULT 578		
ID ADH79814 standard; protein; 720 AA.		
DE Novel human secreted and transmembrane protein PRO1344.		
PN US2003191289-A1.		
PD 09-OCT-2003.		
PA (GETH) GENENTECH INC.		
Query Match	100.0%;	Score 3945; DB 7; Length 720;
Best Local Similarity	100.0%;	Pred. No. 1.9e-204;
RESULT 579		
ID ADI04632 standard; protein; 720 AA.		
DE Novel human secreted and transmembrane protein PRO1344.		
PN US2003171550-A1.		
PD 11-SEP-2003.		
PA (GETH) GENENTECH INC.		
Query Match	100.0%;	Score 3945; DB 7; Length 720;
Best Local Similarity	100.0%;	Pred. No. 1.9e-204;
RESULT 580		
ID ADI02766 standard; protein; 720 AA.		
DE Novel human secreted and transmembrane protein PRO1344.		
PN US2003181651-A1.		
PD 25-SEP-2003.		
PA (GETH) GENENTECH INC.		
Query Match	100.0%;	Score 3945; DB 7; Length 720;
Best Local Similarity	100.0%;	Pred. No. 1.9e-204;
Query Match	100.0%;	Score 3945; DB 7; Length 720;
Best Local Similarity	100.0%;	Pred. No. 1.9e-204;

RESULT 581	ID	ADH78087 standard; protein; 720 AA.
DE	Human PRO polypeptide #19.	
FN	US2003181667-A1.	
PD	25-SEP-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	Best Local Similarity	100.0%; Score 3945; DB 7; Length 720;
RESULT 582	ID	AD125726 standard; protein; 720 AA.
DE	Novel1 human secreted and transmembrane protein PRO1344.	
FN	US2003181670-A1.	
PD	25-SEP-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	Best Local Similarity	100.0%; Score 3945; DB 7; Length 720;
RESULT 583	ID	AD125896 standard; protein; 720 AA.
DE	Novel1 human secreted and transmembrane protein PRO1344.	
FN	US2003181671-A1.	
PD	25-SEP-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	Best Local Similarity	100.0%; Score 3945; DB 7; Length 720;
RESULT 584	ID	ADK5408 standard; protein; 720 AA.
DE	Novel1 human secreted and transmembrane protein PRO1344.	
FN	US2003073821-A1.	
PD	17-APR-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	Best Local Similarity	100.0%; Score 3945; DB 7; Length 720;
RESULT 585	ID	ADH98750 standard; protein; 720 AA.
DE	Novel1 human secreted and transmembrane protein PRO1344.	
FN	US2003191284-A1.	
PD	09-OCT-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	Best Local Similarity	100.0%; Score 3945; DB 7; Length 720;
RESULT 586	ID	ADH79991 standard; protein; 720 AA.
DE	Novel1 human secreted and transmembrane protein PRO1344.	
FN	US2003191287-A1.	
PD	09-OCT-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	Best Local Similarity	100.0%; Score 3945; DB 7; Length 720;
RESULT 587	ID	AD132776 standard; protein; 720 AA.
DE	Novel1 human secreted and transmembrane protein PRO1344.	
FN	US2003207396-A1.	
PD	06-NOV-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	Best Local Similarity	100.0%; Score 3945; DB 7; Length 720;
RESULT 588	ID	ADM30310 standard; protein; 720 AA.
DE	Novel1 human secreted and transmembrane protein PRO1344.	
FN	US2003073813-A1.	
PD	17-APR-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	Best Local Similarity	100.0%; Score 3945; DB 7; Length 720;
RESULT 589	ID	ADU93722 standard; protein; 720 AA.
DE	Novel1 human secreted and transmembrane protein PRO1344.	
FN	US2003040013-A1.	
PD	27-FEB-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	Best Local Similarity	100.0%; Score 3945; DB 7; Length 720;
RESULT 590	ID	ADH78087 standard; protein; 720 AA.
DE	Human PRO polypeptide #19.	
FN	US2003181667-A1.	
PD	25-SEP-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	Best Local Similarity	100.0%; Score 3945; DB 7; Length 720;

ID ADC52176 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003130483-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 591
ID ADE74307 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003211572-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 592
ID ADE74919 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003211574-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 593
ID ADP33557 standard; protein; 720 AA.
DE Human PRO1344 polypeptide.
PN US2003194760-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 594
ID ADG11607 standard; protein; 720 AA.
DE Human PRO1344 polypeptide.
PN US2003226655-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 595
ID ADP96132 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003215909-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 596
ID ADG04403 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003215912-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 597
ID ADG050563 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003215911-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 598
ID ADG06608 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180852-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 599
ID ADH06438 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180853-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 600
ID ADG68659 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180855-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 601
ID ADH27749 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180912-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 602
ID ADH25090 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180913-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 603
ID ADH33722 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003181645-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 604
ID ADG82819 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003215910-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 605
ID ADH02365 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003180839-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 606
ID ADH07972 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180845-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 607
ID ADG69369 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180846-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 608
ID ADH39190 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180917-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;

Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 609
ID ADH26100 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003068770-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 610
ID ADG83930 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003180842-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 611
ID ADH19477 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US2003228656-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 612
ID ADG85474 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003168848-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 613
ID ADH06268 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180854-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 614
ID ADH30098 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180856-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 615
ID ADH24410 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180910-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 616
ID ADH33069 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003068768-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 617
ID ADG69539 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180844-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;

RESULT 618
ID ADH07802 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180851-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 619
ID ADG85814 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180861-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 620
ID ADH33360 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180916-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 621
ID ADH33552 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003181637-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 622
ID ADH33892 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003181644-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 623
ID ADH01102 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003180838-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 624
ID ADG69709 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180843-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 625
ID ADH20970 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US2003224358-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 626
ID ADH02195 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003180841-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 627
ID ADG69199 standard; protein; 720 AA.

DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180847-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 628
ID ADG85984 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180862-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 629
ID ADH24920 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180909-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 630
ID ADH39537 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180915-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 631
ID ADH20010 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US2003219856-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 632
ID ADH02535 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003180840-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 633
ID ADG69029 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180849-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 634
ID ADH07632 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180850-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 635
ID ADG86154 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180863-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 636
ID ADH24750 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003190699-A1.

PN US2003180908-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 637
ID ADH25798 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180911-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 638
ID ADH38364 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180922-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 639
ID ADH51703 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181642-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 640
ID ADH52191 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180921-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 641
ID ADH49557 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180857-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 642
ID ADH90519 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181700-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 643
ID ADI11255 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003181683-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 644
ID ADH98920 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003190698-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 645
ID ADI02150 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003190699-A1.

PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 646
ID ADH90689 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181701-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 647
ID ADJ54808 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2004023321-A1.
PD 05-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 648
ID ADJ98564 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181797-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 649
ID ADJ98734 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003187228-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 650
ID ADH78893 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181703-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 651
ID ADJ99127 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003186408-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 652
ID ADJ99297 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003187196-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 653
ID ADJ99915 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003187242-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 654
ID ADH79063 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181702-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 655
ID ADK00923 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003186407-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 656
ID ADK1444 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003187229-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 657
ID ADJ64579 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2004038337-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 658
ID ADM31475 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2004048334-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 659
ID ADM35522 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2004053358-A1.
PD 18-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 660
ID ADM40327 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2004048335-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 661
ID ADM80893 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2004058411-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 662
ID ADN37935 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2004091959-A1.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 663
ID ADY77733 standard; protein; 720 AA.
DE Neoplastic disease detection protein PRO1344.
PN US2005059102-A1.
PD 17-MAR-2005.
PA (EATO/) EATON D L.

PA (FILV/) FILVAROFF E.
PA (GERR/) GERRITSEN M E.
PA (GODO/) GODDARD A. J.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI J C.
PA (GURN/) GURNEY A L.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W I.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 9; Length 720;
Pred. No. 1.9e-204;
RESULT 664
ID AEA38494 standard; protein; 720 AA.
DE Human secreted/transmembrane protein, #133.
PN US2005112725-A1.
PD 26-MAY-2005.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 9; Length 720;
Pred. No. 1.9e-204;
RESULT 665
ID AED50165 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2005163766-A1.
PD 28-JUL-2005.
PA (EATO/) EATON D L.
PA (FILV/) FILVAROFF E.
PA (GERR/) GERRITSEN M E.
PA (GODO/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI J C.
PA (GURN/) GURNEY A L.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W I.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 10; Length 720;
Pred. No. 1.9e-204;
RESULT 666
ID AEF12564 standard; protein; 720 AA.
DE Human PRO1344 protein SEQ ID NO:38.
PN US200608901-A1.
PD 12-JAN-2006.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 10; Length 720;
Pred. No. 1.9e-204;
RESULT 667
ID AEF74253 standard; protein; 720 AA.
DE Human PRO1344 protein SEQ ID NO:38.
PN US2005260647-A1.
PD 24-NOV-2005.
PA (EATO/) EATON D L.
PA (FILV/) FILVAROFF E.
PA (GERR/) GERRITSEN M E.
PA (GODO/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI J C.
PA (GURN/) GURNEY A L.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W I.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 10; Length 720;
Pred. No. 1.9e-204;
RESULT 668
ID AEG62857 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2006073544-A1.
PD 06-APR-2006.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 10; Length 720;
Pred. No. 1.9e-204;
RESULT 669
ID AEG72680 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2006074226-A1.
PD 06-APR-2006.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 10; Length 720;
Pred. No. 1.9e-204;
RESULT 670
ID AEG62245 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2006073545-A1.
PD 06-APR-2006.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 10; Length 720;
Pred. No. 1.9e-204;
PA (LUX/) LUX X.

RESULT 671
ID AEG88162 standard; protein; 720 AA.
DE Human PRO protein amino acid sequence - SEQ ID 170.
PN US2006074227-A1.
PD 06-APR-2006.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 10; Length 720;
Pred. No. 1.9e-204;
RESULT 672
ID AEF17478 standard; protein; 720 AA.
DE Human tumor overexpressed cDNA protein product PRO1344 SEQ ID NO: 170.
PN US2006094864-A1.
PD 04-MAY-2006.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 10; Length 720;
Pred. No. 1.9e-204;
RESULT 673
ID AEF43591 standard; protein; 720 AA.
DE PRO1344 protein sequence, SEQ ID 38.
PN US200609657-A1.
PD 11-MAY-2006.
PA (EATO/) EATON D L.
PA (FILV/) FILVAROFF E.
PA (GERR/) GERRITSEN M E.
PA (GODO/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI J C.
PA (GURN/) GURNEY A L.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W I.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 10; Length 720;
Pred. No. 1.9e-204;
RESULT 674
ID AEF11916 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2006160186-A1.
PD 20-JUL-2006.
PA (EATO/) EATON D L.
PA (FILV/) FILVAROFF E.
PA (GERR/) GERRITSEN M E.
PA (GODO/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI J C.
PA (GURN/) GURNEY A L.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W I.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 10; Length 720;
Pred. No. 1.9e-204;
RESULT 675
ID AAB70532 standard; protein; 720 AA.
DE Human PRO2 protein sequence SEQ ID NO:4.
PN WO200110902-A2.
PD 15-FEB-2001.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 99.8%; Score 3939; DB 4; Length 720;
Pred. No. 4e-204;
RESULT 676
ID AAU0401 standard; protein; 720 AA.
DE Human secreted protein, POLY13.
PN WO200119856-A2.
PD 22-MAR-2001.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 99.8%; Score 3939; DB 4; Length 720;
Pred. No. 4e-204;
RESULT 677
ID ADH89028 standard; protein; 720 AA.
DE Human POLYX polypeptide #13.
PN US2003198958-A1.
PD 23-OCT-2003.
PA (SHIM/) SHIMKETS R A.
PA (PERN/) FERNANDES E.
PA (HERR/) HERRMANN J L.
PA (LUX/) LUX X.

PA (YANG/) YANG M.
PA (BOLD/) BOLDOG F L.
PA (SMIT/) SMITHSON G.
PA (RAST/) RASTBELL L.
Query Match 99.8%; Score 3939; DB 8; Length 720;
RESULT 678
ID AAY88280 standard; protein; 720 AA.
DE Human TANGO 215 protein.
PN WO200018904-A2.
PD 06-APR-2000.
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
Query Match 99.8%; Score 3936; DB 3; Length 720;
RESULT 679
ID A616805 standard; protein; 720 AA.
DE Human TANGO 215 protein.
PN US2006141575-A1.
PD 29-JUN-2006.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 99.8%; Score 3936; DB 10; Length 720;
RESULT 680
ID ADY80612 standard; protein; 737 AA.
DE Human regeneration-associated muscle protease enzyme - SEQ ID 2.
PN JP2005073574-A.
PD 24-MAR-2005.
PA (TOKR-) ZH TOKYOTO RINSHO IGAKU SOGO KENKYUSHO.
Query Match 99.5%; Score 3926.5; DB 9; Length 737;
RESULT 681
ID AAB85891 standard; protein; 737 AA.
DE Human serine protease-like protein (hc-PLACE1009992).
PN WO200109349-A1.
PD 08-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 99.4%; Score 3921.5; DB 4; Length 737;
RESULT 682
ID AAB93670 standard; protein; 737 AA.
DE Human protein sequence SEQ ID NO:13202.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 99.4%; Score 3921.5; DB 4; Length 737;
RESULT 683
ID ADJ69990 standard; protein; 737 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID1796.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 99.4%; Score 3921.5; DB 7; Length 737;
RESULT 684
ID ADN04640 standard; protein; 737 AA.
DE Antiporiatic protein sequence #505.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH-) GENENTECH INC.
Query Match 99.4%; Score 3921.5; DB 8; Length 737;
RESULT 685
ID ADS85034 standard; protein; 737 AA.
DE Human atopic dermatitis-related protein sequence SeqID36.
PN WO2004031386-A1.
PD 15-APR-2004.
PA (GENO-) GENOX RES INC.
PA (UTJU-) UNIV JUNTENDO.
Query Match 99.4%; Score 3921.5; DB 8; Length 737;
RESULT 686
Best Local Similarity 97.6%; Pred. No. 3.6e-203;

ID ADS85022 standard; protein; 737 AA.
DE Human atopic dermatitis-related protein sequence SeqID24.
PN WO2004031386-A1.
PD 15-APR-2004.
PA (GENO-) GENOX RES INC.
PA (UTJU-) UNIV JUNTENDO.
Query Match 99.4%; Score 3921.5; DB 8; Length 737;
RESULT 687
ID AAB85893 standard; protein; 762 AA.
DE Human serine protease-like protein (hc-PLACE1009992).
PN WO200109349-A1.
PD 08-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 99.4%; Score 3921.5; DB 4; Length 762;
RESULT 688
ID A6168109 standard; protein; 699 AA.
DE Human TANGO 215 mature protein SEQ ID NO: 86.
PN US2006141575-A1.
PD 29-JUN-2006.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 97.0%; Score 3828; DB 10; Length 699;
RESULT 689
ID ADY80614 standard; protein; 720 AA.
DE Mouse regeneration-associated muscle protease enzyme - SEQ ID 4.
PN JP2005073574-A.
PD 24-MAR-2005.
PA (TOKR-) ZH TOKYOTO RINSHO IGAKU SOGO KENKYUSHO.
Query Match 91.7%; Score 3617; DB 9; Length 720;
RESULT 690
ID A6168141 standard; protein; 720 AA.
DE Murine TANGO 215 protein SEQ ID NO: 118.
PN US2006141575-A1.
PD 29-JUN-2006.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 91.7%; Score 3617; DB 10; Length 720;
RESULT 691
ID AAB85892 standard; protein; 720 AA.
DE Mouse serine protease-like protein (mc-PLACE1009992).
PN WO200109349-A1.
PD 08-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 91.6%; Score 3612; DB 4; Length 720;
RESULT 692
ID AAB09927 standard; protein; 719 AA.
DE Murine TANGO 215 protein.
PN WO200018904-A2.
PD 06-APR-2000.
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
Query Match 91.3%; Score 3602.5; DB 3; Length 719;
RESULT 693
ID A6168169 standard; protein; 720 AA.
DE Murine TANGO 215 protein.
PN US2006141575-A1.
PD 29-JUN-2006.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 91.0%; Score 3591; DB 10; Length 720;
RESULT 694
ID AAB19180 standard; protein; 649 AA.
DE Human protease, PRS-17 protein.
PN WO200208396-A2.
PD 31-JAN-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 88.7%; Score 3500.5; DB 5; Length 649;
RESULT 695
Best Local Similarity 90.0%; Pred. No. 1.5e-180;

ID AAB70531 standard; protein; 567 AA.
DE Human PRO1 protein sequence SEQ ID NO:2.
PN WO200110902-A2.
PD 15-FEB-2001.
PA (CURA-) CURAGEN CORP.
Query Match 78.3%; Score 3089.5; DB 4; Length 567;
Best Local Similarity 99.5%; Pred. No. 1.9e-158;
RESULT 696
ID AAB49533 standard; protein; 570 AA.
DE Clone HEPPEY75.
PN WO200061774-A2.
PD 19-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 74.7%; Score 2946.5; DB 3; Length 570;
Best Local Similarity 96.8%; Pred. No. 9.4e-151;
RESULT 697
ID ADR41465 standard; protein; 551 AA.
DE Human CD-like molecule HSDP41, SEQ ID NO:284.
PN WO200226930-A2.
PD 04-APR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 74.6%; Score 2944; DB 5; Length 551;
Best Local Similarity 99.3%; Pred. No. 1.2e-150;
RESULT 698
ID AAM41706 standard; protein; 499 AA.
DE Human polypeptide SEQ ID NO 6637.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 65.3%; Score 2577.5; DB 4; Length 499;
Best Local Similarity 96.6%; Pred. No. 6.2e-131;
RESULT 699
ID AAE20817 standard; protein; 455 AA.
DE Human gene 5 encoded secreted protein HSLGU75, SEQ ID NO:79.
PN WO200218435-A1.
PD 07-MAR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 61.2%; Score 2413; DB 5; Length 455;
Best Local Similarity 99.3%; Pred. No. 4.2e-122;
RESULT 700
ID ABG64652 standard; protein; 455 AA.
DE Human albumin fusion protein #1327.
PN WO200177137-A1.
PD 18-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 61.2%; Score 2413; DB 5; Length 455;
Best Local Similarity 99.3%; Pred. No. 4.2e-122;
RESULT 701
ID ADL77919 standard; protein; 455 AA.
DE Albumin fusion protein related therapeutic protein X, SEQ ID NO 1401.
PN US2004010134-A1.
PD 15-JAN-2004.
PA (ROSE/) ROSEN C A.
PA (HASE/) HASELTINE W A.
Query Match 61.2%; Score 2413; DB 8; Length 455;
Best Local Similarity 99.3%; Pred. No. 4.2e-122;
RESULT 702
ID AEH08193 standard; protein; 455 AA.
DE Therapeutic protein HSLGU75, SEQ ID 1401.
PN US2006084794-A1.
PD 20-APR-2006.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 61.2%; Score 2413; DB 10; Length 455;
Best Local Similarity 99.3%; Pred. No. 4.2e-122;
RESULT 703
ID ADL06662 standard; protein; 417 AA.
DE Human 3T3 cell conversion promoter PP938.
PN CN1403477-A.
PD 19-MAR-2003.
PA (SHAN-) SHANGHAI XINSHIJI GENE TECHN DEV CO LTD.
Query Match 52.2%; Score 2059; DB 7; Length 417;
Best Local Similarity 95.6%; Pred. No. 4.5e-103;
RESULT 704

ID AAM39920 standard; protein; 359 AA.
DE Human polypeptide SEQ ID NO 3065.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 48.4%; Score 1909; DB 4; Length 359;
Best Local Similarity 100.0%; Pred. No. 4.7e-95;
RESULT 705
ID AAM39957 standard; protein; 359 AA.
DE Human polypeptide SEQ ID NO 3102.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 48.4%; Score 1909; DB 4; Length 359;
Best Local Similarity 100.0%; Pred. No. 4.7e-95;
RESULT 706
ID AAE20797 standard; protein; 323 AA.
DE Human gene 5 encoded secreted protein HSLGU75, SEQ ID NO:59.
PN WO200218435-A1.
PD 07-MAR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 43.3%; Score 1708.5; DB 5; Length 323;
Best Local Similarity 94.1%; Pred. No. 2.7e-84;
RESULT 707
ID ABG64653 standard; protein; 323 AA.
DE Human albumin fusion protein #1328.
PN WO200177137-A1.
PD 18-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 43.3%; Score 1708.5; DB 5; Length 323;
Best Local Similarity 94.1%; Pred. No. 2.7e-84;
RESULT 708
ID ADL77920 standard; protein; 323 AA.
DE Albumin fusion protein related therapeutic protein X, SEQ ID NO 1402.
PN US2004010134-A1.
PD 15-JAN-2004.
PA (ROSE/) ROSEN C A.
PA (HASE/) HASELTINE W A.
Query Match 43.3%; Score 1708.5; DB 8; Length 323;
Best Local Similarity 94.1%; Pred. No. 2.7e-84;
RESULT 709
ID AEH08194 standard; protein; 323 AA.
DE Therapeutic protein HSLGU75, SEQ ID 1402.
PN US2006084794-A1.
PD 20-APR-2006.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 43.3%; Score 1708.5; DB 10; Length 323;
Best Local Similarity 94.1%; Pred. No. 2.7e-84;
RESULT 710
ID AAM24485 standard; protein; 234 AA.
DE Human EST encoded protein SEQ ID NO: 2010.
PN WO200154477-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 29.8%; Score 1175.5; DB 4; Length 234;
Best Local Similarity 91.4%; Pred. No. 1e-55;
RESULT 711
ID ABR72332 standard; protein; 1019 AA.
DE Horseshoe crab factor C.
PN WO200302976-A2.
PD 09-JAN-2003.
PA (WHIK-) BIONEER INC.
Query Match 17.0%; Score 672; DB 6; Length 1019;
Best Local Similarity 25.6%; Pred. No. 5.3e-28;
RESULT 712
ID AAM43394 standard; protein; 1019 AA.
DE Singapore horseshoe crab factor C proenzyme (CrFC 21).
PN SG42456-A1.
PD 15-AUG-1997.
PA (UTSI-) UNITV SINGAPORE NAT.
Query Match 16.9%; Score 665; DB 2; Length 1019;
Best Local Similarity 25.4%; Pred. No. 1.3e-27;
RESULT 713

ID AAY05750 standard; protein; 1019 AA.
DE Horseshoe crab Factor C.
PN W09915676-A1.
PD 01-APR-1999.
PA (UYSI-) UNIV SINGAPORE NAT.
Query Match 16.9%; Score 665; DB 2; Length 1019;
Best Local Similarity 25.4%; Pred. No. 1.3e-27;
RESULT 714
ID AAM94302 standard; protein; 1019 AA.
DE Horseshoe crab Factor C protein #2.
PN US5858706-A.
PD 12-JAN-1999.
PA (UYSI-) UNIV SINGAPORE NAT.
Query Match 16.9%; Score 665; DB 2; Length 1019;
Best Local Similarity 25.4%; Pred. No. 1.3e-27;
RESULT 715
ID AAY42490 standard; protein; 1019 AA.
DE Recombinant N-terminally truncated Horseshoe crab Factor C protein.
PN US5985590-A.
PD 16-NOV-1999.
PA (UYSI-) UNIV SINGAPORE NAT.
Query Match 16.9%; Score 665; DB 3; Length 1019;
Best Local Similarity 25.4%; Pred. No. 1.3e-27;
RESULT 716
ID AAB60935 standard; protein; 1019 AA.
DE Horseshoe crab recombinant Factor C #2.
PN W0200127289-A2.
PD 19-APR-2001.
PA (UYSI-) UNIV SINGAPORE NAT.
Query Match 16.9%; Score 665; DB 4; Length 1019;
Best Local Similarity 25.4%; Pred. No. 1.3e-27;
RESULT 717
ID ABP72334 standard; protein; 1019 AA.
DE Horseshoe crab Factor C.
PN W02003002976-A2.
PD 09-JUN-2003.
PA (WHIK) BICWHITTAKER INC.
Query Match 16.9%; Score 665; DB 6; Length 1019;
Best Local Similarity 25.4%; Pred. No. 1.3e-27;
RESULT 718
ID ADM39099 standard; protein; 1019 AA.
DE Southeast Asian horseshoe crab Factor C.
PN W02005003163-A1.
PD 13-JAN-2005.
PA (UYSI-) UNIV SINGAPORE NAT.
Query Match 16.9%; Score 665; DB 9; Length 1019;
Best Local Similarity 25.4%; Pred. No. 1.3e-27;
RESULT 719
ID AAM43393 standard; protein; 1083 AA.
DE Singapore horseshoe crab Factor C proenzyme (CrFC 26).
PN S642456-A1.
PD 15-AUG-1997.
PA (UYSI-) UNIV SINGAPORE NAT.
Query Match 16.9%; Score 665; DB 2; Length 1083;
Best Local Similarity 25.4%; Pred. No. 1.3e-27;
RESULT 720
ID AAY05749 standard; protein; 1083 AA.
DE Horseshoe crab Factor C.
PN W09915676-A1.
PD 01-APR-1999.
PA (UYSI-) UNIV SINGAPORE NAT.
Query Match 16.9%; Score 665; DB 2; Length 1083;
Best Local Similarity 25.4%; Pred. No. 1.3e-27;
RESULT 721
ID AAM94301 standard; protein; 1083 AA.
DE Horseshoe crab Factor C protein #1.
PN US5858706-A.
PD 12-JAN-1999.
PA (UYSI-) UNIV SINGAPORE NAT.
Query Match 16.9%; Score 665; DB 2; Length 1083;
Best Local Similarity 25.4%; Pred. No. 1.3e-27;
RESULT 722
ID AAY42489 standard; protein; 1083 AA.

DE Horseshoe crab recombinant Factor C protein.
PN US5985590-A.
PD 16-NOV-1999.
PA (UYSI-) UNIV SINGAPORE NAT.
Query Match 16.9%; Score 665; DB 3; Length 1083;
Best Local Similarity 25.4%; Pred. No. 1.3e-27;
RESULT 723
ID AAB60934 standard; protein; 1083 AA.
DE Horseshoe crab recombinant Factor C #1.
PN W0200127289-A2.
PD 19-APR-2001.
PA (UYSI-) UNIV SINGAPORE NAT.
Query Match 16.9%; Score 665; DB 4; Length 1083;
Best Local Similarity 25.4%; Pred. No. 1.3e-27;
RESULT 724
ID ABP72333 standard; protein; 1083 AA.
DE Horseshoe crab Factor C.
PN W02003002976-A2.
PD 09-JAN-2003.
PA (WHIK) BICWHITTAKER INC.
Query Match 16.9%; Score 665; DB 6; Length 1083;
Best Local Similarity 25.4%; Pred. No. 1.3e-27;
RESULT 725
ID AAM41743 standard; protein; 146 AA.
DE Human polypeptide SEQ ID NO 6674.
PN W0200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 16.8%; Score 662; DB 4; Length 146;
Best Local Similarity 85.4%; Pred. No. 3e-28;
RESULT 726
ID AAY11743 standard; protein; 103 AA.
DE Human 5' EST secreted protein SEQ ID NO: 343.
PN W09906550-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match 14.7%; Score 580; DB 2; Length 103;
Best Local Similarity 97.1%; Pred. No. 5.6e-24;
RESULT 727
ID AEF13693 standard; protein; 699 AA.
DE Human MBP-associated serine protease 1 (MASP-1) protein.
PN W02005123776-A1.
PD 28-DEC-2005.
PA (OMER-) OMEROS CORP.
PA (UYLR-) UNIV LEICESTER.
Query Match 12.1%; Score 478; DB 10; Length 699;
Best Local Similarity 24.6%; Pred. No. 1.1e-17;
RESULT 728
ID AEB26839 standard; protein; 680 AA.
DE Human MASP-1 protein, SEQ ID NO: 6 #2.
PN US2005158297-A1.
PD 21-JUL-2005.
PA (JENS/) JENSENUS J C.
PA (THIE/) THIEL S.
Query Match 12.1%; Score 476; DB 9; Length 680;
Best Local Similarity 24.6%; Pred. No. 1.3e-17;
RESULT 729
ID ADE87459 standard; protein; 699 AA.
DE Human MBP-associated serine protease-1 protein.
PN EP1344533-A1.
PD 17-SEP-2003.
PA (NATL-) NATLMCONE AS.
Query Match 12.1%; Score 476; DB 7; Length 699;
Best Local Similarity 24.6%; Pred. No. 1.3e-17;
RESULT 730
ID AEB64931 standard; protein; 699 AA.
DE Human p100 serine protease of Ra-reactive factor, SEQ ID 24.
PN JP200525343-A.
PD 22-SEP-2005.
PA (HOKK-) HOKKAIDO TLO KK.
Query Match 12.1%; Score 476; DB 10; Length 699;
Best Local Similarity 24.6%; Pred. No. 1.3e-17;
RESULT 731

ID ADL91028 standard; protein; 699 AA.
DE Human mannose binding lectin amino acid sequence SEQ ID NO:14.
PN WO2004024925-A2.
PD 25-MAR-2004.
PA (NATL-) NATIMMUNE AS.
Query Match 12.0%; Score 475; DB 8; Length 699;
Best Local Similarity 24.6%; Pred. No. 1.5e-17;
RESULT 732
ID AAM83722 standard; protein; 698 AA.
DE Human diagnostic and therapeutic pproteoin SEQ ID NO:3971.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 12.0%; Score 474.5; DB 8; Length 698;
Best Local Similarity 24.4%; Pred. No. 1.6e-17;
RESULT 733
ID AAB85060 standard; protein; 728 AA.
DE Human serine protease MASP-3 polypeptide.
PN WO200140451-A2.
PD 07-JUN-2001.
PA (JENS/) JENSENIUS J C.
Query Match 11.9%; Score 471; DB 4; Length 728;
Best Local Similarity 25.0%; Pred. No. 2.6e-17;
RESULT 734
ID AEB26835 standard; protein; 679 AA.
DE Human MASP-1 protein, SEQ ID NO: 6 #1.
PN US2005158297-A1.
PD 21-JUL-2005.
PA (JENS/) JENSENIUS J C.
Query Match 11.9%; Score 469.5; DB 9; Length 679;
Best Local Similarity 24.4%; Pred. No. 2.9e-17;
RESULT 735
ID ADEB87461 standard; protein; 728 AA.
DE Human MBL-associated serine protease-4 protein.
PN EP1344533-A1.
PD 17-SEP-2003.
PA (NATL-) NATIMMUNE AS.
Query Match 11.9%; Score 468; DB 7; Length 728;
Best Local Similarity 25.0%; Pred. No. 3.8e-17;
RESULT 736
ID ADL91027 standard; protein; 728 AA.
DE Human mannose binding lectin amino acid sequence SEQ ID NO:13.
PN WO2004024925-A2.
PD 25-MAR-2004.
PA (NATL-) NATIMMUNE AS.
Query Match 11.9%; Score 468; DB 8; Length 728;
Best Local Similarity 25.0%; Pred. No. 3.8e-17;
RESULT 737
ID AAB47559 standard; protein; 728 AA.
DE Protease PRS-1.
PN WO200171004-A2.
PD 27-SEP-2001.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 11.7%; Score 461; DB 4; Length 728;
Best Local Similarity 24.9%; Pred. No. 9e-17;
RESULT 738
ID AAG80756 standard; protein; 707 AA.
DE Murine C1r protein.
PN KR2001077614-A.
PD 20-AUG-2001.
PA (BIOC-) BIO CLUE & SOLUTION CO LTD.
Query Match 10.9%; Score 429; DB 5; Length 707;
Best Local Similarity 22.3%; Pred. No. 4.6e-15;
RESULT 739
ID AEF03476 standard; protein; 670 AA.
DE Mature rat MASP-2.
PN WO2005123128-A2.
PD 23-DEC-2005.
PA (OMER-) OMEROS CORP.
Query Match 10.4%; Score 412; DB 10; Length 670;
Best Local Similarity 21.4%; Pred. No. 3.7e-14;
RESULT 740
ID AEF03475 standard; protein; 685 AA.
DE Full length rat MASP-2.
PN WO2005123128-A2.
PD 29-DEC-2005.
PA (OMER-) OMEROS CORP.
Query Match 10.7%; Score 423; DB 10; Length 685;
Best Local Similarity 24.1%; Pred. No. 9.5e-15;
RESULT 741
ID AEF03473 standard; protein; 670 AA.
DE Mature murine MASP-2.
PN WO2005123128-A2.
PD 29-DEC-2005.
PA (OMER-) OMEROS CORP.
Query Match 10.4%; Score 412; DB 10; Length 670;
Best Local Similarity 21.4%; Pred. No. 3.6e-14;
RESULT 742
ID AEF03472 standard; protein; 685 AA.
DE Full length murine MASP-2.
PN WO2005123128-A2.
PD 29-DEC-2005.
PA (OMER-) OMEROS CORP.
Query Match 10.4%; Score 412; DB 10; Length 685;
Best Local Similarity 21.4%; Pred. No. 3.7e-14;
RESULT 743
ID AEB26836 standard; protein; 688 AA.
DE Human C1q-associated serine protease, C1r SEQ ID NO: 7.
PN US2005158297-A1.
PD 21-JUL-2005.
PA (JENS/) JENSENIUS J C.
Query Match 10.2%; Score 403.5; DB 9; Length 688;
Best Local Similarity 22.9%; Pred. No. 1.1e-13;
RESULT 744
ID ABB50288 standard; protein; 705 AA.
DE Complement component 1 r ovarian tumour marker protein, SEQ ID NO:66.
PN WO2001751177-A2.
PD 11-OCT-2001.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match 10.2%; Score 403.5; DB 4; Length 705;
Best Local Similarity 22.9%; Pred. No. 1.1e-13;
RESULT 745
ID AAG80757 standard; protein; 705 AA.
DE Human C1r protein.
PN KR2001077614-A.
PD 20-AUG-2001.
PA (BIOC-) BIO CLUE & SOLUTION CO LTD.
Query Match 10.2%; Score 403.5; DB 5; Length 705;
Best Local Similarity 22.9%; Pred. No. 1.1e-13;
RESULT 746
ID ADP65211 standard; protein; 705 AA.
DE Human complement component 1, r subcomponent.
PN WO2003072827-A1.
PD 04-SEP-2003.
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
Query Match 10.2%; Score 403.5; DB 7; Length 705;
Best Local Similarity 22.6%; Pred. No. 1.1e-13;
RESULT 747
ID AEB13349 standard; protein; 705 AA.
DE Complement component C1r SEQ ID NO 14.
PN WO2005061537-A2.
PD 07-JUL-2005.
PA (GSFU-) GSF FORSCHUNGSZENTRUM UMWELT & GESUNDHEIT.
Query Match 10.2%; Score 403.5; DB 9; Length 705;
Best Local Similarity 22.9%; Pred. No. 1.1e-13;
RESULT 748

Query Match 10.7%; Score 423; DB 10; Length 670;
Best Local Similarity 24.1%; Pred. No. 9.3e-15;
RESULT 740
ID AEF03475 standard; protein; 685 AA.
DE Full length rat MASP-2.
PN WO2005123128-A2.
PD 29-DEC-2005.
PA (OMER-) OMEROS CORP.
Query Match 10.7%; Score 423; DB 10; Length 685;
Best Local Similarity 24.1%; Pred. No. 9.5e-15;
RESULT 741
ID AEF03473 standard; protein; 670 AA.
DE Mature murine MASP-2.
PN WO2005123128-A2.
PD 29-DEC-2005.
PA (OMER-) OMEROS CORP.
Query Match 10.4%; Score 412; DB 10; Length 670;
Best Local Similarity 21.4%; Pred. No. 3.6e-14;
RESULT 742
ID AEF03472 standard; protein; 685 AA.
DE Full length murine MASP-2.
PN WO2005123128-A2.
PD 29-DEC-2005.
PA (OMER-) OMEROS CORP.
Query Match 10.4%; Score 412; DB 10; Length 685;
Best Local Similarity 21.4%; Pred. No. 3.7e-14;
RESULT 743
ID AEB26836 standard; protein; 688 AA.
DE Human C1q-associated serine protease, C1r SEQ ID NO: 7.
PN US2005158297-A1.
PD 21-JUL-2005.
PA (JENS/) JENSENIUS J C.
Query Match 10.2%; Score 403.5; DB 9; Length 688;
Best Local Similarity 22.9%; Pred. No. 1.1e-13;
RESULT 744
ID ABB50288 standard; protein; 705 AA.
DE Complement component 1 r ovarian tumour marker protein, SEQ ID NO:66.
PN WO2001751177-A2.
PD 11-OCT-2001.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match 10.2%; Score 403.5; DB 4; Length 705;
Best Local Similarity 22.9%; Pred. No. 1.1e-13;
RESULT 745
ID AAG80757 standard; protein; 705 AA.
DE Human C1r protein.
PN KR2001077614-A.
PD 20-AUG-2001.
PA (BIOC-) BIO CLUE & SOLUTION CO LTD.
Query Match 10.2%; Score 403.5; DB 5; Length 705;
Best Local Similarity 22.9%; Pred. No. 1.1e-13;
RESULT 746
ID ADP65211 standard; protein; 705 AA.
DE Human complement component 1, r subcomponent.
PN WO2003072827-A1.
PD 04-SEP-2003.
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
Query Match 10.2%; Score 403.5; DB 7; Length 705;
Best Local Similarity 22.6%; Pred. No. 1.1e-13;
RESULT 747
ID AEB13349 standard; protein; 705 AA.
DE Complement component C1r SEQ ID NO 14.
PN WO2005061537-A2.
PD 07-JUL-2005.
PA (GSFU-) GSF FORSCHUNGSZENTRUM UMWELT & GESUNDHEIT.
Query Match 10.2%; Score 403.5; DB 9; Length 705;
Best Local Similarity 22.9%; Pred. No. 1.1e-13;
RESULT 748

ID AED74704 standard; protein; 705 AA.
DE Human placental protein SEQ ID NO:1532.
PN US2005255114-A1.
PD 17-NOV-2005.
PA (NUVE-) NUVELO INC.
Query Match 10.2%; Score 403.5; DB 9; Length 705;
Best Local Similarity 22.9%; Pred. No. 1.1e-13;
RESULT 749
ID ADU18123 standard; protein; 704 AA.
DE Human candidate osteoarthritis marker protein - SEQ ID 154.
PN WO2004092413-A2.
PD 28-OCT-2004.
PA (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS PHARMA GMBH.
Query Match 10.2%; Score 403; DB 8; Length 704;
Best Local Similarity 22.5%; Pred. No. 1.2e-13;
RESULT 750
ID AEG31619 standard; protein; 686 AA.
DE Human mannan-binding lectin associated serine protease-2 protein.
PN US2002082208-A1.
PD 27-JUN-2002.
PA (JENS/) JENSENIUS J C.
PA (THIE/) THIEL S.
Query Match 10.2%; Score 401.5; DB 5; Length 686;
Best Local Similarity 22.7%; Pred. No. 1.4e-13;
RESULT 751
ID AAE14564 standard; protein; 686 AA.
DE Human MASP-2 protein.
PN WO200206460-A2.
PD 24-JAN-2002.
PA (JENS/) JENSENIUS J C.
PA (THIE/) THIEL S.
Query Match 10.2%; Score 401.5; DB 5; Length 686;
Best Local Similarity 22.7%; Pred. No. 1.4e-13;
RESULT 752
ID AEG32115 standard; protein; 686 AA.
DE Mannan-binding lectin associated serine protease-2 (MASP-2).
PN US2002082209-A1.
PD 27-JUN-2002.
PA (JENS/) JENSENIUS J C.
PA (THIE/) THIEL S.
Query Match 10.2%; Score 401.5; DB 5; Length 686;
Best Local Similarity 22.7%; Pred. No. 1.4e-13;
RESULT 753
ID ADL91025 standard; protein; 686 AA.
DE Human mannose binding lectin amino acid sequence SEQ ID NO:11.
PN WO2004024925-A2.
PD 25-MAR-2004.
PA (NATI-) NATIMUNE AS.
Query Match 10.2%; Score 401.5; DB 8; Length 686;
Best Local Similarity 22.7%; Pred. No. 1.4e-13;
RESULT 754
ID AEA17053 standard; protein; 686 AA.
DE Alzheimer's disease associated protein #6.
PN US2005123962-A1.
PD 09-JUN-2005.
PA (AGYT-) AGY THERAPEUTICS INC.
Query Match 10.2%; Score 401.5; DB 9; Length 686;
Best Local Similarity 22.7%; Pred. No. 1.4e-13;
RESULT 755
ID AEB26831 standard; protein; 686 AA.
DE Human mannan binding lectin-associated serine protease-2, SEQ ID NO: 2.
PN US2005158297-A1.
PD 21-JUL-2005.
PA (JENS/) JENSENIUS J C.
PA (THIE/) THIEL S.
Query Match 10.2%; Score 401.5; DB 9; Length 686;
Best Local Similarity 22.7%; Pred. No. 1.4e-13;
RESULT 756
ID AEF03426 standard; protein; 686 AA.
DE Full length MASP-2.
PN WO2005123128-A2.
PD 29-DEC-2005.

PA (OMER-) OMEROS CORP.
PA (UYLE-) UNIV LEICESTER.
Query Match 10.2%; Score 401.5; DB 10; Length 686;
Best Local Similarity 22.7%; Pred. No. 1.4e-13;
RESULT 757
ID AEF13655 standard; protein; 686 AA.
DE Human MB1-associated serine protease 2 (MASP-2) protein.
PN WO2005123776-A1.
PD 29-DEC-2005.
PA (OMER-) OMEROS CORP.
PA (UYLE-) UNIV LEICESTER.
Query Match 10.2%; Score 401.5; DB 10; Length 686;
Best Local Similarity 22.7%; Pred. No. 1.4e-13;
RESULT 758
ID AAE14568 standard; protein; 686 AA.
DE Human MASP-2 protein, alternative version.
PN WO200206460-A2.
PD 24-JAN-2002.
PA (JENS/) JENSENIUS J C.
PA (THIE/) THIEL S.
Query Match 10.2%; Score 400.5; DB 5; Length 686;
Best Local Similarity 22.7%; Pred. No. 1.5e-13;
RESULT 759
ID ADE87460 standard; protein; 686 AA.
DE Human MB1-associated serine protease-2 protein.
PN EPI344531-A1.
PD 17-SEP-2003.
PA (NATI-) NATIMUNE AS.
Query Match 10.2%; Score 400.5; DB 7; Length 686;
Best Local Similarity 22.7%; Pred. No. 1.5e-13;
RESULT 760
ID ADV50598 standard; protein; 686 AA.
DE Human mannan-binding lectin serine protease 2 (MASP2) protein.
PN WO2004106384-A1.
PD 09-DEC-2004.
PA (NATI-) NATIMUNE AS.
Query Match 10.2%; Score 400.5; DB 9; Length 686;
Best Local Similarity 22.7%; Pred. No. 1.5e-13;
RESULT 761
ID ADY62954 standard; protein; 686 AA.
DE human mitogen activated serine protease-2 (MASP-2).
PN WO2005024013-A1.
PD 17-MAR-2005.
PA (NATI-) NATIMUNE AS.
Query Match 10.2%; Score 400.5; DB 9; Length 686;
Best Local Similarity 22.7%; Pred. No. 1.5e-13;
RESULT 762
ID ADQ27010 standard; protein; 671 AA.
DE Human MASP-2 mature polypeptide.
PN WO2004050907-A2.
PD 17-JUN-2004.
PA (UYAA-) UNIV AARHUS.
PA (AARH) AARHUS AMT.
Query Match 10.1%; Score 399.5; DB 8; Length 671;
Best Local Similarity 22.8%; Pred. No. 1.7e-13;
RESULT 763
ID AEB26838 standard; protein; 671 AA.
DE Human mature MASP-2 protein (residues 16-686).
PN US2005158297-A1.
PD 21-JUL-2005.
PA (JENS/) JENSENIUS J C.
PA (THIE/) THIEL S.
Query Match 10.1%; Score 399.5; DB 9; Length 671;
Best Local Similarity 22.8%; Pred. No. 1.7e-13;
RESULT 764
ID AEF03427 standard; protein; 671 AA.
DE Mature MASP-2.
PN WO2005123128-A2.
PD 29-DEC-2005.
PA (OMER-) OMEROS CORP.
PA (UYLE-) UNIV LEICESTER.
Query Match 10.1%; Score 399.5; DB 10; Length 671;
Best Local Similarity 22.8%; Pred. No. 1.7e-13;

RESULT 765
ID AEF13656 standard; protein: 671 AA.
DE Human MBP-associated serine protease 2 (MASP-2) mature protein.
PN W02005123776-A1.
PD 29-DEC-2005.
PA (OMER-) OMEROS CORP.
PA (UYLE-) UNIV LEICESTER.
Query Match
Best Local Similarity 10.1%; Score 399.5; DB 10; Length 671;
RESULT 766
ID AAE14565 standard; peptide: 671 AA.
DE Human mature MASP-2 protein.
PN W0200206460-A2.
PD 24-JAN-2002.
PA (JENS/) JENSENIUS J C.
PA (THIE/) THIEL S.
Query Match
Best Local Similarity 10.1%; Score 398.5; DB 5; Length 671;
RESULT 767
ID AEC95282 standard; protein: 604 AA.
DE Enteropeptidase, SEQ ID 5.
PN JP2005253325-A.
PD 22-SEP-2005.
PA (UYHO-) UNIV HOKKAIDO.
Query Match
Best Local Similarity 9.4%; Score 369.5; DB 9; Length 604;
RESULT 768
ID AEC95280 standard; protein: 1036 AA.
DE Enteropeptidase, SEQ ID 3.
PN JP2005253325-A.
PD 22-SEP-2005.
PA (UYHO-) UNIV HOKKAIDO.
Query Match
Best Local Similarity 9.4%; Score 369.5; DB 9; Length 1036;
RESULT 769
ID ADX26355 standard; protein: 694 AA.
DE Novel cell pain response detection method-related mouse protein SeqID701.
PN W02005014849-A2.
PD 17-FEB-2005.
PA (EURO-) EUROCELTIQUE SA.
Query Match
Best Local Similarity 9.2%; Score 364; DB 9; Length 694;
RESULT 770
ID ADE56422 standard; protein: 694 AA.
DE Rat Protein BAA25797, SEQ ID NO 2275.
PN W02003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match
Best Local Similarity 8.6%; Score 340.5; DB 7; Length 694;
RESULT 771
ID ADE83526 standard; protein: 694 AA.
DE Rat Protein BAA25797, SEQ ID NO 11123.
PN W02003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match
Best Local Similarity 8.6%; Score 340.5; DB 7; Length 694;
RESULT 772
ID ADX26430 standard; protein: 694 AA.
DE Novel cell pain response detection method-related rat protein SeqID776.
PN W02005014849-A2.
PD 17-FEB-2005.
PA (EURO-) EUROCELTIQUE SA.
Query Match
Best Local Similarity 8.6%; Score 340.5; DB 9; Length 694;
RESULT 773
ID ADE56418 standard; protein: 695 AA.
DE Rat Protein DB8250, SEQ ID NO 2271.
PN W02003016475-A2.
PD 27-FEB-2003.

PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match
Best Local Similarity 8.6%; Score 340.5; DB 7; Length 695;
RESULT 774
ID ADD45338 standard; protein: 695 AA.
DE Rat Protein DB8250, SEQ ID NO 10771.
PN W02003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match
Best Local Similarity 8.6%; Score 340.5; DB 7; Length 695;
RESULT 775
ID AAB43579 standard; protein: 760 AA.
DE Human cancer associated protein sequence SEQ ID NO:1024.
PN W020053530-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 8.5%; Score 336; DB 3; Length 760;
RESULT 776
ID AEB26837 standard; protein: 673 AA.
DE Human C1q-associated serine protease, C1s SEQ ID NO: 8.
PN US2005158297-A1.
PD 21-JUL-2005.
PA (JENS/) JENSENIUS J C.
PA (THIE/) THIEL S.
Query Match
Best Local Similarity 8.5%; Score 334; DB 9; Length 673;
RESULT 777
ID ADD45340 standard; protein: 688 AA.
DE Human Protein O9UCV3, SEQ ID NO 10773.
PN W02003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match
Best Local Similarity 8.5%; Score 334; DB 7; Length 688;
RESULT 778
ID ADE56420 standard; protein: 688 AA.
DE Human Protein O9UCV3, SEQ ID NO 2273.
PN W02003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match
Best Local Similarity 8.5%; Score 334; DB 7; Length 688;
RESULT 779
ID ADP65315 standard; protein: 688 AA.
DE Human complement c1s component precursor (c1 esterase).
PN W02003072827-A1.
PD 04-SEP-2003.
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
Query Match
Best Local Similarity 8.5%; Score 334; DB 7; Length 688;
RESULT 780
ID ADU75392 standard; protein: 688 AA.
DE Marker gene related amino acid sequence SEQ ID NO:644.
PN EP1394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Query Match
Best Local Similarity 8.5%; Score 334; DB 8; Length 688;
RESULT 781
ID ADU91020 standard; protein: 688 AA.
DE Human mannosyl binding lectin amino acid sequence SEQ ID NO:6.
PN W02004024925-A2.
PD 25-MAR-2004.
PA (NATT-) NATIMUNE AS.
Query Match
Best Local Similarity 8.5%; Score 334; DB 8; Length 688;
RESULT 782
ID ADU91020 standard; protein: 688 AA.
DE Human mannosyl binding lectin amino acid sequence SEQ ID NO:6.
PN W02004024925-A2.
PD 25-MAR-2004.

ID AEM8137 standard; protein; 688 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO2660, SEQ:3453.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 334; DB 8; Length 688;
Best Local Similarity 21.7%; Pred. No. 5.9e-10;
RESULT 783
ID ADU06459 standard; protein; 688 AA.
DE Novel bronchial cancer-associated human protein SeqID683.
PN DE10316701-A1.
PD 04-NOV-2004.
PA (HINZ) HINZMANN B.
PA (HERM) HERMANN K.
PA (CAST) HEIDEN CASTANOS-VELEZ E.
Query Match 8.5%; Score 334; DB 8; Length 688;
Best Local Similarity 21.7%; Pred. No. 5.9e-10;
RESULT 784
ID ADX26285 standard; protein; 688 AA.
DE Novel cell pain response detection method-related human protein SeqID631.
PN WO2005014849-A2.
PD 17-FEB-2005.
PA (EURO-) EUROCELTIQUE SA.
Query Match 8.5%; Score 334; DB 9; Length 688;
Best Local Similarity 21.7%; Pred. No. 5.9e-10;
RESULT 785
ID ADZ80432 standard; protein; 688 AA.
DE Mature complement C1s (C1 esterase) SEQ ID NO 45.
PN WO2005040422-A2.
PD 06-MAY-2005.
PA (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS PHARMA GMBH.
Query Match 8.5%; Score 334; DB 9; Length 688;
Best Local Similarity 21.7%; Pred. No. 5.9e-10;
RESULT 786
ID AED74705 standard; protein; 688 AA.
DE Human placental protein SEQ ID NO:1533.
PN US2005255114-A1.
PD 17-NOV-2005.
PA (NUVE-) NUVELO INC.
Query Match 8.5%; Score 334; DB 9; Length 688;
Best Local Similarity 21.7%; Pred. No. 5.9e-10;
RESULT 787
ID AEX17066 standard; protein; 688 AA.
DE Human C1s fragment SEQ ID NO 821.
PN WO2005072340-A2.
PD 11-AUG-2005.
PA (COMP-) COMPUGEN LTD.
PA (COMP-) COMPUGEN INC.
Query Match 8.5%; Score 334; DB 10; Length 688;
Best Local Similarity 21.7%; Pred. No. 5.9e-10;
RESULT 788
ID ADI16884 standard; protein; 855 AA.
DE Human NOVX protein homologue SeqID 420.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 8.4%; Score 332; DB 5; Length 855;
Best Local Similarity 21.6%; Pred. No. 9.3e-10;
RESULT 789
ID ADI16818 standard; protein; 855 AA.
DE Human NOVX protein homologue SeqID 354.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 8.4%; Score 332; DB 5; Length 855;
Best Local Similarity 21.6%; Pred. No. 9.3e-10;
RESULT 790
ID AEF27702 standard; protein; 855 AA.
DE Human prostamlin, SEQ:132.
PN US2006009634-A1.
PD 12-JAN-2006.
PA (KEKU/) KEKUDA R.

PA (ALSO/) ALSOBROOK J.
PA (TCHX/) TCHERNY V.
PA (LITX/) LIT X.
PA (SPYT/) SPYTEK K.
PA (PATT/) PATTURAJAN M.
PA (GROS/) GROSSE W.
PA (LEPL/) LEPELEY D.
PA (BURG/) BURGESS C.
PA (VERN/) VERNET C.
PA (LITL/) LI L.
PA (GORM/) GORMAN L.
PA (EDIN/) EDINGER S.
PA (SCIO/) SCIORE P.
PA (ELLE/) EILERMAN K.
PA (MALY/) MALYANKAR U.
PA (ROTH/) ROTHENBERG M.
PA (STON/) STONE D.
PA (BOLD/) BOLDOG F.
PA (GUOX/) GUO X.
PA (SHEN/) SHENOY S.
PA (ANDE/) ANDERSON D.
PA (PADI/) PADIGARU M.
PA (TAUP/) TAUPIER R.
PA (MILL/) MILLER C.
PA (EISE/) EISEN A.
Query Match 8.4%; Score 332; DB 10; Length 855;
Best Local Similarity 21.6%; Pred. No. 9.3e-10;
RESULT 791
ID AAE06940 standard; protein; 1019 AA.
DE Human enterokinase protein.
PN WO200157194-A2.
PD 09-AUG-2001.
PA (CORV-) CORVAS INT INC.
Query Match 8.4%; Score 331.5; DB 4; Length 1019;
Best Local Similarity 22.9%; Pred. No. 1.2e-09;
RESULT 792
ID ADA83985 standard; protein; 1019 AA.
DE Human PRSS7 protein.
PN WO2002103028-A2.
PD 27-DEC-2002.
PA (BION-) BIONEEDICAL CENT.
Query Match 8.4%; Score 331.5; DB 6; Length 1019;
Best Local Similarity 22.9%; Pred. No. 1.2e-09;
RESULT 793
ID ADI10400 standard; protein; 1019 AA.
DE Human cell surface protease #16.
PN WO200295007-A2.
PD 28-NOV-2002.
PA (CORV-) CORVAS INT INC.
Query Match 8.4%; Score 331.5; DB 7; Length 1019;
Best Local Similarity 22.9%; Pred. No. 1.2e-09;
RESULT 794
ID ADJ46924 standard; protein; 1019 AA.
DE Human transmembrane serine protease (MTSP)-related polypeptide #6.
PN US2004001801-A1.
PD 01-JAN-2004.
PA (CORV-) CORVAS INT INC.
Query Match 8.4%; Score 331.5; DB 8; Length 1019;
Best Local Similarity 22.9%; Pred. No. 1.2e-09;
RESULT 795
ID AAE25673 standard; protein; 1019 AA.
DE Human serine protease PRSS7 SEQ ID NO 18.
PN WO2005110338-A2.
PD 24-NOV-2005.
PA (GANY-) GANYMED PHARM AG.
Query Match 8.4%; Score 331.5; DB 10; Length 1019;
Best Local Similarity 22.9%; Pred. No. 1.2e-09;
RESULT 796
ID AAE83015 standard; protein; 1019 AA.
DE Human enteropeptidase.
PN WO2006050999-A2.
PD 18-MAY-2006.
PA (OBER-) OBE THERAPY BIOTECHNOLOGY SAS.

Query Match 8.4%; Score 331.5; DB 10; Length 1019;
Best Local Similarity 22.9%; Pred. No. 1.2e-09;
RESULT 797
ID ADJ70437 standard; protein, 1019 AA.
DE Human heat mitochondrial protein as a therapeutic target SegID2243.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
Query Match 8.4%; Score 330.5; DB 7; Length 1019;
Best Local Similarity 22.9%; Pred. No. 1.3e-09;
RESULT 798
ID ADJ70480 standard; protein, 3389 AA.
DE Human heat mitochondrial protein as a therapeutic target SegID2286.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
Query Match 8.4%; Score 329.5; DB 7; Length 3389;
Best Local Similarity 20.8%; Pred. No. 4.6e-09;
RESULT 799
ID ABE02790 standard; protein, 3566 AA.
DE Human S-100 beta binding protein, SEQ ID NO:33.
PN WO2005106473-A1.
PD 10-NOV-2005.
PA (ONOX) ONO PHARM CO LTD.
Query Match 8.4%; Score 329.5; DB 9; Length 3566;
Best Local Similarity 20.8%; Pred. No. 4.8e-09;
RESULT 800
ID ADH72216 standard; protein, 3567 AA.
DE Human protein of the invention NOV54b SEQ ID NO:1112.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 8.4%; Score 329.5; DB 8; Length 3567;
Best Local Similarity 20.8%; Pred. No. 4.8e-09;
RESULT 801
ID AAR13623 standard; protein, 460 AA.
DE Human Protein C zymogen SC.
PN EP43875-A.
PD 28-AUG-1991.
PA (LILLY) LILLY & CO ELI.
Query Match 8.3%; Score 329; DB 2; Length 460;
Best Local Similarity 25.5%; Pred. No. 7.6e-10;
RESULT 802
ID ABG76507 standard; protein, 1274 AA.
DE DNA encoding protein modification and maintenance molecule #11.
PN WO200260942-A2.
PD 08-AUG-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 8.3%; Score 328.5; DB 5; Length 1274;
Best Local Similarity 20.8%; Pred. No. 2.1e-09;
RESULT 803
ID AAU11815 standard; protein, 1783 AA.
DE Cancer and neurogenesis associated gene, variant 5G-3V3.
PN WO200190354-A1.
PD 29-NOV-2001.
PA (UYLE-) UNIV LEEDS.
Query Match 8.3%; Score 328.5; DB 5; Length 1783;
Best Local Similarity 20.8%; Pred. No. 2.9e-09;
RESULT 804
ID AAU11813 standard; protein, 1800 AA.
DE Cancer and neurogenesis associated gene, variant 5G-3V1.
PN WO200190354-A1.
PD 29-NOV-2001.
PA (UYLE-) UNIV LEEDS.
Query Match 8.3%; Score 328.5; DB 5; Length 1800;
Best Local Similarity 20.8%; Pred. No. 2.9e-09;
RESULT 805
ID AAU11812 standard; protein, 1826 AA.
DE Cancer and neurogenesis associated gene.
PN WO200190354-A1.
PD 29-NOV-2001.

PA (UYLE-) UNIV LEEDS.
Query Match 8.3%; Score 328.5; DB 5; Length 1826;
Best Local Similarity 20.8%; Pred. No. 2.9e-09;
RESULT 806
ID AAU11814 standard; protein, 2008 AA.
DE Cancer and neurogenesis associated gene, variant 5G-3V2.
PN WO200190354-A1.
PD 29-NOV-2001.
PA (UYLE-) UNIV LEEDS.
Query Match 8.3%; Score 328.5; DB 5; Length 2008;
Best Local Similarity 20.8%; Pred. No. 3.2e-09;
RESULT 807
ID AAU11817 standard; protein, 2306 AA.
DE Cancer and neurogenesis associated gene, variant 5R23V2.
PN WO200190354-A1.
PD 29-NOV-2001.
PA (UYLE-) UNIV LEEDS.
Query Match 8.3%; Score 328.5; DB 5; Length 2306;
Best Local Similarity 20.8%; Pred. No. 3.6e-09;
RESULT 808
ID AAU11816 standard; protein, 2352 AA.
DE Cancer and neurogenesis associated gene, variant 5R-3V2.
PN WO200190354-A1.
PD 29-NOV-2001.
PA (UYLE-) UNIV LEEDS.
Query Match 8.3%; Score 328.5; DB 5; Length 2352;
Best Local Similarity 20.8%; Pred. No. 3.7e-09;
RESULT 809
ID AAB19551 standard; protein, 683 AA.
DE Human matrixase (truncated form).
PN WO200053232-A1.
PD 14-SEP-2000.
PA (GEOU) UNIV GEORGETOWN.
Query Match 8.3%; Score 328; DB 3; Length 683;
Best Local Similarity 21.4%; Pred. No. 1.2e-09;
RESULT 810
ID AAY90284 standard; protein, 762 AA.
DE Human peptidase, HPEP-1 protein sequence.
PN WO200042201-A2.
PD 20-JUL-2000.
PA (INCY-) INCYTE PHARM INC.
Query Match 8.3%; Score 328; DB 3; Length 762;
Best Local Similarity 21.4%; Pred. No. 1.4e-09;
RESULT 811
ID AAM25628 standard; protein, 851 AA.
DE Human protein sequence SEQ ID NO:1143.
PN WO200153455-A2.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 8.3%; Score 328; DB 4; Length 851;
Best Local Similarity 21.6%; Pred. No. 1.5e-09;
RESULT 812
ID ABB1428 standard; peptide, 851 AA.
DE Human membrane-type Ser kinase homologue, SEQ ID NO:1798.
PN WO200157188-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 8.3%; Score 328; DB 4; Length 851;
Best Local Similarity 21.6%; Pred. No. 1.5e-09;
RESULT 813
ID ADO55145 standard; protein, 853 AA.
DE Protein #47 with increased gene expression in renal cell carcinoma.
PN WO200603842-A2.
PD 22-APR-2004.
PA (VAND-) VAN ANDEL INST.
Query Match 8.3%; Score 328; DB 8; Length 853;
Best Local Similarity 21.4%; Pred. No. 1.5e-09;
RESULT 814
ID AAB19552 standard; protein, 855 AA.
DE Human matrixase.
PN WO200053232-A1.
PD 14-SEP-2000.
PA (GEOU) UNIV GEORGETOWN.

Query Match
 Best Local Similarity 21.4%; Pred. No. 1.5e-09; Length 855;
 RESULT 815
 ID AAB35465 standard; protein; 855 AA.
 DE Human membrane-type serine protease MT-SP1.
 PN W0200123524-A2.
 PD 05-APR-2001.
 PA (REGC) UNIV CALIFORNIA.
 Query Match
 Best Local Similarity 21.4%; Pred. No. 1.5e-09; Length 855;
 RESULT 816
 ID AD116817 standard; protein; 855 AA.
 DE Human NOVX protein homologue SegID 353.
 PN W0200268649-A2.
 PD 06-SEP-2002.
 PA (CURA-) CURAGEN CORP.
 Query Match
 Best Local Similarity 21.4%; Pred. No. 1.5e-09; Length 855;
 RESULT 817
 ID AD116883 standard; protein; 855 AA.
 DE Human NOVX protein homologue SegID 419.
 PN W0200268649-A2.
 PD 06-SEP-2002.
 PA (CURA-) CURAGEN CORP.
 Query Match
 Best Local Similarity 21.4%; Pred. No. 1.5e-09; Length 855;
 RESULT 818
 ID AD116876 standard; protein; 855 AA.
 DE Human NOVX protein homologue SegID 412.
 PN W0200268649-A2.
 PD 06-SEP-2002.
 PA (CURA-) CURAGEN CORP.
 Query Match
 Best Local Similarity 21.4%; Pred. No. 1.5e-09; Length 855;
 RESULT 819
 ID ADN39867 standard; protein; 855 AA.
 DE Cancer/angiogenesis/fibrosis-related polypeptide, SRQ ID NO:C237.
 PN W02003042661-A2.
 PD 22-MAY-2003.
 PA (E0SB-) EOS BIOTECHNOLOGY INC.
 Query Match
 Best Local Similarity 21.4%; Pred. No. 1.5e-09; Length 855;
 RESULT 820
 ID ADN04754 standard; protein; 855 AA.
 DE Antisporiatic protein sequence #558.
 PN W02004028479-A2.
 PD 08-APR-2004.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 21.4%; Pred. No. 1.5e-09; Length 855;
 RESULT 821
 ID ADP23334 standard; protein; 855 AA.
 DE PRO polypeptide SEQ ID NO:428.
 PN W02004041170-A2.
 PD 21-MAY-2004.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 21.4%; Pred. No. 1.5e-09; Length 855;
 RESULT 822
 ID AE146688 standard; protein; 855 AA.
 DE Human cancer-associated protease Matrilptase.
 PN W02006068975-A2.
 PD 29-JUN-2006.
 PA (ABGE-) ABGENIX INC.
 Query Match
 Best Local Similarity 21.4%; Pred. No. 1.5e-09; Length 855;
 RESULT 823
 ID ABR66721 standard; protein; 863 AA.
 DE Human prostatic carcinoma derived protein SEQ ID 233 #3.
 PN W02004076614-A2.
 PD 10-SEP-2004.
 PA (HINZ/) HINZMANN B.

PA (DAHL/) DAHL E.
 PA (ROSE/) ROSENTHAL A.
 PA (HERM/) HERMANN K.
 PA (PILA/) PILARSKY C.
 Query Match
 Best Local Similarity 21.4%; Pred. No. 1.5e-09; Length 863;
 RESULT 824
 ID ADR66379 standard; protein; 863 AA.
 DE Human prostatic carcinoma derived protein SEQ ID 233 #2.
 PN W02004076614-A2.
 PD 10-SEP-2004.
 PA (HINZ/) HINZMANN B.
 PA (DAHL/) DAHL E.
 PA (ROSE/) ROSENTHAL A.
 PA (HERM/) HERMANN K.
 PA (PILA/) PILARSKY C.
 Query Match
 Best Local Similarity 21.4%; Pred. No. 1.5e-09; Length 863;
 RESULT 825
 ID AAB58274 standard; protein; 449 AA.
 DE Lung cancer associated polypeptide sequence SEQ ID 612.
 PN W0200055180-A2.
 PD 21-SEP-2000.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match
 Best Local Similarity 23.3%; Pred. No. 8.9e-10; Length 449;
 RESULT 826
 ID ADL64961 standard; protein; 688 AA.
 DE Human complement component 1 protein, CIS.
 PN US2004033582-A1.
 PD 19-FEB-2004.
 PA (EDMO/) EDMONDS M.
 PA (HUI/) HUI L.
 PA (PERR/) PERRONE M.
 PA (POME/) POMEIL J R.
 PA (RAMA/) RAMANTHAN C S.
 PA (SWAN/) SWANSON B.
 PA (TSUC/) TSUCHIHASHI Z.
 PA (ZERR/) ZERBA K.
 Query Match
 Best Local Similarity 21.7%; Pred. No. 1.4e-09; Length 688;
 RESULT 827
 ID AD116508 standard; protein; 757 AA.
 DE Human NOVX protein to treat human pathological conditions SegID44.
 PN W0200268649-A2.
 PD 06-SEP-2002.
 PA (CURA-) CURAGEN CORP.
 Query Match
 Best Local Similarity 21.6%; Pred. No. 1.5e-09; Length 757;
 RESULT 828
 ID AAY06671 standard; protein; 855 AA.
 DE Tumour antigen derived gene-15 (TADG-15) protein.
 PN W09942120-A1.
 PD 26-AUG-1999.
 PA (UYAR-) UNIV ARKANSAS.
 Query Match
 Best Local Similarity 21.6%; Pred. No. 1.7e-09; Length 855;
 RESULT 829
 ID AAB98500 standard; protein; 855 AA.
 DE Human TADG-15.
 PN W0200129056-A1.
 PD 26-APR-2001.
 PA (UYAR-) UNIV ARKANSAS.
 Query Match
 Best Local Similarity 21.6%; Pred. No. 1.7e-09; Length 855;
 RESULT 830
 ID AAE06930 standard; protein; 855 AA.
 DE Human membrane-type serine protease (MTSP) 1.
 PN W0200157194-A2.
 PD 09-AUG-2001.
 PA (CORV-) CORVAS INT INC.
 Query Match
 Best Local Similarity 21.6%; Pred. No. 1.7e-09; Length 855;

Best Local Similarity 21.6%; Pred. No. 1.7e-09;
RESULT 831
ID AAO22929 standard; protein; 855 AA.
DE Type II transmembrane serine protease 1 protein SEQ ID NO. 2.
PN WO200272786-A2.
PD 19-SEP-2002.
PA (CORV-) CORVAS INT INC.
Query Match 8.3%; Score 327; DB 5; Length 855;
Best Local Similarity 21.6%; Pred. No. 1.7e-09;
RESULT 832
ID ADI16816 standard; protein; 855 AA.
DE Human NOVX protein homologue SeqID 352.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 8.3%; Score 327; DB 5; Length 855;
Best Local Similarity 21.6%; Pred. No. 1.7e-09;
RESULT 833
ID ADI16882 standard; protein; 855 AA.
DE Human NOVX protein homologue SeqID 418.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 8.3%; Score 327; DB 5; Length 855;
Best Local Similarity 21.6%; Pred. No. 1.7e-09;
RESULT 834
ID ADI16875 standard; protein; 855 AA.
DE Human NOVX protein homologue SeqID 411.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 8.3%; Score 327; DB 5; Length 855;
Best Local Similarity 21.6%; Pred. No. 1.7e-09;
RESULT 835
ID ABB56619 standard; protein; 855 AA.
DE Human membrane-type serine protease MTSP1 protein SEQ ID NO.2.
PN WO200292841-A2.
PD 21-NOV-2002.
PA (CORV-) CORVAS INT INC.
Query Match 8.3%; Score 327; DB 6; Length 855;
Best Local Similarity 21.6%; Pred. No. 1.7e-09;
RESULT 836
ID AAO30146 standard; protein; 855 AA.
DE Human membrane-type serine protease MTSP1 protein.
PN WO2003044179-A2.
PD 30-MAY-2003.
PA (CORV-) CORVAS INT INC.
Query Match 8.3%; Score 327; DB 6; Length 855;
Best Local Similarity 21.6%; Pred. No. 1.7e-09;
RESULT 837
ID AAE29820 standard; protein; 855 AA.
DE Human membrane-type serine protease 1 (MTSP1).
PN WO200277287-A2.
PD 03-OCT-2002.
PA (CORV-) CORVAS INT INC.
Query Match 8.3%; Score 327; DB 6; Length 855;
Best Local Similarity 21.6%; Pred. No. 1.7e-09;
RESULT 838
ID AAE29791 standard; protein; 855 AA.
DE Human membrane-type serine protease, MTSP1.
PN WO200277263-A2.
PD 03-OCT-2002.
PA (CORV-) CORVAS INT INC.
Query Match 8.3%; Score 327; DB 6; Length 855;
Best Local Similarity 21.6%; Pred. No. 1.7e-09;
RESULT 839
ID ABB72376 standard; protein; 855 AA.
DE Transmembrane serine protease 1 (MTSP1).
PN WO2003004681-A2.
PD 16-JAN-2003.
PA (CORV-) CORVAS INT INC.
Query Match 8.3%; Score 327; DB 6; Length 855;
Best Local Similarity 21.6%; Pred. No. 1.7e-09;

RESULT 840
ID ABB97551 standard; protein; 855 AA.
DE Human MTSP1, SEQ ID NO:2.
PN WO2003031585-A2.
PD 17-APR-2003.
PA (CORV-) CORVAS INT INC.
Query Match 8.3%; Score 327; DB 7; Length 855;
Best Local Similarity 21.6%; Pred. No. 1.7e-09;
RESULT 841
ID ADI10371 standard; protein; 855 AA.
DE Human cell surface protease #1.
PN WO200295007-A2.
PD 28-NOV-2002.
PA (CORV-) CORVAS INT INC.
Query Match 8.3%; Score 327; DB 7; Length 855;
Best Local Similarity 21.6%; Pred. No. 1.7e-09;
RESULT 842
ID ADG65326 standard; protein; 855 AA.
DE Human MTSP1.
PN WO2003104394-A2.
PD 18-DEC-2003.
PA (DENB-) DENBREON SAN DIEGO LLC.
Query Match 8.3%; Score 327; DB 8; Length 855;
Best Local Similarity 21.6%; Pred. No. 1.7e-09;
RESULT 843
ID ADI28861 standard; protein; 855 AA.
DE Human matrixase (MTSP1) serine protease.
PN WO2004005471-A2.
PD 15-JAN-2004.
PA (DENB-) DENBREON SAN DIEGO LLC.
Query Match 8.3%; Score 327; DB 8; Length 855;
Best Local Similarity 21.6%; Pred. No. 1.7e-09;
RESULT 844
ID ADJ46695 standard; protein; 855 AA.
DE Human transmembrane serine protease (MTSP) polypeptide #1.
PN US2004001801-A1.
PD 01-JAN-2004.
PA (CORV-) CORVAS INT INC.
Query Match 8.3%; Score 327; DB 8; Length 855;
Best Local Similarity 21.6%; Pred. No. 1.7e-09;
RESULT 845
ID AEB61724 standard; protein; 855 AA.
DE Human membrane-type serine protease 1.
PN WO2005100556-A2.
PD 27-OCT-2005.
PA (CATALY-) CATALYST BIOSCIENCES.
Query Match 8.3%; Score 327; DB 9; Length 855;
Best Local Similarity 21.6%; Pred. No. 1.7e-09;
RESULT 846
ID AEE05739 standard; protein; 855 AA.
DE Wild type human membrane-type serine protease 1 (MT-SPI).
PN WO2005110453-A2.
PD 24-NOV-2005.
PA (CATALY-) CATALYST BIOSCIENCES.
Query Match 8.3%; Score 327; DB 9; Length 855;
Best Local Similarity 21.6%; Pred. No. 1.7e-09;
RESULT 847
ID AAE20788 standard; protein; 3095 AA.
DE Rat C3b/C4b complement receptor like protein.
PN WO200210199-A2.
PD 07-FEB-2002.
PA (AMGE-) AMGEN INC.
Query Match 8.2%; Score 324; DB 5; Length 3095;
Best Local Similarity 20.1%; Pred. No. 8.3e-09;
RESULT 848
ID ADN42162 standard; protein; 757 AA.
DE Human novel protein NOV 8.
PN US2004033493-A1.
PD 19-FEB-2004.
PA (TCHE/) TCHERNEV V T.
PA (SPYT/) SPYTEK K A.
PA (ZERH/) ZERHUSEN B D.
PA (PATV/) PATURBAJAN M.

PA (SHIM/) SHIMKETS R. A.
PA (LILL/) LI L.
PA (GANG/) GANGOLI E. A.
PA (PAD/) PADIGARU M.
PA (ANDE/) ANDERSON D. W.
PA (RAST/) RASTELI L.
PA (MILL/) MILLER C. E.
PA (GERL/) GERLACH V.
PA (TAUP/) TAUPIER R. J.
PA (GUSE/) GUSEV V. Y.
PA (COLM/) COLMAN S. D.
PA (WOLE/) WOLENC A. R.
PA (PENA/) PENNA C. E. A.
PA (FURT/) FURTA K. W.
PA (GROS/) GROSSE W. M.
PA (ALSO/) ALSOBROOK J. P.
PA (LEPL/) LEPPLEY D. M.
PA (RIEG/) RIEGER D. K.
PA (BURG/) BURGESS C. E.
Query Match
Best Local Similarity 8.1%; Score 323; DB 8; Length 757;
Pred. No. 2.5e-09;
RESULT 849
ID ADH71146 standard; protein; 3130 AA.
DE Human protein of the invention NOV4f SEQ ID NO:42.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 8.1%; Score 321; DB 8; Length 3130;
Pred. No. 1.2e-08;
RESULT 850
ID ADH71144 standard; protein; 3483 AA.
DE Human protein of the invention NOV4e SEQ ID NO:40.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 8.1%; Score 321; DB 8; Length 3483;
Pred. No. 1.4e-08;
RESULT 851
ID ADH71136 standard; protein; 3546 AA.
DE Human protein of the invention NOV4a SEQ ID NO:32.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 8.1%; Score 321; DB 8; Length 3546;
Pred. No. 1.4e-08;
RESULT 852
ID AAE20787 standard; protein; 3069 AA.
DE Human C3b/C4b complement receptor like protein #1.
PN WO200210199-A2.
PD 07-FEB-2002.
PA (AMGE-) AMGEN INC.
Query Match
Best Local Similarity 8.1%; Score 320.5; DB 5; Length 3069;
Pred. No. 1.3e-08;
RESULT 853
ID AAE20789 standard; protein; 3100 AA.
DE Human C3b/C4b complement receptor like protein #2.
PN WO200210199-A2.
PD 07-FEB-2002.
PA (AMGE-) AMGEN INC.
Query Match
Best Local Similarity 8.1%; Score 320.5; DB 5; Length 3100;
Pred. No. 1.3e-08;
RESULT 854
ID AAU99088 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant G383N/G385T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match
Best Local Similarity 8.1%; Score 319.5; DB 5; Length 419;
Pred. No. 2.3e-09;
RESULT 855
ID AAU99080 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant L349N/D351T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match
Best Local Similarity 8.1%; Score 318.5; DB 5; Length 419;
Pred. No. 2.5e-09;
RESULT 858
ID ADH71142 standard; protein; 2612 AA.
DE Human protein of the invention NOV4d SEQ ID NO:38.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 8.1%; Score 318; DB 8; Length 2612;
Pred. No. 1.5e-08;
RESULT 859
ID ABG79169 standard; protein; 2669 AA.
DE Human cub and sushi domain containing protein #2.
PN WO200264791-A2.
PD 22-AUG-2002.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 8.1%; Score 318; DB 5; Length 2669;
Pred. No. 1.5e-08;
RESULT 860
ID ADH71140 standard; protein; 2669 AA.
DE Human protein of the invention NOV4c SEQ ID NO:36.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 8.1%; Score 318; DB 8; Length 2669;
Pred. No. 1.5e-08;
RESULT 861
ID ABG79168 standard; protein; 3104 AA.
DE Human cub and sushi domain containing protein #1.
PN WO200264791-A2.
PD 22-AUG-2002.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 8.1%; Score 318; DB 5; Length 3104;
Pred. No. 1.8e-08;
RESULT 862
ID ADH71168 standard; protein; 3104 AA.
DE Human protein of the invention NOV4g SEQ ID NO:64.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 8.1%; Score 318; DB 8; Length 3104;
Pred. No. 1.8e-08;
RESULT 863
ID ADH71166 standard; protein; 3104 AA.
DE Human protein of the invention NOV4p SEQ ID NO:62.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 8.1%; Score 318; DB 8; Length 3104;
Pred. No. 1.8e-08;
RESULT 864
ID ADH71138 standard; protein; 3104 AA.

DE Human protein of the invention NOV4b SEQ ID NO:34.
PN W02003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 8.1%; Score 318; DB 8; Length 3104;
Best Local Similarity 22.6%; Pred. No. 1.8e-08;
RESULT 865
ID AAU9906 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant D189N/K191T.
PN W020032461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 8.0%; Score 317.5; DB 5; Length 419;
Best Local Similarity 24.4%; Pred. No. 2.9e-09;
RESULT 866
ID AAU9906 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant T315N/V317T.
PN W020032461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 8.0%; Score 317.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 2.9e-09;
RESULT 867
ID ADM28524 standard; protein; 421 AA.
DE Human Protein C variant #2.
PN W0200411385-A1.
PD 29-DEC-2004.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 8.0%; Score 317.5; DB 9; Length 421;
Best Local Similarity 24.7%; Pred. No. 2.9e-09;
RESULT 868
ID AEA20987 standard; protein; 627 AA.
DE Novel human polypeptide SEQ ID NO 1681.
PN W02005049806-A2.
PD 02-JUN-2005.
PA (NUVE-) NUVELO INC.
Query Match 8.0%; Score 317.5; DB 9; Length 627;
Best Local Similarity 21.3%; Pred. No. 4.2e-09;
RESULT 869
ID AAR57283 standard; protein; 798 AA.
DE Bovine enterokinase.
PN W09416083-A1.
PD 21-JUL-1994.
PA (GENY-) GENETICS INST INC.
Query Match 8.0%; Score 317.5; DB 2; Length 798;
Best Local Similarity 24.6%; Pred. No. 5.3e-09;
RESULT 870
ID AAE20900 standard; protein; 3069 AA.
DE Human C3b/C4b complement receptor like protein #1, alternative version.
PN W0200210199-A2.
PD 07-FEB-2002.
PA (AMGE-) AMGEN INC.
Query Match 8.0%; Score 317.5; DB 5; Length 3069;
Best Local Similarity 20.7%; Pred. No. 1.9e-08;
RESULT 871
ID AAE20901 standard; protein; 3100 AA.
DE Human C3b/C4b complement receptor like protein #2, alternative version.
PN W0200210199-A2.
PD 07-FEB-2002.
PA (AMGE-) AMGEN INC.
Query Match 8.0%; Score 317.5; DB 5; Length 3100;
Best Local Similarity 20.7%; Pred. No. 1.9e-08;
RESULT 872
ID AAU99076 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant M338N/S340T.
PN W020032461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 8.0%; Score 316.5; DB 5; Length 419;
Best Local Similarity 23.3%; Pred. No. 4.2e-09;
RESULT 881
ID AAU99053 standard; protein; 419 AA.

Best Local Similarity 24.7%; Pred. No. 3.3e-09;
RESULT 873
ID AAU99022 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant K217N/L219T.
PN W020032461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 8.0%; Score 316.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 3.3e-09;
RESULT 874
ID AAU99026 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant L220N/R222T.
PN W020032461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 8.0%; Score 315.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 875
ID AAU99081 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant D351N/Q353S.
PN W020032461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 8.0%; Score 315.5; DB 5; Length 419;
Best Local Similarity 24.7%; Pred. No. 3.7e-09;
RESULT 876
ID AAU99071 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant S336N/M338S.
PN W020032461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 8.0%; Score 315.5; DB 5; Length 419;
Best Local Similarity 24.7%; Pred. No. 3.7e-09;
RESULT 877
ID AAU99087 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant G383N/G385S.
PN W020032461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 8.0%; Score 315.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 878
ID AAU99079 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant L349N/D351S.
PN W020032461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 8.0%; Score 315.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 879
ID AAR62653 standard; protein; 461 AA.
DE Human Protein C.
PN US358932-A.
PD 25-OCT-1994.
PA (ZYMO-) ZYMOGENETICS INC.
Query Match 8.0%; Score 315.5; DB 5; Length 461;
Best Local Similarity 24.5%; Pred. No. 4e-09;
RESULT 880
ID AAR35760 standard; protein; 419 AA.
DE Protein C (PC).
PN W09309804-A1.
PD 27-MAY-1993.
PA (SCRI-) SCRIPPS RES INST.
Query Match 8.0%; Score 314.5; DB 2; Length 419;
Best Local Similarity 23.3%; Pred. No. 4.2e-09;
RESULT 881
ID AAU99053 standard; protein; 419 AA.

DE Human Protein C zymogen protein mutant R306N/K308S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 8.0%; Score 314.5; DB 5; Length 419;
Best Local Similarity 24.7%; Pred. No. 4.2e-09;
RESULT 892
ID AAU99007 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant S190N/K192S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 8.0%; Score 314.5; DB 5; Length 419;
Best Local Similarity 24.4%; Pred. No. 4.2e-09;
RESULT 893
ID AAU99077 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant I348N/G350S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 8.0%; Score 314.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 4.2e-09;
RESULT 894
ID AAU99043 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant L296N.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 8.0%; Score 314.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 4.2e-09;
RESULT 895
ID ADG83832 standard; protein; 454 AA.
DE Red belly black snake venom protease.
PN WO2003082914-A1.
PD 09-OCT-2003.
PA (UYOU) UNIV QUEENSLAND.
Query Match 8.0%; Score 314.5; DB 8; Length 454;
Best Local Similarity 23.0%; Pred. No. 4.5e-09;
RESULT 896
ID ADM77504 standard; protein; 461 AA.
DE Human protein C variant #2 amino acid sequence.
PN WO200310666-A2.
PD 24-DEC-2003.
PA (MAXY-) MAXYGEN APS.
Query Match 8.0%; Score 314.5; DB 8; Length 461;
Best Local Similarity 24.5%; Pred. No. 4.6e-09;
RESULT 897
ID ADM28523 standard; protein; 420 AA.
DE Human protein C variant #1.
PN WO2004113385-A1.
PD 29-DEC-2004.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 8.0%; Score 314; DB 9; Length 420;
Best Local Similarity 24.5%; Pred. No. 4.5e-09;
RESULT 898
ID AAE23083 standard; protein; 855 AA.
DE Bpichin protein.
PN WO200203787-A2.
PD 17-JAN-2002.
PA (DELT-) DELTAGEN INC.
Query Match 8.0%; Score 314; DB 5; Length 855;
Best Local Similarity 21.4%; Pred. No. 8.7e-09;
RESULT 899
ID ADL16819 standard; protein; 855 AA.
DE Murine NOVX protein homologue Segid 355.
PN WO200268649-A2.
PD 06-SEP-2002.

PA (CURA-) CURAGEN CORP.
Query Match 8.0%; Score 314; DB 5; Length 855;
Best Local Similarity 21.4%; Pred. No. 8.7e-09;
RESULT 890
ID ADL16877 standard; protein; 855 AA.
DE Murine NOVX protein homologue Segid 413.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 8.0%; Score 314; DB 5; Length 855;
Best Local Similarity 21.4%; Pred. No. 8.7e-09;
RESULT 891
ID AAW72753 standard; protein; 419 AA.
DE Primary structure of activated human protein C.
PN EP875563-A2.
PD 04-NOV-1998.
PA (ELIL) LILLY & CO ELI.
Query Match 7.9%; Score 313.5; DB 2; Length 419;
Best Local Similarity 23.3%; Pred. No. 4.7e-09;
RESULT 892
ID AAU99005 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant D189N/K191S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.9%; Score 313.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 4.7e-09;
RESULT 893
ID AAU99025 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant L220N/R222S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.9%; Score 313.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 4.7e-09;
RESULT 894
ID AAU99065 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant T315N/V317S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.9%; Score 313.5; DB 5; Length 419;
Best Local Similarity 24.3%; Pred. No. 4.7e-09;
RESULT 895
ID AAU99016 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant D214N/S216T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.9%; Score 313.5; DB 5; Length 419;
Best Local Similarity 24.7%; Pred. No. 4.7e-09;
RESULT 896
ID AAU99023 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant K218N/L220S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 313.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 4.7e-09;
RESULT 897
ID AEH44151 standard; protein; 419 AA.
DE Human protein C analog with A264I substitution.
PN WO2006044294-A2.
PD 27-APR-2006.
PA (ELIL) LILLY & CO ELI.
Query Match 7.9%; Score 313.5; DB 10; Length 419;
Best Local Similarity 24.5%; Pred. No. 4.7e-09;
RESULT 898

ID AAR1083 standard; protein; 509 AA.
DE PAP-I-protein C fusion construct.
PN WO9109953-A.
PD 11-JUL-1991.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 7.9%; Score 313; DB 2; Length 509;
Best Local Similarity 23.5%; Pred. No. 6e-09;
RESULT 899
ID AD116820 standard; protein; 855 AA.
DE Rat NOVX protein homologue SeqID 356.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 7.9%; Score 313; DB 5; Length 855;
Best Local Similarity 21.4%; Pred. No. 9.8e-09;
RESULT 900
ID AD116881 standard; protein; 855 AA.
DE Rat NOVX protein homologue SeqID 417.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 7.9%; Score 313; DB 5; Length 855;
Best Local Similarity 21.4%; Pred. No. 9.8e-09;
RESULT 901
ID AD116878 standard; protein; 855 AA.
DE Rat NOVX protein homologue SeqID 414.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 7.9%; Score 313; DB 5; Length 855;
Best Local Similarity 21.4%; Pred. No. 9.8e-09;
RESULT 902
ID AAU99072 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant S336N/M338T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.9%; Score 312.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 5.4e-09;
RESULT 903
ID AAU99097 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant D189N/K191N.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.9%; Score 312.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 5.4e-09;
RESULT 904
ID AAU99009 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant K191N/K193S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.9%; Score 312.5; DB 5; Length 419;
Best Local Similarity 24.2%; Pred. No. 5.4e-09;
RESULT 905
ID AAU99064 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant R312N/R314T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.9%; Score 312.5; DB 5; Length 419;
Best Local Similarity 24.9%; Pred. No. 5.4e-09;
RESULT 906
ID AAU99069 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant V334N.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.

PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 312.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 5.4e-09;
RESULT 907
ID AAU99082 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant D351N/Q353T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.9%; Score 312.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 5.4e-09;
RESULT 908
ID AAU99096 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant M338A.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.9%; Score 312.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 5.4e-09;
RESULT 909
ID AAU99091 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant L387N/N389S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.9%; Score 312.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 5.4e-09;
RESULT 910
ID AAU99024 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant K218N/L220T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.9%; Score 312.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 5.4e-09;
RESULT 911
ID AAU99048 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant H303N/S305T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.9%; Score 312.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 5.4e-09;
RESULT 912
ID AAU99067 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant F316N/L318S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.9%; Score 312.5; DB 5; Length 419;
Best Local Similarity 24.3%; Pred. No. 5.4e-09;
RESULT 913
ID AAU99075 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant M338N.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.9%; Score 312.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 5.4e-09;
RESULT 914
ID AAU99092 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant L387N/N389T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.9%; Score 312.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 5.4e-09;
RESULT 915
ID AAU99092 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant L387N/N389T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN HOLDINGS LTD.

Query Match
Best Local Similarity 7.9%; Score 312.5; DB 5; Length 419;
RESULT 915
ID AAU99011 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant K192N/L194S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match
Best Local Similarity 7.9%; Score 312.5; DB 5; Length 419;
RESULT 916
ID AAU99032 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant S250N/S252T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match
Best Local Similarity 7.9%; Score 312.5; DB 5; Length 419;
RESULT 917
ID ADM77507 standard; protein; 461 AA.
DE Human protein C variant #5 amino acid sequence.
PN WO200310666-A2.
PD 24-DEC-2003.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match
Best Local Similarity 7.9%; Score 312.5; DB 8; Length 461;
RESULT 918
ID ADM77505 standard; protein; 461 AA.
DE Human protein C variant #3 amino acid sequence.
PN WO200310666-A2.
PD 24-DEC-2003.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match
Best Local Similarity 7.9%; Score 312.5; DB 8; Length 461;
RESULT 919
ID AEK16852 standard; protein; 622 AA.
DE Human HUMCIRS_P6 protein SEQ ID NO 95.
PN WO2005072340-A2.
PD 11-AUG-2005.
PA (COMP-) COMPUGEN LTD.
PA (COMP-) COMPUGEN INC.
Query Match
Best Local Similarity 7.9%; Score 312.5; DB 10; Length 622;
RESULT 920
ID AEK17063 standard; protein; 622 AA.
DE Human HUMCIRS_PEA_1_P22 protein fragment SEQ ID NO 818.
PN WO2005072340-A2.
PD 11-AUG-2005.
PA (COMP-) COMPUGEN LTD.
PA (COMP-) COMPUGEN INC.
Query Match
Best Local Similarity 7.9%; Score 312.5; DB 10; Length 622;
RESULT 921
ID AAB82677 standard; protein; 419 AA.
DE Human protein C derivative (H100/S11G/Q32E/N33D/L194S).
PN WO200151793-A2.
PD 09-AUG-2001.
PA (ELIL) LILLY & CO ELI.
Query Match
Best Local Similarity 7.9%; Score 312; DB 4; Length 419;
RESULT 922
ID AAR3537 standard; protein; 460 AA.
DE Human Protein C zymogen N.
PN EP443875-A.
PD 28-AUG-1991.
PA (ELIL) LILLY & CO ELI.
Query Match
Best Local Similarity 7.9%; Score 312; DB 2; Length 460;
RESULT 923
ID AAB82677 standard; protein; 467 AA.
DE Coarctal taiwan venom protease.
PN WO2003082914-A1.
PD 09-OCT-2003.
PA (UYOU) UNIV QUEENSLAND.
Query Match
Best Local Similarity 7.9%; Score 312; DB 8; Length 467;
RESULT 924
ID ABB60993 standard; protein; 1031 AA.
DE Novel human protein. SEQ ID 80.
PN WO200250105-A1.
PD 27-JUN-2002.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
PA (GLAXO) GLAXO GROUP LTD.
Query Match
Best Local Similarity 7.9%; Score 312; DB 5; Length 1031;
RESULT 925
ID AAU99008 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant S190N/K192T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match
Best Local Similarity 7.9%; Score 311.5; DB 5; Length 419;
RESULT 926
ID AAU99039 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant T254N/N256S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match
Best Local Similarity 7.9%; Score 311.5; DB 5; Length 419;
RESULT 927
ID AAU99047 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant H303N.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match
Best Local Similarity 7.9%; Score 311.5; DB 5; Length 419;
RESULT 928
ID AAU99070 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant V334N/S336T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match
Best Local Similarity 7.9%; Score 311.5; DB 5; Length 419;
RESULT 929
ID AAU99017 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant E215N/K217S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match
Best Local Similarity 7.9%; Score 311.5; DB 5; Length 419;
RESULT 930
ID AAU99044 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant L296N/T298S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match
Best Local Similarity 7.9%; Score 311.5; DB 5; Length 419;
RESULT 931
ID AAU99014 standard; protein; 419 AA.

DE Human Protein C zymogen protein mutant K193N/A195T.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 311.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.1e-09;
RESULT 932
ID AAU99031 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant S250N.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 311.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.1e-09;
RESULT 933
ID AAU99057 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant K306N/A310S.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 311.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.1e-09;
RESULT 934
ID AAU99054 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant R306N/K308T.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 311.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.1e-09;
RESULT 935
ID AAU99095 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant D214A.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 311.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.1e-09;
RESULT 936
ID AAU99015 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant D214N.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 311.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.1e-09;
RESULT 937
ID AAP81205 standard; protein; 461 AA.
DE Human protein C.
PN EP266190-A.
PD 04-MAY-1988.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 7.9%; Score 311.5; DB 1; Length 461;
Best Local Similarity 24.5%; Pred. No. 6.6e-09;
RESULT 938
ID AAR13539 standard; protein; 461 AA.
DE Human Protein C zymogen LIN.
PN EP443875-A.
PD 28-AUG-1991.
PA (ELIL) LILLY & CO ELI.
Query Match 7.9%; Score 311.5; DB 2; Length 461;
Best Local Similarity 24.5%; Pred. No. 6.6e-09;
RESULT 939
ID AAR13997 standard; protein; 461 AA.
DE Human protein C zymogen Q329.
PN EP443874-A.
PD 28-AUG-1991.

PA (ELIL) LILLY & CO ELI.
Query Match 7.9%; Score 311.5; DB 2; Length 461;
Best Local Similarity 24.5%; Pred. No. 6.6e-09;
RESULT 940
ID ADM77503 standard; protein; 461 AA.
DE Human protein C variant #1 amino acid sequence.
PN W0200310666-A2.
PD 24-DEC-2003.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 311.5; DB 8; Length 461;
Best Local Similarity 24.5%; Pred. No. 6.6e-09;
RESULT 941
ID AAB82678 standard; protein; 419 AA.
DE Human protein C derivative (H100/S116/Q32E/N33D/L194S/T254S).
PN W0200157193-A2.
PD 09-AUG-2001.
PA (ELIL) LILLY & CO ELI.
Query Match 7.9%; Score 311; DB 4; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.5e-09;
RESULT 942
ID AAB82675 standard; protein; 419 AA.
DE Human protein C derivative (S116/Q32E/N33D/L194S).
PN W0200157193-A2.
PD 09-AUG-2001.
PA (ELIL) LILLY & CO ELI.
Query Match 7.9%; Score 311; DB 4; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.5e-09;
RESULT 943
ID ADX39090 standard; protein; 446 AA.
DE Rat factor VII.
PN W02005014775-A2.
PD 17-FEB-2005.
PA (UYFL) UNIV FLORIDA RES FOUND INC.
Query Match 7.9%; Score 311; DB 9; Length 446;
Best Local Similarity 23.3%; Pred. No. 6.8e-09;
RESULT 944
ID ADC40013 standard; protein; 409 AA.
DE Human activated protein C-related protein #2.
PN W02003075834-A2.
PD 18-SEP-2003.
PA (ELIL) LILLY & CO ELI.
Query Match 7.9%; Score 310.5; DB 7; Length 409;
Best Local Similarity 24.5%; Pred. No. 6.7e-09;
RESULT 945
ID ADC40012 standard; protein; 410 AA.
DE Human activated protein C-related protein #1.
PN W02003075834-A2.
PD 18-SEP-2003.
PA (ELIL) LILLY & CO ELI.
Query Match 7.9%; Score 310.5; DB 7; Length 410;
Best Local Similarity 24.5%; Pred. No. 6.7e-09;
RESULT 946
ID AAY56803 standard; protein; 415 AA.
DE Truncated human protein C polypeptide.
PN W09963070-A1.
PD 09-DEC-1999.
PA (ELIL) LILLY & CO ELI.
Query Match 7.9%; Score 310.5; DB 3; Length 415;
Best Local Similarity 24.5%; Pred. No. 6.8e-09;
RESULT 947
ID AAB82673 standard; protein; 419 AA.
DE Wild-type human protein C.
PN W0200157193-A2.
PD 09-AUG-2001.
PA (ELIL) LILLY & CO ELI.
Query Match 7.9%; Score 310.5; DB 4; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.9e-09;
RESULT 948
ID AAB36896 standard; protein; 419 AA.
DE Human protein C derivative 3.
PN W0200066754-A1.
PD 09-NOV-2000.

PA (ELIL) LILLY & CO ELI.
Query Match 7.9%; Score 310.5; DB 4; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.9e-09;
RESULT 949
ID AAB36894 standard; protein; 419 AA.
DE Human protein C derivative 1.
PN W0200066754-A1.
PD 09-NOV-2000.
PA (ELIL) LILLY & CO ELI.
Query Match 7.9%; Score 310.5; DB 4; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.9e-09;
RESULT 950
ID AAE08625 standard; protein; 419 AA.
DE Human mature wild type protein C.
PN W0200159084-A1.
PD 16-AUG-2001.
PA (ELIL) LILLY & CO ELI.
Query Match 7.9%; Score 310.5; DB 4; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.9e-09;
RESULT 951
ID AAU99063 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant R312N/R314S.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 310.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.9e-09;
RESULT 952
ID AAU99012 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant K192N/L194T.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 310.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.9e-09;
RESULT 953
ID AAU99050 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant S304N/R306T.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 310.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.9e-09;
RESULT 954
ID AAU99010 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant K191N/K193T.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 310.5; DB 5; Length 419;
Best Local Similarity 24.2%; Pred. No. 6.9e-09;
RESULT 955
ID AAU99040 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant T254N/N256T.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 310.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.9e-09;
RESULT 956
ID AAU99060 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant E309N/K311T.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 310.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.9e-09;

RESULT 957
ID AAU99055 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant E307N/E309S.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 310.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.9e-09;
RESULT 958
ID AAU99056 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant E307N/E309T.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 310.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.9e-09;
RESULT 959
ID AAU99059 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant E309N/K311S.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 310.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.9e-09;
RESULT 960
ID AAU99002 standard; protein; 419 AA.
DE Human Protein C zymogen protein.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 310.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.9e-09;
RESULT 961
ID AAU99051 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant S305N/E307S.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 310.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.9e-09;
RESULT 962
ID AAU99052 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant S305N/E307T.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 310.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.9e-09;
RESULT 963
ID ABR55547 standard; protein; 419 AA.
DE Amino acid sequence of mature human protein C (PC).
PN FR2831170-A1.
PD 25-APR-2003.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
Query Match 7.9%; Score 310.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.9e-09;
RESULT 964
ID ADC40014 standard; protein; 419 AA.
DE Human activated protein C-related protein #3.
PN W02003075834-A2.
PD 18-SEP-2003.
PA (ELIL) LILLY & CO ELI.
Query Match 7.9%; Score 310.5; DB 7; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.9e-09;
RESULT 965
ID ADO18786 standard; protein; 419 AA.
DE Mature human zymogen-like protein C.

PN WO200404190-A2.
PD 27-MAY-2004.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match
Best Local Similarity 7.9%; Score 310.5; DB 8; Length 419;
RESULT 966
ID ADM28521 standard; protein; 419 AA.
DE Human protein C.
PN WO200411385-A1.
PD 29-DEC-2004.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
PA (MAXY-) MAXYGEN APS.
Query Match
Best Local Similarity 7.9%; Score 310.5; DB 9; Length 419;
RESULT 967
ID ADY52283 standard; protein; 419 AA.
DE Human activated protein C (APC).
PN WO2005023308-A1.
PD 17-MAR-2005.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
PA (MAXY-) MAXYGEN APS.
Query Match
Best Local Similarity 7.9%; Score 310.5; DB 9; Length 419;
RESULT 968
ID AEH44147 standard; protein; 419 AA.
DE Human protein C analog with S3Y substitution.
PN WO2006044294-A2.
PD 27-APR-2006.
PA (ELIL) LILLY & CO ELI.
Query Match
Best Local Similarity 7.9%; Score 310.5; DB 10; Length 419;
RESULT 969
ID AEH44149 standard; protein; 419 AA.
DE Human protein C analog with L8W substitution.
PN WO2006044294-A2.
PD 27-APR-2006.
PA (ELIL) LILLY & CO ELI.
Query Match
Best Local Similarity 7.9%; Score 310.5; DB 10; Length 419;
RESULT 970
ID AEH44146 standard; protein; 419 AA.
DE Wild-type human protein C zymogen.
PN WO2006044294-A2.
PD 27-APR-2006.
PA (ELIL) LILLY & CO ELI.
Query Match
Best Local Similarity 7.9%; Score 310.5; DB 10; Length 419;
RESULT 971
ID AEH44148 standard; protein; 419 AA.
DE Human protein C analog with S3F substitution.
PN WO2006044294-A2.
PD 27-APR-2006.
PA (ELIL) LILLY & CO ELI.
Query Match
Best Local Similarity 7.9%; Score 310.5; DB 10; Length 419;
RESULT 972
ID AEH44154 standard; protein; 419 AA.
DE Human protein C analog with V375I substitution.
PN WO2006044294-A2.
PD 27-APR-2006.
PA (ELIL) LILLY & CO ELI.
Query Match
Best Local Similarity 7.9%; Score 310.5; DB 10; Length 419;
RESULT 973
ID ADG83834 standard; protein; 453 AA.
DE Mainland tiger snake venom protease.
PN WO2003082914-A1.
PD 09-OCT-2003.
PA (UYOU) UNIV QUEENSLAND.
Query Match
Best Local Similarity 7.9%; Score 310.5; DB 8; Length 453;
RESULT 974
ID AAR34295 standard; protein; 461 AA.
DE Sequence of human protein C.
PN JP63263083-A.
PD 31-OCT-1988.
PA (FARH) HOECHST JAPAN LTD.
Query Match
Best Local Similarity 7.9%; Score 310.5; DB 1; Length 460;
RESULT 975
ID AAM25086 standard; protein; 460 AA.
DE Human protein C.
PN WO9720043-A1.
PD 05-JUN-1997.
PA (ZYMO) ZYMOGENETICS INC.
PA (PPLT-) PPL THERAPEUTICS.
Query Match
Best Local Similarity 7.9%; Score 310.5; DB 2; Length 460;
RESULT 976
ID AAP60001 standard; protein; 461 AA.
DE Sequence of polypeptide with human protein C activity.
PN EP191606-A.
PD 20-AUG-1986.
PA (ELIL) LILLY & CO ELI.
Query Match
Best Local Similarity 7.9%; Score 310.5; DB 1; Length 461;
RESULT 977
ID AAP70855 standard; protein; 461 AA.
DE Human protein C.
PN EP215548-A.
PD 25-MAR-1987.
PA (ZYMO) ZYMOGENETICS INC.
PA (UNIW) UNIV WASHINGTON.
Query Match
Best Local Similarity 7.9%; Score 310.5; DB 1; Length 461;
RESULT 978
ID AAP90401 standard; protein; 461 AA.
DE Zymogen form of human protein C.
PN EP323149-A.
PD 05-JUL-1989.
PA (ELIL) LILLY & CO ELI.
Query Match
Best Local Similarity 7.9%; Score 310.5; DB 1; Length 461;
RESULT 979
ID AAR13622 standard; protein; 461 AA.
DE Human protein C.
PN WO9112320-A.
PD 22-AUG-1991.
PA (ZYMO) ZYMOGENETICS INC.
PA (TEIJ) TEIJIN LTD.
Query Match
Best Local Similarity 7.9%; Score 310.5; DB 2; Length 461;
RESULT 980
ID AAR13081 standard; protein; 461 AA.
DE Human protein C.
PN WO9109953-A.
PD 11-JUL-1991.
PA (ZYMO) ZYMOGENETICS INC.
Query Match
Best Local Similarity 7.9%; Score 310.5; DB 2; Length 461;
RESULT 981
ID AAR13074 standard; protein; 461 AA.
DE Protein C precursor.
PN WO9109951-A.
PD 11-JUL-1991.
PA (ZYMO) ZYMOGENETICS INC.
PA (TEIJ) TEIJIN LTD.
Query Match
Best Local Similarity 7.9%; Score 310.5; DB 2; Length 461;
RESULT 982
ID AAR34295 standard; protein; 461 AA.
DE Protein C.
PN JP05064588-A.
PD 19-MAR-1993.
PA (TEIJ) TEIJIN LTD.

ID AAP81104 standard; protein; 460 AA.
DE Sequence of human protein C.
PN JP63263083-A.
PD 31-OCT-1988.
PA (FARH) HOECHST JAPAN LTD.
Query Match
Best Local Similarity 7.9%; Score 310.5; DB 1; Length 460;
RESULT 975
ID AAM25086 standard; protein; 460 AA.
DE Human protein C.
PN WO9720043-A1.
PD 05-JUN-1997.
PA (ZYMO) ZYMOGENETICS INC.
PA (PPLT-) PPL THERAPEUTICS.
Query Match
Best Local Similarity 7.9%; Score 310.5; DB 2; Length 460;
RESULT 976
ID AAP60001 standard; protein; 461 AA.
DE Sequence of polypeptide with human protein C activity.
PN EP191606-A.
PD 20-AUG-1986.
PA (ELIL) LILLY & CO ELI.
Query Match
Best Local Similarity 7.9%; Score 310.5; DB 1; Length 461;
RESULT 977
ID AAP70855 standard; protein; 461 AA.
DE Human protein C.
PN EP215548-A.
PD 25-MAR-1987.
PA (ZYMO) ZYMOGENETICS INC.
PA (UNIW) UNIV WASHINGTON.
Query Match
Best Local Similarity 7.9%; Score 310.5; DB 1; Length 461;
RESULT 978
ID AAP90401 standard; protein; 461 AA.
DE Zymogen form of human protein C.
PN EP323149-A.
PD 05-JUL-1989.
PA (ELIL) LILLY & CO ELI.
Query Match
Best Local Similarity 7.9%; Score 310.5; DB 1; Length 461;
RESULT 979
ID AAR13622 standard; protein; 461 AA.
DE Human protein C.
PN WO9112320-A.
PD 22-AUG-1991.
PA (ZYMO) ZYMOGENETICS INC.
PA (TEIJ) TEIJIN LTD.
Query Match
Best Local Similarity 7.9%; Score 310.5; DB 2; Length 461;
RESULT 980
ID AAR13081 standard; protein; 461 AA.
DE Human protein C.
PN WO9109953-A.
PD 11-JUL-1991.
PA (ZYMO) ZYMOGENETICS INC.
Query Match
Best Local Similarity 7.9%; Score 310.5; DB 2; Length 461;
RESULT 981
ID AAR13074 standard; protein; 461 AA.
DE Protein C precursor.
PN WO9109951-A.
PD 11-JUL-1991.
PA (ZYMO) ZYMOGENETICS INC.
PA (TEIJ) TEIJIN LTD.
Query Match
Best Local Similarity 7.9%; Score 310.5; DB 2; Length 461;
RESULT 982
ID AAR34295 standard; protein; 461 AA.
DE Protein C.
PN JP05064588-A.
PD 19-MAR-1993.
PA (TEIJ) TEIJIN LTD.

Query Match
Best Local Similarity 7.9%; Score 310.5; DB 2; Length 461;
PA (MAXY-) MAXYGEN HOLDINGS LTD.
RESULT 983
ID AAW02600 standard; protein; 461 AA.
DE Human protein C.
PN US5516650-A.
PD 14-MAY-1996.
PA (ZYMO) ZYMOGENETICS INC.
Query Match
Best Local Similarity 7.9%; Score 310.5; DB 2; Length 461;
RESULT 984
ID AAY49561 standard; protein; 461 AA.
DE Human lecithin cholesterol acyltransferase protein sequence.
PN W0930454-A2.
PD 07-OCT-1999.
PA (WHEB) WHITEHEAD INST BIOMEDICAL RES.
Query Match
Best Local Similarity 7.9%; Score 310.5; DB 2; Length 461;
RESULT 985
ID AAB82674 standard; protein; 461 AA.
DE Wild-type human protein C.
PN W0200157193-A2.
PD 09-AUG-2001.
PA (BLIL) LILLY & CO ELI.
Query Match
Best Local Similarity 7.9%; Score 310.5; DB 4; Length 461;
RESULT 986
ID AAB36895 standard; protein; 461 AA.
DE Human protein C derivative 2.
PN W020006754-A1.
PD 09-NOV-2000.
PA (BLIL) LILLY & CO ELI.
Query Match
Best Local Similarity 7.9%; Score 310.5; DB 4; Length 461;
RESULT 987
ID AAB08626 standard; protein; 461 AA.
DE Human wild type protein C.
PN W0200159084-A1.
PD 16-AUG-2001.
PA (BLIL) LILLY & CO ELI.
Query Match
Best Local Similarity 7.9%; Score 310.5; DB 4; Length 461;
RESULT 988
ID AAU99001 standard; protein; 461 AA.
DE Human Protein C precursor protein.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match
Best Local Similarity 7.9%; Score 310.5; DB 5; Length 461;
RESULT 989
ID ADW77502 standard; protein; 461 AA.
DE Human protein C wild-type amino acid sequence.
PN W02003106666-A2.
PD 24-DEC-2003.
PA (MAXY-) MAXYGEN APS.
Query Match
Best Local Similarity 7.9%; Score 310.5; DB 8; Length 461;
RESULT 990
ID ADO18787 standard; protein; 461 AA.
DE Human zymogen-like protein C.
PN W02004044190-A2.
PD 27-MAY-2004.
PA (MAXY-) MAXYGEN APS.
Query Match
Best Local Similarity 7.9%; Score 310.5; DB 8; Length 461;
RESULT 991
ID ADW28520 standard; protein; 461 AA.
DE Human protein C precursor.
PN W02004113385-A1.
PD 29-DEC-2004.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match
Best Local Similarity 7.9%; Score 310.5; DB 9; Length 461;
RESULT 992
ID ADM28522 standard; protein; 461 AA.
DE Human protein C precursor 139R/K mutant.
PN W02004113385-A1.
PD 29-DEC-2004.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match
Best Local Similarity 7.9%; Score 310.5; DB 9; Length 461;
RESULT 993
ID AED96684 standard; protein; 461 AA.
DE Human C-reactive protein (CRP) associated marker SEQ ID NO 866.
PN W02005107364-A2.
PD 17-NOV-2005.
PA (COMP-) COMPUGEN LTD.
Query Match
Best Local Similarity 7.9%; Score 310.5; DB 9; Length 461;
RESULT 994
ID AEF72258 standard; protein; 461 AA.
DE Human target protein #99.
PN W02005119262-A2.
PD 15-DEC-2005.
PA (GALA-) GALAPAGOS GENOMICS NV.
Query Match
Best Local Similarity 7.9%; Score 310.5; DB 10; Length 461;
RESULT 995
ID AEG02811 standard; protein; 461 AA.
DE Human Protein C.
PN W02006018204-A1.
PD 23-FEB-2006.
PA (ZLBB-) ZLB BEHRING GMBH.
Query Match
Best Local Similarity 7.9%; Score 310.5; DB 10; Length 461;
RESULT 996
ID AEJ1612 standard; protein; 461 AA.
DE Human protein C.
PN W02006072137-A1.
PD 13-JUL-2006.
PA (NSYD-) NORTHERN SYDNEY & CENT COAST AREA HEALTH.
Query Match
Best Local Similarity 7.9%; Score 310.5; DB 10; Length 461;
RESULT 997
ID AEC01736 standard; protein; 506 AA.
DE PC-GPI cassette protein.
PN W02005073375-A1.
PD 11-AUG-2005.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match
Best Local Similarity 7.9%; Score 310.5; DB 9; Length 506;
RESULT 998
ID AEC01741 standard; protein; 507 AA.
DE PCUAC-GPI-4stop cassette.
PN W02005073375-A1.
PD 11-AUG-2005.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match
Best Local Similarity 7.9%; Score 310.5; DB 9; Length 507;
RESULT 999
ID AEC01737 standard; protein; 507 AA.
DE PC-UGAC-GPI-4stop cassette protein.
PN W02005073375-A1.
PD 11-AUG-2005.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match
Best Local Similarity 7.9%; Score 310.5; DB 9; Length 507;
RESULT 1000
ID AEC01737 standard; protein; 507 AA.
DE PC-UGAC-GPI-4stop cassette protein.
PN W02005073375-A1.
PD 11-AUG-2005.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match
Best Local Similarity 7.9%; Score 310.5; DB 9; Length 507;

```
Best Local Similarity 24.5%; Pred. No. 8.2e-09;
RESULT 1000
ID AER17219 standard; protein, 557 AA.
DE Human HMWCLRS_PEA_1_P22 protein.
PD WO2005072340-A2.
PD 11-AUG-2005.
PA (COMP-) COMPUGEN LTD.
PA (COMP-) COMPUGEN INC.
Query Match
Best Local Similarity 7.9%; Score 310.5; DB 10; Length 557;
RESULT 1001
ID AAB82676 standard; protein, 419 AA.
DE Human protein C derivative (S1IG/Q32E/N33D/L194S/T254S).
PD WO200157193-A2.
PD 09-AUG-2001.
PA (ELIL) LILLY & CO ELI.
Query Match
Best Local Similarity 7.9%; Score 310; DB 4; Length 419;
RESULT 1002
ID AAE08630 standard; protein, 419 AA.
DE Human protein C derivative #4.
PD WO200159084-A1.
PD 16-AUG-2001.
PA (ELIL) LILLY & CO ELI.
Query Match
Best Local Similarity 7.9%; Score 310; DB 4; Length 419;
RESULT 1003
ID AAR13538 standard; protein, 460 AA.
DE Human Protein C zymogen FN.
PD EP43875-A.
PD 28-AUG-1991.
PA (ELIL) LILLY & CO ELI.
Query Match
Best Local Similarity 7.9%; Score 310; DB 2; Length 460;
RESULT 1004
ID AAB36897 standard; protein, 419 AA.
DE Human protein C derivative 4.
PD WO200066754-A1.
PD 09-NOV-2000.
PA (ELIL) LILLY & CO ELI.
Query Match
Best Local Similarity 7.8%; Score 309.5; DB 4; Length 419;
RESULT 1005
ID AAB36898 standard; protein, 419 AA.
DE Human protein C derivative 5.
PD WO200066754-A1.
PD 09-NOV-2000.
PA (ELIL) LILLY & CO ELI.
Query Match
Best Local Similarity 7.8%; Score 309.5; DB 4; Length 419;
RESULT 1006
ID AAU99018 standard; protein, 419 AA.
DE Human Protein C zymogen protein mutant E215N/K217T.
PD WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match
Best Local Similarity 7.8%; Score 309.5; DB 5; Length 419;
RESULT 1007
ID AAU99013 standard; protein, 419 AA.
DE Human Protein C zymogen protein mutant K251N.
PD WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match
Best Local Similarity 7.8%; Score 309.5; DB 5; Length 419;
RESULT 1008
ID AAU99013 standard; protein, 419 AA.
DE Human Protein C zymogen protein mutant K193N/A195S.
PD WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match
Best Local Similarity 7.8%; Score 309.5; DB 5; Length 419;
RESULT 1009
ID AAU99068 standard; protein, 419 AA.
DE Human Protein C zymogen protein mutant F316N/L318T.
PD WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match
Best Local Similarity 7.8%; Score 309.5; DB 5; Length 419;
RESULT 1010
ID AAU99062 standard; protein, 419 AA.
DE Human Protein C zymogen protein mutant A310N/R312T.
PD WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match
Best Local Similarity 7.8%; Score 309.5; DB 5; Length 419;
RESULT 1011
ID AAU99020 standard; protein, 419 AA.
DE Human Protein C zymogen protein mutant S216N/K218T.
PD WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match
Best Local Similarity 7.8%; Score 309.5; DB 5; Length 419;
RESULT 1012
ID AAU99035 standard; protein, 419 AA.
DE Human Protein C zymogen protein mutant S252N.
PD WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match
Best Local Similarity 7.8%; Score 309.5; DB 5; Length 419;
RESULT 1013
ID AAU99085 standard; protein, 419 AA.
DE Human Protein C zymogen protein mutant E357N/D359S.
PD WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match
Best Local Similarity 7.8%; Score 309.5; DB 5; Length 419;
RESULT 1014
ID AAU99058 standard; protein, 419 AA.
DE Human Protein C zymogen protein mutant K308N/A310T.
PD WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match
Best Local Similarity 7.8%; Score 309.5; DB 5; Length 419;
RESULT 1015
ID AAU99019 standard; protein, 419 AA.
DE Human Protein C zymogen protein mutant S216N/K218S.
PD WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match
Best Local Similarity 7.8%; Score 309.5; DB 5; Length 419;
RESULT 1016
ID AAU99094 standard; protein, 419 AA.
DE Human Protein C zymogen protein mutant H388N/Y390T.
PD WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
```


PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.8%; Score 309.5; DB 5; Length 419;
Best Local Similarity 24.7%; Pred. No. 7.8e-09;
RESULT 1017
ID AAU99089 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant L386N/H388S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.8%; Score 309.5; DB 5; Length 419;
Best Local Similarity 24.8%; Pred. No. 7.8e-09;
RESULT 1018
ID AEH44153 standard; protein; 419 AA.
DE Human protein C analog with Q353R substitution.
PN WO2006044294-A2.
PD 27-APR-2006.
PA (ELIL) LILLY & CO ELI.
Query Match 7.8%; Score 309.5; DB 10; Length 419;
Best Local Similarity 24.5%; Pred. No. 7.8e-09;
RESULT 1019
ID AAP90070 standard; protein; 461 AA.
DE Human protein C.
PN EP31312-A.
PD 07-JUN-1989.
PA (ELIL) LILLY & CO ELI.
Query Match 7.8%; Score 309.5; DB 1; Length 461;
Best Local Similarity 24.5%; Pred. No. 8.5e-09;
RESULT 1020
ID AAR13540 standard; protein; 461 AA.
DE Human Protein C zymogen FLIN.
PN EP443875-A.
PD 28-AUG-1991.
PA (ELIL) LILLY & CO ELI.
Query Match 7.8%; Score 309.5; DB 2; Length 461;
Best Local Similarity 24.5%; Pred. No. 8.5e-09;
RESULT 1021
ID ADI16874 standard; protein; 799 AA.
DE Murine NOVX protein homologue SegID 410.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 7.8%; Score 309.5; DB 5; Length 799;
Best Local Similarity 21.6%; Pred. No. 1.4e-08;
RESULT 1022
ID ADI16880 standard; protein; 799 AA.
DE Murine NOVX protein homologue SegID 416.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 7.8%; Score 309.5; DB 5; Length 799;
Best Local Similarity 21.6%; Pred. No. 1.4e-08;
RESULT 1023
ID AAE08627 standard; protein; 419 AA.
DE Human protein C derivative #1.
PN WO200159084-A1.
PD 16-AUG-2001.
PA (ELIL) LILLY & CO ELI.
Query Match 7.8%; Score 309; DB 4; Length 419;
Best Local Similarity 24.5%; Pred. No. 8.3e-09;
RESULT 1024
ID AAE08629 standard; protein; 419 AA.
DE Human protein C derivative #3.
PN WO200159084-A1.
PD 16-AUG-2001.
PA (ELIL) LILLY & CO ELI.
Query Match 7.8%; Score 309; DB 4; Length 419;
Best Local Similarity 24.5%; Pred. No. 8.3e-09;
RESULT 1025
ID AAU99049 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant S304N/R306S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (ELIL) LILLY & CO ELI.

PA (MAXY-) MAXYGEN APS.
Query Match 7.8%; Score 308.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 8.8e-09;
RESULT 1026
ID AAU99061 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant A310N/R312S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.8%; Score 308.5; DB 5; Length 419;
Best Local Similarity 24.1%; Pred. No. 8.8e-09;
RESULT 1027
ID AAU99090 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant L386N/H388T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.8%; Score 308.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 8.8e-09;
RESULT 1028
ID AAU99086 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant E357N/D359T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.8%; Score 308.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 8.8e-09;
RESULT 1029
ID AAU99036 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant S252N/T254S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.8%; Score 308.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 8.8e-09;
RESULT 1030
ID AAU99045 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant Y302N.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.8%; Score 308.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 8.8e-09;
RESULT 1031
ID AAU99034 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant K251N/T253S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.8%; Score 308.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 8.8e-09;
RESULT 1032
ID ADM77506 standard; protein; 461 AA.
DE Human protein C variant #4 amino acid sequence.
PN WO200310666-A2.
PD 24-DEC-2003.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.8%; Score 308.5; DB 8; Length 461;
Best Local Similarity 24.5%; Pred. No. 9.6e-09;
RESULT 1033
ID AAE08628 standard; protein; 419 AA.
DE Human protein C derivative #2.
PN WO200159084-A1.
PD 16-AUG-2001.
PA (ELIL) LILLY & CO ELI.

Query Match 7.8%; Score 308; DB 4; Length 419;
Best Local Similarity 24.5%; Pred. No. 9.4e-09;
RESULT 1034
ID AAU99084 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant R352N/D354T.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.8%; Score 307.5; DB 5; Length 419;
Best Local Similarity 24.6%; Pred. No. 1e-08;
RESULT 1035
ID AAU99021 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant K217N/L219S.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.8%; Score 307.5; DB 5; Length 419;
Best Local Similarity 24.4%; Pred. No. 1e-08;
RESULT 1036
ID AAU99046 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant Y302N/S304T.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.8%; Score 307.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 1e-08;
RESULT 1037
ID AAU99093 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant H388N/Y390S.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.8%; Score 307.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 1e-08;
RESULT 1038
ID AAU99083 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant R352N/D354S.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.8%; Score 306.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 1.1e-08;
RESULT 1039
ID AAU99074 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant V339T.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.8%; Score 306.5; DB 5; Length 419;
Best Local Similarity 24.4%; Pred. No. 1.1e-08;
RESULT 1040
ID AAU99003 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant D172N/K174S.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.8%; Score 306.5; DB 5; Length 419;
Best Local Similarity 24.4%; Pred. No. 1.1e-08;
RESULT 1041
ID A6H44152 standard; protein; 419 AA.
DE Human protein C analog with N13K substitution.
PN W02006044294-A2.
PD 27-APR-2006.
PA (ELIL) LILLY & CO ELI.
Query Match 7.8%; Score 306.5; DB 10; Length 419;
Best Local Similarity 24.1%; Pred. No. 1.1e-08;

RESULT 1042
ID AAR13585 standard; protein; 461 AA.
DE Human Protein C zymogen Q313.
PN EP443874-A.
PD 28-AUG-1991.
PA (ELIL) LILLY & CO ELI.
Query Match 7.8%; Score 306.5; DB 2; Length 461;
Best Local Similarity 24.1%; Pred. No. 1.2e-08;
RESULT 1043
ID A6M83654 standard; protein; 495 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:3903.
PN W02004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 7.8%; Score 306.5; DB 8; Length 495;
Best Local Similarity 24.8%; Pred. No. 1.3e-08;
RESULT 1044
ID A6D96686 standard; protein; 495 AA.
DE Human C-reactive protein (CRP) associated marker SEQ ID NO 868.
PN W02005107364-A2.
PD 17-NOV-2005.
PA (COMP-) COMPUEN LTD.
PA (COHE/) COHEN Y.
Query Match 7.8%; Score 306.5; DB 9; Length 495;
Best Local Similarity 24.8%; Pred. No. 1.3e-08;
RESULT 1045
ID AAU99004 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant D172N/K174T.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.7%; Score 305.5; DB 5; Length 419;
Best Local Similarity 24.4%; Pred. No. 1.3e-08;
RESULT 1046
ID AAU99073 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant V339S.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.7%; Score 305.5; DB 5; Length 419;
Best Local Similarity 24.4%; Pred. No. 1.3e-08;
RESULT 1047
ID A6H44150 standard; protein; 419 AA.
DE Human protein C analog with Q32M substitution.
PN W02006044294-A2.
PD 27-APR-2006.
PA (ELIL) LILLY & CO ELI.
Query Match 7.7%; Score 305.5; DB 10; Length 419;
Best Local Similarity 24.4%; Pred. No. 1.3e-08;
RESULT 1048
ID A6X20109 standard; protein; 667 AA.
DE Novel human polypeptide SEQ ID NO 803.
PN W02005049806-A2.
PD 02-JUN-2005.
PA (NUVE-) NUVELO INC.
Query Match 7.7%; Score 305; DB 9; Length 667;
Best Local Similarity 20.8%; Pred. No. 2.1e-08;
RESULT 1049
ID A6G02812 standard; protein; 419 AA.
DE Mature Protein C polypeptide.
PN W02006018204-A1.
PD 23-FEB-2006.
PA (ZLBB-) ZLB BEHRING GMBH.
Query Match 7.7%; Score 304.5; DB 10; Length 419;
Best Local Similarity 24.9%; Pred. No. 1.4e-08;
RESULT 1050
ID AAR13582 standard; protein; 461 AA.
DE Human protein C zymogen Q097.
PN EP443874-A.
PD 28-AUG-1991.
PA (ELIL) LILLY & CO ELI.

Query Match 7.7%; Score 304.5; DB 2; Length 461;
Best Local Similarity 24.4%; Pred. No. 1.6e-08;
RESULT 1051
ID AAR13584 standard; protein; 461 AA.
DE Human protein C zymogen Q248.
PN EP43874-A.
PD 28-AUG-1991.
PA (ELIL) LILLY & CO ELI.
Query Match 7.7%; Score 304.5; DB 2; Length 461;
Best Local Similarity 24.4%; Pred. No. 1.6e-08;
RESULT 1052
ID AAU99037 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant T253N/D255S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.7%; Score 302.5; DB 5; Length 419;
Best Local Similarity 24.4%; Pred. No. 1.9e-08;
RESULT 1053
ID AAU99028 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant V243N/V245T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.7%; Score 302.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 1.9e-08;
RESULT 1054
ID AAU99027 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant V243N/V245S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.6%; Score 301.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 2.1e-08;
RESULT 1055
ID AAU99038 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant T253N/D255T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.6%; Score 301.5; DB 5; Length 419;
Best Local Similarity 24.4%; Pred. No. 2.1e-08;
RESULT 1056
ID AAP93714 standard; protein; 461 AA.
DE Hybrid protein of protein-C and Factor-X.
PN EP296413-A.
PD 28-DEC-1988.
PA (FARK) HOECHST JAPAN LTD.
Query Match 7.6%; Score 301.5; DB 1; Length 461;
Best Local Similarity 24.7%; Pred. No. 2.3e-08;
RESULT 1057
ID ADX3909 standard; protein; 681 AA.
DE Mouse factor VII mutant.
PN WO2005014775-A2.
PD 17-FEB-2005.
PA (UYFL) UNIV FLORIDA RES FOUND INC.
Query Match 7.6%; Score 301.5; DB 9; Length 681;
Best Local Similarity 22.3%; Pred. No. 3.3e-08;
RESULT 1058
ID ADX39094 standard; protein; 446 AA.
DE Mouse factor VII.
PN WO2005014775-A2.
PD 17-FEB-2005.
PA (UYFL) UNIV FLORIDA RES FOUND INC.
Query Match 7.6%; Score 300.5; DB 9; Length 446;
Best Local Similarity 22.3%; Pred. No. 2.5e-08;
RESULT 1059
ID AAU99041 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant D255N/D257S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.6%; Score 299.5; DB 5; Length 419;
Best Local Similarity 24.2%; Pred. No. 2.7e-08;
RESULT 1060
ID ADX39097 standard; protein; 443 AA.
DE Rabbit factor VII.
PN WO2005014775-A2.
PD 17-FEB-2005.
PA (UYFL) UNIV FLORIDA RES FOUND INC.
Query Match 7.6%; Score 299.5; DB 9; Length 443;
Best Local Similarity 24.0%; Pred. No. 2.8e-08;
RESULT 1061
ID AAU99029 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant V245N/P247S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.6%; Score 298.5; DB 5; Length 419;
Best Local Similarity 24.4%; Pred. No. 3e-08;
RESULT 1062
ID AAU99030 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant V245N/P247T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.6%; Score 298.5; DB 5; Length 419;
Best Local Similarity 24.4%; Pred. No. 3e-08;
RESULT 1063
ID AAU99042 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant D255N/D257T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.6%; Score 298.5; DB 5; Length 419;
Best Local Similarity 24.2%; Pred. No. 3e-08;
RESULT 1064
ID ADX39092 standard; protein; 433 AA.
DE Danio factor VII.
PN WO2005014775-A2.
PD 17-FEB-2005.
PA (UYFL) UNIV FLORIDA RES FOUND INC.
Query Match 7.6%; Score 298.5; DB 9; Length 433;
Best Local Similarity 23.0%; Pred. No. 3.1e-08;
RESULT 1065
ID ADB65750 standard; protein; 397 AA.
DE Human protein encoded by clone UTERU20087070.
PN EP1308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
Query Match 7.6%; Score 298; DB 7; Length 397;
Best Local Similarity 24.1%; Pred. No. 3.1e-08;
RESULT 1066
ID AEL57571 standard; protein; 543 AA.
DE Human t-Plasminogen activator precursor, SEQ ID NO: 2034.
PN US2006216722-A1.
PD 28-SEP-2006.
PA (BETS/) BETSHOLTZ C.
PA (TRYG/) TRYGVASON K.
PA (TRAK/) TAKEMOTO M.
PA (HELI/) HE L.
PA (PATR/) PATRAKAS J.
Query Match 7.5%; Score 297.5; DB 10; Length 543;
Best Local Similarity 23.0%; Pred. No. 4.4e-08;
RESULT 1067
ID ADL1268 standard; protein; 230 AA.
DE Polypeptide homologous to a human NOVX domain SegID 804.

PN W0200268649-A2.
PA (CURA-) CURAGEN CORP.
Query Match 7.5%; Score 296; DB 5; Length 230;
Best Local Similarity 32.3%; Pred. No. 2.4e-08;
RESULT 1068
ID AD117276 standard; protein; 230 AA.
DE Polypeptide homologous to a human NOVX domain Segid 812.
PN W0200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 7.5%; Score 296; DB 5; Length 230;
Best Local Similarity 32.3%; Pred. No. 2.4e-08;
RESULT 1069
ID ADJ83075 standard; protein; 230 AA.
DE Trypsin-like serine protease protein - SEQ ID 66.
PN US2003170630-A1.
PD 11-SEP-2003.
PA (ALSO-) ALSOOROOK J P.
PA (TCHE-) TCHERNEV V T.
PA (LIUX-) LIU X.
PA (SPYT-) SPYTEK K A.
PA (ZERH-) ZERHUSEN B D.
PA (PATY-) PATTURAJAN M.
PA (LEPL-) LEPLEY D M.
PA (BURG-) BURGESS C E.
PA (SHIM-) SHIMKETS R A.
PA (GROS-) GROSSE W M.
PA (SZEK-) SZEKERES E S.
PA (VERN-) VERNET C A M.
PA (LILF-) LI L.
PA (CASW-) CASMAN S J.
PA (BOLD-) BOLDOG F L.
PA (GORM-) GORMAN L.
PA (GANG-) GANGOULI E A.
PA (FERN-) FERNANDES E R.
PA (RIEG-) RIEGER D K.
PA (EDIN-) EDINGER S R.
PA (GUNT-) GUNTHER E.
PA (MILT-) MILLET I.
PA (SCIO-) SCIORE P.
PA (ELLE-) ELLERMAN K.
PA (MACD-) MACDOUGALL J R.
PA (SMIT-) SMITHSON G.
Query Match 7.5%; Score 296; DB 7; Length 230;
Best Local Similarity 32.3%; Pred. No. 2.4e-08;
RESULT 1070
ID AEF27705 standard; protein; 230 AA.
DE Trypsin-like serine protease consensus sequence, SEQ.135.
PN US200609634-A1.
PD 12-JAN-2006.
PA (KEKU-) KEKUDA R.
PA (ALSO-) ALSOOROOK J.
PA (TCHE-) TCHERNEV V.
PA (LIUX-) LIU X.
PA (SPYT-) SPYTEK K.
PA (PATY-) PATTURAJAN M.
PA (GROS-) GROSSE W.
PA (LEPL-) LEPLEY D.
PA (BURG-) BURGESS C.
PA (VERN-) VERNET C.
PA (LILF-) LI L.
PA (GORM-) GORMAN L.
PA (EDIN-) EDINGER S.
PA (SCIO-) SCIORE P.
PA (ELLE-) ELLERMAN K.
PA (MALY-) MALYANKAR U.
PA (ROTH-) ROTHENBERG M.
PA (STON-) STONE D.
PA (BOLD-) BOLDOG F.
PA (GUOX-) GUO X.
PA (SHEN-) SHENY S.
PA (ANDE-) ANDERSON D.

PA (PADI-) PADIGARU M.
PA (TAUP-) TAUPIER R.
PA (MILT-) MILLER C.
PA (RISE-) EISEN A.
Query Match 7.5%; Score 296; DB 10; Length 230;
Best Local Similarity 32.3%; Pred. No. 2.4e-08;
RESULT 1071
ID AEG02859 standard; protein; 451 AA.
DE Factor VII/X fusion protein SEQ ID NO:53.
PN W02006018204-A1.
PD 23-FEB-2006.
PA (ZLIB-) ZLB BEHRING GMBH.
Query Match 7.5%; Score 296; DB 10; Length 451;
Best Local Similarity 25.2%; Pred. No. 4.4e-08;
RESULT 1072
ID ADM64351 standard; protein; 527 AA.
DE Mutant human plasminogen activator protein - SEQ ID 3.
PN CN1526726-A.
PD 08-SEP-2004.
PA (LIBA-) LI B.
Query Match 7.5%; Score 296; DB 8; Length 527;
Best Local Similarity 23.4%; Pred. No. 5.1e-08;
RESULT 1073
ID ABE21442 standard; protein; 932 AA.
DE Novel human diagnostic protein #21433.
PN W0200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 7.5%; Score 296; DB 4; Length 932;
Best Local Similarity 21.4%; Pred. No. 8.8e-08;
RESULT 1074
ID ADX39096 standard; protein; 425 AA.
DE Chicken factor VII.
PN W02005014775-A2.
PD 17-FEB-2005.
PA (UVFL-) UNIV FLORIDA RES FOUND INC.
Query Match 7.5%; Score 295; DB 9; Length 425;
Best Local Similarity 23.4%; Pred. No. 4.8e-08;
RESULT 1075
ID AAR09290 standard; protein; 562 AA.
DE Sequence of tissue plasminogen activator analogue Gr6 (Ileu 66, Asp 67, Thr 68, Gln 117).
PN W08912681-A.
PD 28-DEC-1989.
PA (BRBI-) BRIT BIO-TECHN LTD.
Query Match 7.5%; Score 294; DB 2; Length 562;
Best Local Similarity 23.3%; Pred. No. 7e-08;
RESULT 1076
ID ADX39099 standard; protein; 407 AA.
DE Bovine factor VII.
PN W02005014775-A2.
PD 17-FEB-2005.
PA (UVFL-) UNIV FLORIDA RES FOUND INC.
Query Match 7.4%; Score 293.5; DB 9; Length 407;
Best Local Similarity 24.1%; Pred. No. 5.5e-08;
RESULT 1077
ID ABU12065 standard; protein; 986 AA.
DE Human NOV12a CG92293-01 protein SEQ ID 50.
PN W0200281625-A2.
PD 17-OCT-2002.
PA (CURA-) CURAGEN CORP.
Query Match 7.4%; Score 293; DB 6; Length 986;
Best Local Similarity 21.8%; Pred. No. 1.3e-07;
RESULT 1078
ID AAR70903 standard; protein; 527 AA.
DE Human c-pa variant (N103,A432,A434).
PN US5385732-A.
PD 31-JAN-1995.
PA (GERTH-) GENENTECH INC.
Query Match 7.4%; Score 292; DB 2; Length 527;
Best Local Similarity 23.4%; Pred. No. 8.4e-08;
RESULT 1079
ID AAR70895 standard; protein; 527 AA.

DE Human t-PA variant (N103,A331,A332) .
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.4%; Score 292; DB 2; Length 527;
RESULT 1080
ID ADM03787 standard; protein; 516 AA.
DE Antisporadic protein sequence #90.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.4%; Score 291.5; DB 8; Length 516;
RESULT 1081
ID ABM80985 standard; protein; 516 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO81669, SEQ:2539.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.4%; Score 291.5; DB 8; Length 516;
RESULT 1082
ID ADQ3246 standard; protein; 516 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 909.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPIERA CORP.
Query Match
Best Local Similarity 7.4%; Score 291.5; DB 8; Length 516;
RESULT 1083
ID ABL57575 standard; protein; 516 AA.
DE Human t-plasminogen activator precursor, SEQ ID NO: 2038.
PN US2006216722-A1.
PD 28-SEP-2006.
PA (BETS/) BETSHOLTZ C.
PA (TRYG/) TRYGVASON K.
PA (TAKE/) TAKEMOTO M.
PA (HELL/) HE L.
PA (PATR/) PATRAKAS J.
Query Match
Best Local Similarity 7.4%; Score 291.5; DB 10; Length 516;
RESULT 1084
ID AAR13921 standard; protein; 522 AA.
DE Delta (466-470) tPA variant with H432A and R434A substns.
PN WO91133149-A.
PD 05-SEP-1991.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.4%; Score 291.5; DB 2; Length 522;
RESULT 1085
ID AAP70475 standard; protein; 564 AA.
DE Sequence of tissue plasminogen (TPA) analogue.
PN WO8703906-A.
PD 02-JUL-1987.
PA (URJO) UPJOHN CO.
PA (MARO/) MAROTTI K R.
Query Match
Best Local Similarity 7.4%; Score 291.5; DB 1; Length 564;
RESULT 1086
ID ADG838 standard; protein; 376 AA.
DE Rough scale snake venom prothrombin activator, trocarin.
PN WO2003082914-A1.
PD 09-OCT-2003.
PA (UYOU) UNIV QUEENSLAND.
Query Match
Best Local Similarity 7.4%; Score 291; DB 8; Length 376;
RESULT 1087
ID AAP6614 standard; protein; 516 AA.
DE Plasmid pDAF3 encoded sequence.
PN JP61139386-A.
PD 26-JUN-1986.
PA (TOYJ) TOYO SODA MFG CO LTD.

PA (SAGA) SAGAMI CHEM RES CENTRE.
PA (CENG) CENTRAL GLASS CO LTD.
PA (HODO) HODOGAYA CHEM IND CO LTD.
Query Match
Best Local Similarity 7.4%; Score 290.5; DB 1; Length 516;
RESULT 1088
ID AAP70257 standard; protein; 516 AA.
DE Sequence of human tissue plasminogen activator (TPA) and leader.
PN EP231883-A.
PD 12-AUG-1987.
PA (SAGA) SAGAMI CHEM RES CENTRE.
PA (NIPS) NIPPON SODA CO.
PA (CENG) CENTRAL GLASS CO LTD.
PA (TOYJ) TOYO SODA MFG CO LTD.
PA (NISC) NISSAN CHEM IND LTD.
PA (NISC) NISSAN CHEMICAL INDS KK.
Query Match
Best Local Similarity 7.4%; Score 290.5; DB 1; Length 516;
RESULT 1089
ID AAR70878 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N103,D184,E275,1277) .
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.4%; Score 290; DB 2; Length 483;
RESULT 1090
ID AAR70885 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N103,D184,E275,1277) .
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.4%; Score 290; DB 2; Length 483;
RESULT 1091
ID AAR70894 standard; protein; 527 AA.
DE Human t-PA variant (N103,A303,A304) .
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.4%; Score 290; DB 2; Length 527;
RESULT 1092
ID ADM64350 standard; protein; 527 AA.
DE Mutant human plasminogen activator protein - SEQ ID 2.
PN CN1526726-A.
PD 08-SEP-2004.
PA (LIBB/) LI B.
Query Match
Best Local Similarity 7.4%; Score 290; DB 8; Length 527;
RESULT 1093
ID ADL00357 standard; protein; 520 AA.
DE Human tissue type plasminogen activator (h-tPA) mutant polypeptide.
PN CN1397564-A.
PD 19-FEB-2003.
PA (LIBB/) LI B.
Query Match
Best Local Similarity 7.3%; Score 289.5; DB 7; Length 520;
RESULT 1094
ID AAR12340 standard; protein; 559 AA.
DE 7-PA variant contg. fibronectin for thrombolytic lysis (1) .
PN JP03061482-A.
PD 18-MAR-1991.
PA (FUJI) FUJISAWA PHARM CO LTD.
Query Match
Best Local Similarity 7.3%; Score 289.5; DB 2; Length 559;
RESULT 1095
ID AAR22664 standard; protein; 564 AA.
DE tPA analogue KK2A.
PN US5106741-A.
PD 21-APR-1992.
PA (URJO) UPJOHN CO.
Query Match
Best Local Similarity 7.3%; Score 289.5; DB 2; Length 564;

Best Local Similarity 23.4%; Pred. No. 1.2e-07;
RESULT 1096
ID AAE06934 standard; protein; 658 AA.
DE Human membrane-type serine protease (MTSP) 4-S splice variant.
PN W0200157194-A2.
PD 09-AUG-2001.
PA (CORV-) CORVAS INT INC.
Query Match 7.3%; Score 289.5; DB 4; Length 658;
Best Local Similarity 22.7%; Pred. No. 1.4e-07;
RESULT 1097
ID AD110379 standard; protein; 658 AA.
DE Human cell surface protease #5.
PN W0200295007-A2.
PD 28-NOV-2002.
PA (CORV-) CORVAS INT INC.
Query Match 7.3%; Score 289.5; DB 7; Length 658;
Best Local Similarity 22.7%; Pred. No. 1.4e-07;
RESULT 1098
ID ADJ46903 standard; protein; 658 AA.
DE Human transmembrane serine protease (MTSP) polypeptide #5.
PN US2004001801-A1.
PD 01-JAN-2004.
PA (CORV-) CORVAS INT INC.
Query Match 7.3%; Score 289.5; DB 8; Length 658;
Best Local Similarity 22.7%; Pred. No. 1.4e-07;
RESULT 1099
ID AAE06933 standard; protein; 802 AA.
DE Human membrane-type serine protease (MTSP) 4-L splice variant.
PN W0200157194-A2.
PD 03-AUG-2001.
PA (CORV-) CORVAS INT INC.
Query Match 7.3%; Score 289.5; DB 4; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.7e-07;
RESULT 1100
ID AD110377 standard; protein; 802 AA.
DE Human cell surface protease #4.
PN W0200295007-A2.
PD 28-NOV-2002.
PA (CORV-) CORVAS INT INC.
Query Match 7.3%; Score 289.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.7e-07;
RESULT 1101
ID ADJ46901 standard; protein; 802 AA.
DE Human transmembrane serine protease (MTSP) polypeptide #4.
PN US2004001801-A1.
PD 01-JAN-2004.
PA (CORV-) CORVAS INT INC.
Query Match 7.3%; Score 289.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.7e-07;
RESULT 1102
ID AAR21598 standard; protein; 527 AA.
DE rPA variant - T103N, D236A, D238A, K240A.
PN W09202612-A.
PD 20-FEB-1992.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 289; DB 2; Length 527;
Best Local Similarity 23.4%; Pred. No. 1.2e-07;
RESULT 1103
ID AAR09217 standard; protein; 529 AA.
DE c-PA insertion variant I304 HH.
PN W09002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 289; DB 2; Length 529;
Best Local Similarity 23.4%; Pred. No. 1.2e-07;
RESULT 1104
ID AAB85076 standard; peptide; 296 AA.
DE Amino acid sequence of MASP-1 polypeptide.
PN W0200140451-A2.
PD 07-JUN-2001.
PA (JENS/) JENSENIUS J C.
PA (THIE/) THIEL S.
Query Match 7.3%; Score 288.5; DB 4; Length 296;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;

Best Local Similarity 29.3%; Pred. No. 7.6e-08;
RESULT 1105
ID AAY41710 standard; protein; 802 AA.
DE Human PRO618 protein sequence.
PN W09946281-A2.
PD 16-SEP-1999.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 2; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1106
ID AAB44266 standard; protein; 802 AA.
DE Human PRO618 (UNQ354) protein sequence SEQ ID NO:169.
PN W0200053756-A2.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 3; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1107
ID AAB24052 standard; protein; 802 AA.
DE Human PRO618 protein sequence SEQ ID NO:24.
PN W0200053754-A1.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 3; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1108
ID AAU82755 standard; protein; 802 AA.
DE Amino acid sequence of novel human protease #54.
PN W0200200860-A2.
PD 03-JAN-2002.
PA (SUGE-) SUGEN INC.
Query Match 7.3%; Score 288.5; DB 5; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1109
ID ABO25212 standard; protein; 802 AA.
DE Novel human secreted and transmembrane protein PRO618.
PN US2003050239-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 6; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1110
ID ABU72218 standard; protein; 802 AA.
DE Novel human secreted and transmembrane protein PRO618.
PN US2002192706-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 6; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1111
ID ABU84898 standard; protein; 802 AA.
DE Human secreted and transmembrane polypeptide PRO618.
PN US2002177553-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 6; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1112
ID ABU61096 standard; protein; 802 AA.
DE Human PRO618 polypeptide.
PN US2002169284-A1.
PD 14-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 6; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1113
ID ABU80365 standard; protein; 802 AA.
DE Human secreted/transmembrane protein PRO618.
PN US2003004102-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 6; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;

RESULT 1114
ID ADA24708 standard; protein; 802 AA.
DE Novel human secreted and transmembrane protein PRO618.
PN US2003050241-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 6; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1115
ID ABO19667 standard; protein; 802 AA.
DE Novel human secreted and transmembrane protein PRO618.
PN US2003050240-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 6; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1116
ID ADA12369 standard; protein; 802 AA.
DE Human secreted/transmembrane polypeptide PRO618.
PN US2003055216-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 6; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1117
ID ABO19558 standard; protein; 802 AA.
DE Novel human secreted and transmembrane polypeptide #26.
PN US2003049633-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 6; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1118
ID ADB73675 standard; protein; 802 AA.
DE Human PRO polypeptide #26.
PN US2003045462-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1119
ID ADB76391 standard; protein; 802 AA.
DE Human PRO polypeptide #26.
PN US2003083248-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1120
ID ADC43817 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003054986-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1121
ID ADC61577 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003049684-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1122
ID ADC63541 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003054405-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1123
ID ADC66641 standard; protein; 802 AA.

DE Human secreted/transmembrane protein, PRO618.
PN US2003060406-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1124
ID ADC68765 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003064407-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1125
ID ADC62825 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003068648-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1126
ID ADC67890 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003068178-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1127
ID ADC41210 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003072745-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1128
ID ADC67265 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003073131-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1129
ID ADC62201 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003073624-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1130
ID ADC41834 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003104998-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1131
ID ADE49203 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003096744-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1132
ID ADE35257 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.

PN US2003203434-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1133
ID ADE16371 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003203435-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1134
ID ADD72986 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003203436-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1135
ID ADD72344 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003194781-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1136
ID ADE16995 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003203433-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1137
ID ADF47009 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003195333-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1138
ID ADF32766 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003216561-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1139
ID ADG60086 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003206915-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1140
ID ADI60846 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003077700-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1141
ID ADE48503 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003104536-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1142
ID ADE89604 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US200310181-A1.
PD 10-JUL-2003.
PA (ASHK/) ASHKENAZI A J.
PA (BAKE/) BAKER K P.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GIRM/) GIRMALDI J C.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (KUOS/) KUO S S.
PA (NAPI/) NAPIER M A.
PA (PANU/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (SHEL/) SHELTON D L.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1143
ID ADF61244 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003195345-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1144
ID ADF39936 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003198994-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1145
ID ADF45732 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003195148-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1146
ID ADF24128 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003204055-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1147
ID ADF40560 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.

PN US2003199021-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1148
ID ADF23504 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003203402-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1149
ID ADF33487 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003194780-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1150
ID ADF26954 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003199436-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1151
ID ADF27590 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003199437-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1152
ID ADF4184 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003199435-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1153
ID ADF32863 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003211091-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1154
ID ADF25229 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003211092-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1155
ID ADF26330 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003199674-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1156
ID ADF34119 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003194410-A1.

PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1157
ID ADF46356 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003195344-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1158
ID ADG50342 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003207803-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1159
ID ADG49718 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003215905-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1160
ID ADG51590 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003215908-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1161
ID ADG49094 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003216305-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1162
ID ADG48470 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003216560-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1163
ID ADG50966 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2004005312-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1164
ID ADG58910 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2004005657-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1165
ID ADG62366 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2004006219-A1.
PD 08-JAN-2004.

PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1166
ID ADH25391 standard; protein; 802 AA.
DE Human neurotrophin homologue related protein sequence SEQ ID NO:169.
PN EP1386931-A1.
PD 04-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1167
ID ADM17168 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2004048332-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1168
ID ADL07002 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2004063921-A1.
PD 01-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1169
ID ADT91615 standard; protein; 802 AA.
DE Human PRO618 protein sequence.
PN AU2002317529-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1170
ID ADU50124 standard; protein; 802 AA.
DE PRO618, SEQ ID 169.
PN US2004233964-A1.
PD 11-NOV-2004.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1171
ID ADM49403 standard; protein; 802 AA.
DE PRO618 protein, SEQ ID 169.
PN US2005014226-A1.
PD 20-JAN-2005.
PA (ASHK/) ASHKENAZI A J.
PA (BAKE/) BAKER K P.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATC/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODO/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI J C.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (KUOS/) KUO S S.
PA (NAPI/) NAPIER M A.
PA (NAPI/) NAPIER M A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (SHEL/) SHELTON D L.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.

PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 7.3%; Score 288.5; DB 9; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1172
ID ADZ52064 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2005084935-A1.
PD 21-APR-2005.
PA (ASHK/) ASHKENAZI A J.
PA (BAKE/) BAKER K P.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATC/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODO/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI J C.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (KUOS/) KUO S S.
PA (NAPI/) NAPIER M A.
PA (NAPI/) NAPIER M A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (SHEL/) SHELTON D L.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 7.3%; Score 288.5; DB 9; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1173
ID AED47892 standard; protein; 802 AA.
DE Human PRO618 amino acid sequence.
PN US2005227342-A1.
PD 13-OCT-2005.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 9; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1174
ID AEH18123 standard; protein; 802 AA.
DE Human PRO protein amino acid sequence - SEQ ID 169.
PN US2006078964-A1.
PD 13-APR-2006.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 10; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1175
ID AAB98507 standard; protein; 902 AA.
DE Murine epithin.
PN WO200129056-A1.
PD 26-APR-2001.
PA (UYAR-) UNIV ARKANSAS.
Query Match 7.3%; Score 288.5; DB 4; Length 902;
Best Local Similarity 21.4%; Pred. No. 2.2e-07;
RESULT 1176
ID AAU80517 standard; protein; 902 AA.
DE Mouse epithilin-like serine protease.
PN WO200196378-A2.
PD 20-DEC-2001.
PA (FARB) BAYER AG.
Query Match 7.3%; Score 288.5; DB 5; Length 902;
Best Local Similarity 21.4%; Pred. No. 2.2e-07;
RESULT 1177
ID AAU77549 standard; protein; 902 AA.
DE Murine type II membrane serine protease, epithin.

PN W0200212461-A2.
PD 14-FEB-2002.
PA (FARB) BAYER AG.
Query Match 7.3%; Score 288.5; DB 5; Length 902;
Best Local Similarity 21.4%; Pred. No. 2.2e-07;
RESULT 1178
ID AAR05489 standard; protein; 527 AA.
DE tPA024 precursor protein.
PN E8373896-A.
PD 20-JUN-1990.
PA (YAMA) YAMANOUCHI PHARM CO LTD.
PA (YAMA) NIPPON STEEL CORP.
Query Match 7.3%; Score 288; DB 2; Length 527;
Best Local Similarity 23.6%; Pred. No. 1.4e-07;
RESULT 1179
ID AAR21599 standard; protein; 527 AA.
DE tPA variant - N117Q, D236A, D238A, K240A.
PN W09202612-A.
PD 20-FEB-1992.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288; DB 2; Length 527;
Best Local Similarity 23.4%; Pred. No. 1.4e-07;
RESULT 1180
ID AAR20220 standard; protein; 527 AA.
DE t-PA analogue expressed by pCDM8-012.
PN JP03285680-A.
PD 16-DEC-1991.
PA (SUMU) SUMITOMO SEIYAKU KK.
Query Match 7.3%; Score 288; DB 2; Length 527;
Best Local Similarity 23.2%; Pred. No. 1.4e-07;
RESULT 1181
ID AAR20219 standard; protein; 527 AA.
DE t-PA analogue expressed by pCDM8-011.
PN JP03285680-A.
PD 16-DEC-1991.
PA (SUMU) SUMITOMO SEIYAKU KK.
Query Match 7.3%; Score 288; DB 2; Length 527;
Best Local Similarity 23.2%; Pred. No. 1.4e-07;
RESULT 1182
ID AAR20217 standard; protein; 527 AA.
DE t-PA analogue expressed by pCDM8-009.
PN JP03285680-A.
PD 16-DEC-1991.
PA (SUMU) SUMITOMO SEIYAKU KK.
Query Match 7.3%; Score 288; DB 2; Length 527;
Best Local Similarity 23.2%; Pred. No. 1.4e-07;
RESULT 1183
ID AAR20218 standard; protein; 527 AA.
DE t-PA analogue expressed by pCDM8-010.
PN JP03285680-A.
PD 16-DEC-1991.
PA (SUMU) SUMITOMO SEIYAKU KK.
Query Match 7.3%; Score 288; DB 2; Length 527;
Best Local Similarity 23.2%; Pred. No. 1.4e-07;
RESULT 1184
ID AAR70901 standard; protein; 527 AA.
DE Human t-PA variant (N103,A416,A417,A418).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288; DB 2; Length 527;
Best Local Similarity 23.5%; Pred. No. 1.4e-07;
RESULT 1185
ID AAR70904 standard; protein; 527 AA.
DE Human t-PA variant (N103,A440).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288; DB 2; Length 527;
Best Local Similarity 23.4%; Pred. No. 1.4e-07;
RESULT 1186
ID AAY9558 standard; protein; 356 AA.
DE Human protein C protein sequence.

PN W0950454-A2.
PD 07-OCT-1999.
PA (WHEE) WHITEHEAD INST BIOMEDICAL RES.
Query Match 7.3%; Score 287.5; DB 2; Length 356;
Best Local Similarity 24.5%; Pred. No. 1e-07;
RESULT 1187
ID AAM52187 standard; protein; 406 AA.
DE Human FVII mutant K143N/N145T/R315N/V317T.
PN W0200158935-A2.
PD 16-AUG-2001.
PA (MAXY-) MAXYGEN APS.
Query Match 7.3%; Score 287.5; DB 4; Length 406;
Best Local Similarity 23.0%; Pred. No. 1.2e-07;
RESULT 1188
ID ADJ56078 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant K143N/ N145T/ R290N/ A292T.
PN W02004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.3%; Score 287.5; DB 8; Length 406;
Best Local Similarity 23.0%; Pred. No. 1.2e-07;
RESULT 1189
ID ADV44720 standard; protein; 406 AA.
DE Human factor VII mutant K143N/N145T/R315N/V317T.
PN W02004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.3%; Score 287.5; DB 9; Length 406;
Best Local Similarity 23.0%; Pred. No. 1.2e-07;
RESULT 1190
ID ADY74310 standard; protein; 406 AA.
DE Human Factor VII variant polypeptide #253.
PN W02005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.3%; Score 287.5; DB 9; Length 406;
Best Local Similarity 23.0%; Pred. No. 1.2e-07;
RESULT 1191
ID AEF15066 standard; protein; 406 AA.
DE Variant human coagulation Factor VII protein #35.
PN W02005123916-A2.
PD 29-DEC-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.3%; Score 287.5; DB 10; Length 406;
Best Local Similarity 23.0%; Pred. No. 1.2e-07;
RESULT 1192
ID AAR13918 standard; protein; 522 AA.
DE Delta (466-470) tPA variant with K416A, H417A and E418A substns.
PN W09113149-A.
PD 05-SEP-1991.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 287.5; DB 2; Length 522;
Best Local Similarity 22.9%; Pred. No. 1.5e-07;
RESULT 1193
ID ABP43952 standard; protein; 795 AA.
DE Human PRO618.
PN W0200231111-A2.
PD 18-APR-2002.
PA (HYSE-) HYSEQ INC.
Query Match 7.3%; Score 287.5; DB 5; Length 795;
Best Local Similarity 22.7%; Pred. No. 2.2e-07;
RESULT 1194
ID ADG83828 standard; protein; 467 AA.
DE Coastal taipan venom protease.
PN W02003082914-A1.
PD 09-OCT-2003.
PA (UYOU) UNIV QUEENSLAND.
Query Match 7.3%; Score 287; DB 8; Length 467;
Best Local Similarity 22.5%; Pred. No. 1.4e-07;
RESULT 1195
ID AAR70879 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N103,S184,E275).
PN US5385732-A.

PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 287; DB 2; Length 483;
Best Local Similarity 23.4%; Pred. No. 1.4e-07;
RESULT 1196
ID AAR70883 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N103,K210,E275) .
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 287; DB 2; Length 483;
Best Local Similarity 23.4%; Pred. No. 1.4e-07;
RESULT 1197
ID AAR70884 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N103,E275,I277) .
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 287; DB 2; Length 483;
Best Local Similarity 23.4%; Pred. No. 1.4e-07;
RESULT 1198
ID AAR70886 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N103,S184,E275,I277) .
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 287; DB 2; Length 483;
Best Local Similarity 23.4%; Pred. No. 1.4e-07;
RESULT 1199
ID AAR70877 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N103,E275) .
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 287; DB 2; Length 483;
Best Local Similarity 23.4%; Pred. No. 1.4e-07;
RESULT 1200
ID AAR70887 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N103,K213,E275,I277) .
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 287; DB 2; Length 483;
Best Local Similarity 23.4%; Pred. No. 1.4e-07;
RESULT 1201
ID AAR70881 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N103,R210,A211,R212,R213,E275) .
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 287; DB 2; Length 483;
Best Local Similarity 23.4%; Pred. No. 1.4e-07;
RESULT 1202
ID AAR70882 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N103,R252,E275) .
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 287; DB 2; Length 483;
Best Local Similarity 23.4%; Pred. No. 1.4e-07;
RESULT 1203
ID AAR70889 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N103,R252,E275,O277) .
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 287; DB 2; Length 483;
Best Local Similarity 23.4%; Pred. No. 1.4e-07;
RESULT 1204
ID AAR70888 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N103,R210,A211,R212,R213,E275,I277) .
PN US5385732-A.
PD 31-JAN-1995.

PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 287; DB 2; Length 483;
Best Local Similarity 23.1%; Pred. No. 1.4e-07;
RESULT 1205
ID AAR70890 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N103,K210,E275,I277) .
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 287; DB 2; Length 483;
Best Local Similarity 23.4%; Pred. No. 1.4e-07;
RESULT 1206
ID AAR70880 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N103,K213,E275) .
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 287; DB 2; Length 483;
Best Local Similarity 23.4%; Pred. No. 1.4e-07;
RESULT 1207
ID AAR70907 standard; protein; 527 AA.
DE Human t-PA variant (N103,A460,A462) .
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 287; DB 2; Length 527;
Best Local Similarity 23.4%; Pred. No. 1.6e-07;
RESULT 1208
ID AAR70874 standard; protein; 527 AA.
DE Human t-PA variant (N67,N103) .
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 287; DB 2; Length 527;
Best Local Similarity 23.4%; Pred. No. 1.6e-07;
RESULT 1209
ID AAR70892 standard; protein; 527 AA.
DE Human t-PA variant (N103,A283,A287) .
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 287; DB 2; Length 527;
Best Local Similarity 23.4%; Pred. No. 1.6e-07;
RESULT 1210
ID AAM52182 standard; protein; 406 AA.
DE Human FVII mutant K143N/N145T.
PN WO200158935-A2.
PD 16-AUG-2001.
PA (MAXY-) MAXYGEN APS.
Query Match 7.3%; Score 286.5; DB 4; Length 406;
Best Local Similarity 23.0%; Pred. No. 1.3e-07;
RESULT 1211
ID ADU56073 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant K143N/N145T.
PN WO200400366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.3%; Score 286.5; DB 8; Length 406;
Best Local Similarity 23.0%; Pred. No. 1.3e-07;
RESULT 1212
ID ADO10589 standard; protein; 406 AA.
DE Human factor VII/VIII protein mutant #25.
PN WO2004029091-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.3%; Score 286.5; DB 8; Length 406;
Best Local Similarity 23.0%; Pred. No. 1.3e-07;
RESULT 1213
ID ADV44715 standard; protein; 406 AA.
DE Human factor VII mutant K143N/N145T.
PN WO2004110469-A2.
PD 23-DEC-2004.

PA (NOVO) NOVO NORDISK AS.
Query Match 7.3%; Score 286.5; DB 9; Length 406;
Best Local Similarity 23.0%; Pred. No. 1.3e-07;
RESULT 1214
ID ADY74305 standard; protein; 406 AA.
DE Human Factor VII variant polypeptide #248.
PN W02005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.3%; Score 286.5; DB 9; Length 406;
Best Local Similarity 23.0%; Pred. No. 1.3e-07;
RESULT 1215
ID AEF15046 standard; protein; 406 AA.
DE Variant human coagulation Factor VII protein #15.
PN W02005123916-A2.
PD 29-DEC-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.3%; Score 286.5; DB 10; Length 406;
Best Local Similarity 23.0%; Pred. No. 1.3e-07;
RESULT 1216
ID ADG83826 standard; protein; 467 AA.
DE Brown snake venom protease.
PN W02003082914-A1.
PD 09-OCT-2003.
PA (UYOU) UNIV QUEENSLAND.
Query Match 7.3%; Score 286.5; DB 8; Length 467;
Best Local Similarity 22.2%; Pred. No. 1.5e-07;
RESULT 1217
ID AAR14486 standard; protein; 522 AA.
DE Delta (466-470) CPA variant with Y67N substitution.
PN W09113149-A.
PD 05-SEP-1991.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 286.5; DB 2; Length 522;
Best Local Similarity 22.7%; Pred. No. 1.7e-07;
RESULT 1218
ID AAR44816 standard; protein; 527 AA.
DE Human CPA variant (N67,N103).
PN US5270198-A.
PD 14-DEC-1993.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 286; DB 2; Length 527;
Best Local Similarity 23.2%; Pred. No. 1.8e-07;
RESULT 1219
ID AAR44812 standard; protein; 527 AA.
DE Human CPA variant N103.
PN US5270198-A.
PD 14-DEC-1993.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 286; DB 2; Length 527;
Best Local Similarity 23.2%; Pred. No. 1.8e-07;
RESULT 1220
ID AAR70868 standard; protein; 527 AA.
DE Human t-PA variant (N67,A432,A434).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 286; DB 2; Length 527;
Best Local Similarity 23.2%; Pred. No. 1.8e-07;
RESULT 1221
ID AAR70860 standard; protein; 527 AA.
DE Human t-PA variant (N67,A331,A332).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 286; DB 2; Length 527;
Best Local Similarity 23.4%; Pred. No. 1.8e-07;
RESULT 1222
ID AAR70900 standard; protein; 527 AA.
DE Human t-PA variant (N103,A410).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.

Query Match 7.2%; Score 285; DB 2; Length 527;
Best Local Similarity 23.1%; Pred. No. 1.8e-07;
RESULT 1223
ID AAR09220 standard; protein; 529 AA.
DE t-PA insertion variant 1304H, 1305H.
PN W09002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 286; DB 2; Length 529;
Best Local Similarity 23.2%; Pred. No. 1.8e-07;
RESULT 1224
ID AAP70449 standard; protein; 530 AA.
DE Sequence encoded by of synthetic gene for mature human tissue plasminogen activator (tPA).
PN W08705934-A.
PD 08-OCT-1987.
PA (CREA/) CREA R.
Query Match 7.2%; Score 286; DB 1; Length 530;
Best Local Similarity 22.9%; Pred. No. 1.8e-07;
RESULT 1225
ID AAR12342 standard; protein; 561 AA.
DE T-PA with -ve charged finger and/or kringle domain (1).
PN JF03061483-A.
PD 18-MAR-1991.
PA (FUT) FUJISAWA PHARM CO LTD.
Query Match 7.2%; Score 286; DB 2; Length 561;
Best Local Similarity 22.1%; Pred. No. 1.9e-07;
RESULT 1226
ID AAR09289 standard; protein; 562 AA.
DE Sequence of tissue plasminogen activator analogue BBNT12 (Asp 67, Thr 68).
PN W08912681-A.
PD 28-DEC-1989.
PA (BRRI-) BRIT BIO-TECHN LTD.
Query Match 7.2%; Score 286; DB 2; Length 562;
Best Local Similarity 23.3%; Pred. No. 1.9e-07;
RESULT 1227
ID AAP70880 standard; protein; 527 AA.
DE Thrombolytic proteins 1-9-1-11 having t-PA activity and R275 is deleted or replaced and containing a modified N-linked glycosylation site.
PN W08704722-A.
PD 13-AUG-1987.
PA (GEMV) GENETICS INST INC.
PA (LARS/) LARSEN G R.
Query Match 7.2%; Score 285.5; DB 1; Length 527;
Best Local Similarity 23.1%; Pred. No. 1.9e-07;
RESULT 1228
ID AAP91683 standard; protein; 527 AA.
DE Sequence of tissue plasminogen activator (tPA).
PN W08911531-A.
PD 30-NOV-1989.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 285; DB 1; Length 527;
Best Local Similarity 23.2%; Pred. No. 2e-07;
RESULT 1229
ID AAR09270 standard; protein; 527 AA.
DE t-PA variant H331A, H332A.
PN W09002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 285; DB 2; Length 527;
Best Local Similarity 23.2%; Pred. No. 2e-07;
RESULT 1230
ID AAR09278 standard; protein; 527 AA.
DE t-PA variant H432A, R434A.
PN W09002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 285; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 2e-07;
RESULT 1231
ID ADW64349 standard; protein; 527 AA.
DE Mutant human plasminogen activator protein - SEQ ID 1.

PN CN1526726-A.
PD 08-SEP-2004.
PA (LIBA/) LI B.
Query Match 7.2%; Score 285; DB 8; Length 527;
Best Local Similarity 23.0%; Pred. No. 2e-07;
RESULT 1232
ID AAR71449 standard; protein; 528 AA.
DE Modified human tissue plasminogen activator.
PN EP238304-A.
PD 23-SEP-1987.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 285; DB 1; Length 528;
Best Local Similarity 23.4%; Pred. No. 2e-07;
RESULT 1233
ID AAR13148 standard; protein; 556 AA.
DE T-PA variant contg. fibrinectin for thrombosis lysis (2).
PN JF03061482-A.
PD 18-MAR-1991.
PA (FUJI) FUJISAWA PHARM CO LTD.
Query Match 7.2%; Score 285; DB 2; Length 556;
Best Local Similarity 21.9%; Pred. No. 2.1e-07;
RESULT 1234
ID AAB11710 standard; protein; 264 AA.
DE Human serine protease BSSPS (HBSSPS) SEQ ID NO:2.
PN WO200031243-A1.
PD 02-JUN-2000.
PA (FUJO) FUJO PHARM IND LTD.
Query Match 7.2%; Score 284.5; DB 3; Length 264;
Best Local Similarity 28.0%; Pred. No. 1.1e-07;
RESULT 1235
ID AAP91961 standard; protein; 518 AA.
DE Sequence of des 1-44E275 t-PA mutant.
PN WO8909266-A.
PD 05-OCT-1989.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 284.5; DB 1; Length 518;
Best Local Similarity 22.9%; Pred. No. 2.1e-07;
RESULT 1236
ID AAM84749 standard; protein; 629 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:4998.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 7.2%; Score 284.5; DB 8; Length 629;
Best Local Similarity 19.5%; Pred. No. 2.5e-07;
RESULT 1237
ID AAM82817 standard; protein; 629 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:3066.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 7.2%; Score 284; DB 2; Length 483;
Best Local Similarity 23.1%; Pred. No. 2.1e-07;
RESULT 1238
ID AAR70851 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N67,D184,E275,I277).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 284; DB 2; Length 483;
Best Local Similarity 23.1%; Pred. No. 2.1e-07;
RESULT 1239
ID AAR70844 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N67,D184,E275).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 284; DB 2; Length 483;
Best Local Similarity 23.1%; Pred. No. 2.1e-07;
RESULT 1240
ID AAR44809 standard; protein; 527 AA.
DE Human tPA variant (N65, S67).
PN US5270198-A.

PD 14-DEC-1993.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 284; DB 2; Length 527;
Best Local Similarity 23.1%; Pred. No. 2.3e-07;
RESULT 1241
ID AAR70908 standard; protein; 527 AA.
DE Human t-PA variant (N103,A477).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 284; DB 2; Length 527;
Best Local Similarity 23.4%; Pred. No. 2.3e-07;
RESULT 1242
ID AAR70859 standard; protein; 527 AA.
DE Human t-PA variant (N67,A303,A304).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 284; DB 2; Length 527;
Best Local Similarity 23.8%; Pred. No. 2.3e-07;
RESULT 1243
ID AAR70893 standard; protein; 527 AA.
DE Human t-PA variant (N103,A296,A297,A298,A299).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 284; DB 2; Length 527;
Best Local Similarity 23.5%; Pred. No. 2.3e-07;
RESULT 1244
ID AAR70891 standard; protein; 527 AA.
DE Human t-PA variant (N103,A267).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 284; DB 2; Length 527;
Best Local Similarity 23.7%; Pred. No. 2.3e-07;
RESULT 1245
ID AAP70474 standard; protein; 562 AA.
DE Sequence of tissue plasminogen (TPA) analogue.
PN WO8703906-A.
PD 02-JUL-1987.
PA (UPJO) UPJOHN CO.
PA (MARCO/) MAROTTI K R.
Query Match 7.2%; Score 284; DB 1; Length 562;
Best Local Similarity 23.0%; Pred. No. 2.4e-07;
RESULT 1246
ID AAR09286 standard; protein; 562 AA.
DE Sequence of tissue plasminogen activator analogue BBNTS (Ser 67, Ser 68).
PN WO8912681-A.
PD 28-DEC-1989.
PA (BBNT-) BRIT BIO-TECHN LTD.
Query Match 7.2%; Score 284; DB 2; Length 562;
Best Local Similarity 23.1%; Pred. No. 2.4e-07;
RESULT 1247
ID AAR23807 standard; protein; 562 AA.
DE t-PA (Tyr 297) mutant.
PN WO9206203-A.
PD 16-APR-1992.
PA (TEXA) UNIV TEXAS SYSTEM.
Query Match 7.2%; Score 284; DB 2; Length 562;
Best Local Similarity 23.2%; Pred. No. 2.4e-07;
RESULT 1248
ID AAB80068 standard; protein; 406 AA.
DE Human coagulation factor VII mutant L305V/M306D/D309S.
PN WO200183725-A1.
PD 08-NOV-2001.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.2%; Score 283.5; DB 5; Length 406;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1249
ID AAG73125 standard; protein; 406 AA.
DE Human coagulation Factor VII mutant polypeptide L305V/M306D/D309S.
PN WO20027218-A1.

PD 03-OCT-2002.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.2%; Score 283.5; DB 6; Length 406;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1250
ID ADJ55852 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant L305V/ M306D/ D309S.
PN MO2004000386-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.2%; Score 283.5; DB 8; Length 406;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1251
ID ADV44489 standard; protein; 406 AA.
DE Human factor VII mutant L305V/M306D/D309S.
PN MO2004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.2%; Score 283.5; DB 9; Length 406;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1252
ID ADY74078 standard; protein; 406 AA.
DE Human factor VII variant polypeptide #21.
PN MO2005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.2%; Score 283.5; DB 9; Length 406;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1253
ID ADE83543 standard; protein; 482 AA.
DE Rat Protein NP 058839, SEQ ID NO 11161.
PN MO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 7.2%; Score 283.5; DB 7; Length 482;
Best Local Similarity 22.8%; Pred. No. 2.2e-07;
RESULT 1254
ID AAR13917 standard; peptide; 522 AA.
DE Delta (466-470) tPA variant with K296A, H297A, R298A and R299A substitutions.
PN MO9113149-A.
PD 05-SEP-1991.
PA (GEHT) GENENTECH INC.
Query Match 7.2%; Score 283.5; DB 2; Length 522;
Best Local Similarity 22.8%; Pred. No. 2.4e-07;
RESULT 1255
ID AAP90169 standard; peptide; 571 AA.
DE Tissue plasminogen activator mutant 2G.
PN MO8907146-A.
PD 10-AUG-1989.
PA (INTE-) INTEG GENETICS INC.
Query Match 7.2%; Score 283.5; DB 1; Length 571;
Best Local Similarity 22.4%; Pred. No. 2.6e-07;
RESULT 1256
ID ADM20190 standard; protein; 407 AA.
DE Human factor VII (FVII) protein variant sequence #28.
PN MO2004111242-A1.
PD 23-DEC-2004.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
PA (MAXY-) MAXYGEN APS.
Query Match 7.2%; Score 283; DB 9; Length 407;
Best Local Similarity 22.2%; Pred. No. 2e-07;
RESULT 1257
ID AAR09257 standard; protein; 483 AA.
DE t-PA variant dl-44, N184D, I210R, G211A, K212R, V213R, T252R, F305H.
PN MO9002798-A.
PD 22-MAR-1990.
PA (GEHT) GENENTECH INC.
Query Match 7.2%; Score 283; DB 2; Length 483;
Best Local Similarity 23.2%; Pred. No. 2.4e-07;
RESULT 1258
ID AAR09269 standard; protein; 527 AA.

DE t-PA variant E303A, R304A.
PN MO9002798-A.
PD 22-MAR-1990.
PA (GEHT) GENENTECH INC.
Query Match 7.2%; Score 283; DB 2; Length 527;
Best Local Similarity 23.7%; Pred. No. 2.6e-07;
RESULT 1259
ID AAR44810 standard; protein; 527 AA.
DE Human tPA variant (N65, T67).
PN US5270198-A.
PD 14-DEC-1993.
PA (GEHT) GENENTECH INC.
Query Match 7.2%; Score 283; DB 2; Length 527;
Best Local Similarity 23.1%; Pred. No. 2.6e-07;
RESULT 1260
ID AAR44817 standard; protein; 527 AA.
DE Human tPA variant (N67, A296, A297, A298, A299).
PN US5270198-A.
PD 14-DEC-1993.
PA (GEHT) GENENTECH INC.
Query Match 7.2%; Score 283; DB 2; Length 527;
Best Local Similarity 23.4%; Pred. No. 2.6e-07;
RESULT 1261
ID AAR44814 standard; protein; 527 AA.
DE Human tPA variant (N105, T107).
PN US5270198-A.
PD 14-DEC-1993.
PA (GEHT) GENENTECH INC.
Query Match 7.2%; Score 283; DB 2; Length 527;
Best Local Similarity 23.6%; Pred. No. 2.6e-07;
RESULT 1262
ID AAR70899 standard; protein; 527 AA.
DE Human t-PA variant (N103, A408).
PN US5385732-A.
PD 31-JAN-1995.
PA (GEHT) GENENTECH INC.
Query Match 7.2%; Score 283; DB 2; Length 527;
Best Local Similarity 22.9%; Pred. No. 2.6e-07;
RESULT 1263
ID AAR12341 standard; protein; 560 AA.
DE T-PA variant contg. fibronectin for thrombosis lysis (3).
PN JP03061483-A.
PD 18-MAR-1991.
PA (FUJI) FUJISAWA PHARM CO LTD.
Query Match 7.2%; Score 283; DB 2; Length 560;
Best Local Similarity 22.1%; Pred. No. 2.7e-07;
RESULT 1264
ID AAR12367 standard; protein; 561 AA.
DE T-PA with -ve charged finger and/or kringle domain (7).
PN JP03061483-A.
PD 18-MAR-1991.
PA (FUJI) FUJISAWA PHARM CO LTD.
Query Match 7.2%; Score 283; DB 2; Length 561;
Best Local Similarity 22.1%; Pred. No. 2.7e-07;
RESULT 1265
ID ADM42867 standard; protein; 925 AA.
DE Human corin protein deletion region 569-1042.
PN MO2004111225-A1.
PD 23-DEC-2004.
PA (SCHD) SCHERING AG.
Query Match 7.2%; Score 283; DB 9; Length 925;
Best Local Similarity 20.5%; Pred. No. 4.4e-07;
RESULT 1266
ID AEG02852 standard; protein; 436 AA.
DE Factor VII/IX fusion protein SEQ ID NO:46.
PN MO2006018204-A1.
PD 23-FEB-2006.
PA (ZLBB-) ZLB BEHRING GMBH.
Query Match 7.2%; Score 282.5; DB 10; Length 436;
Best Local Similarity 24.2%; Pred. No. 2.3e-07;
RESULT 1267
ID ARG02835 standard; peptide; 436 AA.
DE Factor VII/IX fusion protein SEQ ID NO:29.

PN W02006018204-A1.
PD 23-FEB-2006.
PA (ZLBB-) ZLB BEHRING GMBH.
Query Match 7.2%; Score 282.5; DB 10; Length 436;
Best Local Similarity 24.2%; Pred. No. 2.3e-07;
RESULT 1268
ID AAR09231 standard; protein; 524 AA.
DE c-PA deletion variant d297-299.
PN W09002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 282.5; DB 2; Length 524;
Best Local Similarity 22.8%; Pred. No. 2.7e-07;
RESULT 1269
ID ADM20177 standard; protein; 406 AA.
DE Human factor VII (FVII) protein variant sequence #15.
PN W02004111242-A1.
PD 23-DEC-2004.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
PA (MAXY-) MAXYGEN APS.
Query Match 7.1%; Score 282; DB 9; Length 406;
Best Local Similarity 22.1%; Pred. No. 2.3e-07;
RESULT 1270
ID ABL92410 standard; protein; 406 AA.
DE Human factor VII protein variant, P10D.
PN W02006114105-A2.
PD 02-NOV-2006.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.1%; Score 282; DB 10; Length 406;
Best Local Similarity 22.3%; Pred. No. 2.3e-07;
RESULT 1271
ID AAR09246 standard; protein; 483 AA.
DE c-PA variant d1-44, N184D, F305H.
PN W09002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 282; DB 2; Length 483;
Best Local Similarity 23.0%; Pred. No. 2.7e-07;
RESULT 1272
ID AAR09254 standard; protein; 483 AA.
DE c-PA variant d1-44, I210R, G211H, K212Q, V213K, F305H.
PN W09002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 282; DB 2; Length 483;
Best Local Similarity 22.8%; Pred. No. 2.7e-07;
RESULT 1273
ID AAR09230 standard; protein; 525 AA.
DE c-PA deletion variant d297-298.
PN W09002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 282; DB 2; Length 525;
Best Local Similarity 23.4%; Pred. No. 2.9e-07;
RESULT 1274
ID AAR09255 standard; protein; 527 AA.
DE c-PA variant I210R, G211H, K212Q, V213K, F305H.
PN W09002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 282; DB 2; Length 527;
Best Local Similarity 22.8%; Pred. No. 2.9e-07;
RESULT 1275
ID AAR21600 standard; protein; 527 AA.
DE c-PA variant - E94A, D95A, T103N.
PN W09202612-A.
PD 20-FEB-1992.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 282; DB 2; Length 527;
Best Local Similarity 23.2%; Pred. No. 2.9e-07;
RESULT 1276
ID AAR70866 standard; protein; 527 AA.
DE Human c-PA variant (N67,A416,A417,A418).

PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 282; DB 2; Length 527;
Best Local Similarity 23.4%; Pred. No. 2.9e-07;
RESULT 1277
ID AAR70902 standard; protein; 527 AA.
DE Human c-PA variant (N103,A426,A427,A429,A430).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 282; DB 2; Length 527;
Best Local Similarity 23.4%; Pred. No. 2.9e-07;
RESULT 1278
ID AAR70869 standard; protein; 527 AA.
DE Human c-PA variant (N67,A440).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 282; DB 2; Length 527;
Best Local Similarity 23.2%; Pred. No. 2.9e-07;
RESULT 1279
ID AAP82582 standard; protein; 562 AA.
DE Tissue plasminogen activator with S-119 substd for M and QG196-98 substd for NGT.
PN JP63230083-A.
PD 26-SEP-1988.
PA (EISA) EISAI CO LTD.
Query Match 7.1%; Score 282; DB 1; Length 562;
Best Local Similarity 23.2%; Pred. No. 3.1e-07;
RESULT 1280
ID AAR09287 standard; protein; 562 AA.
DE Sequence of tissue plasminogen activator analogue BBNT6 (Thr 67, Asp 68).
PN W08912681-A.
PD 28-DEC-1989.
PA (BRBI-) BRIT BIO-TECHN LTD.
Query Match 7.1%; Score 282; DB 2; Length 562;
Best Local Similarity 23.1%; Pred. No. 3.1e-07;
RESULT 1281
ID AAR23808 standard; protein; 562 AA.
DE c-PA (Glu 298) mutant.
PN W09206203-A.
PD 16-APR-1992.
PA (TEXA) UNIV TEXAS SYSTEM.
Query Match 7.1%; Score 282; DB 2; Length 562;
Best Local Similarity 23.5%; Pred. No. 3.1e-07;
RESULT 1282
ID AAR23810 standard; protein; 562 AA.
DE c-PA (Gly 301) mutant.
PN W09206203-A.
PD 16-APR-1992.
PA (TEXA) UNIV TEXAS SYSTEM.
Query Match 7.1%; Score 282; DB 2; Length 562;
Best Local Similarity 23.6%; Pred. No. 3.1e-07;
RESULT 1283
ID AAB84869 standard; protein; 406 AA.
DE Mutant blood coagulant factor VII (FVII-30).
PN JP2001061479-A.
PD 13-MAR-2001.
PA (KAGA) ZH KAGAKU & KESSER RYOH KENKYUSHO.
Query Match 7.1%; Score 281.5; DB 4; Length 406;
Best Local Similarity 22.8%; Pred. No. 2.4e-07;
RESULT 1284
ID AAM52185 standard; protein; 406 AA.
DE Human FVII mutant G291N.
PN W0200158935-A2.
PD 16-AUG-2001.
PA (MAXY-) MAXYGEN APS.
Query Match 7.1%; Score 281.5; DB 4; Length 406;
Best Local Similarity 22.8%; Pred. No. 2.4e-07;
RESULT 1285
ID AAO30584 standard; protein; 406 AA.
DE Human coagulation factor VII variant (S314E/L305V/V158D/K337A/M298Q).

PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.4e-07;
RESULT 1286
ID AAO30626 standard; protein; 406 AA.
DE Human coagulation factor VII variant (K316Q/L305V/V158T/K337A/M298Q).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.4e-07;
RESULT 1287
ID AAO30582 standard; protein; 406 AA.
DE Human coagulation factor VII variant (S314E/L305V/V158T/K337A/M298Q).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.4e-07;
RESULT 1288
ID AAO30616 standard; protein; 406 AA.
DE Human coagulation factor VII variant (K316Q/L305V/K337A/M298Q).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.4e-07;
RESULT 1289
ID AAO30572 standard; protein; 406 AA.
DE Human coagulation factor VII variant (S314E/L305V/K337A/M298Q).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.4e-07;
RESULT 1290
ID AAO30628 standard; protein; 406 AA.
DE Human coagulation factor VII variant (K316Q/L305V/V158D/K337A/M298Q).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.4e-07;
RESULT 1291
ID ADJ55926 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant V158T/ M298Q/ L305V/ S314E/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.4e-07;
RESULT 1292
ID ADJ55927 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant V158D/ M298Q/ L305V/ S314E/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.4e-07;
RESULT 1293
ID ADJ55915 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant M298Q/ L305V/ S314E/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.4e-07;
RESULT 1294
ID ADJ55970 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant V158T/ M298Q/ L305V/ K316Q/ K337A.
PN WO2004000366-A1.

PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.4e-07;
RESULT 1295
ID ADJ56063 standard; protein; 406 AA.
DE Human factor VII protein mutant F374Y/ V158D/ M298Q/ L305V/ S314E/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.4e-07;
RESULT 1296
ID ADJ55959 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant M298Q/ L305V/ K316Q/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.4e-07;
RESULT 1297
ID ADJ56067 standard; protein; 406 AA.
DE Human factor VII protein mutant F374Y/ V158T/ M298Q/ L305V/ S314E/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.4e-07;
RESULT 1298
ID ADJ55971 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant V158D/ M298Q/ L305V/ K316Q/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.4e-07;
RESULT 1299
ID ADJ56033 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant F374Y/ S314E/ M298Q/ L305V/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.4e-07;
RESULT 1300
ID ADJ56076 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant G291N.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.4e-07;
RESULT 1301
ID ADO10585 standard; protein; 406 AA.
DE Human factor VII/VIIa protein mutant #21.
PN WO2004029091-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN APS.
Query Match 7.1%; Score 281.5; DB 8; Length 406;
Best Local Similarity 22.8%; Pred. No. 2.4e-07;
RESULT 1302
ID ADO10626 standard; protein; 406 AA.
DE Human factor VII/VIIa protein mutant #62.
PN WO2004029091-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.1%; Score 281.5; DB 8; Length 406;
Best Local Similarity 22.8%; Pred. No. 2.4e-07;
RESULT 1303
ID ADJ512886 standard; protein; 406 AA.
DE Human factor VII G237L mutant.

PN WO2004083361-A2.
PD 30-SEP-2004.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.1%; Score 281.5; DB 8; Length 406;
Best Local Similarity 22.6%; Pred. No. 2.4e-07;
RESULT 1304
ID ADV44566 standard; protein; 406 AA.
DE Human factor VII mutant S314E/L305V/V158T/K337A/M298Q.
PN WO2004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.4e-07;
RESULT 1305
ID ADV44707 standard; protein; 406 AA.
DE Human factor VII mutant F374Y/V158D/M298QV/S314E/K337A/L305V.
PN WO2004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.4e-07;
RESULT 1306
ID ADV44568 standard; protein; 406 AA.
DE Human factor VII mutant S314E/L305V/V158D/K337A/M298Q.
PN WO2004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.4e-07;
RESULT 1307
ID ADV44718 standard; protein; 406 AA.
DE Human factor VII mutant G291N.
PN WO2004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 9; Length 406;
Best Local Similarity 22.8%; Pred. No. 2.4e-07;
RESULT 1308
ID ADV44610 standard; protein; 406 AA.
DE Human factor VII mutant K316Q/L305V/V158T/K337A/M298Q.
PN WO2004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.4e-07;
RESULT 1309
ID ADV44612 standard; protein; 406 AA.
DE Human factor VII mutant K316Q/L305V/V158D/K337A/M298Q.
PN WO2004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.4e-07;
RESULT 1310
ID ADV44673 standard; protein; 406 AA.
DE Human factor VII mutant F374Y/L305V/M298Q/K337A/S314E.
PN WO2004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.4e-07;
RESULT 1311
ID ADV44556 standard; protein; 406 AA.
DE Human factor VII mutant S314E/L305V/K337A/M298Q.
PN WO2004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.4e-07;
RESULT 1312
ID ADV44704 standard; protein; 406 AA.
DE Human factor VII mutant F374Y/V158T/S314E/M298Q/K337A/L305V.

PN WO2004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.4e-07;
RESULT 1313
ID ADV44600 standard; protein; 406 AA.
DE Human factor VII mutant K316Q/L305V/K337A/M298Q.
PN WO2004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.4e-07;
RESULT 1314
ID ADV74145 standard; protein; 406 AA.
DE Human factor VII variant polypeptide #88.
PN WO2005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 281.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.4e-07;
RESULT 1315
ID ADV74296 standard; protein; 406 AA.
DE Human factor VII variant polypeptide #239.
PN WO2005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 281.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.4e-07;
RESULT 1316
ID ADV74155 standard; protein; 406 AA.
DE Human factor VII variant polypeptide #98.
PN WO2005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 281.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.4e-07;
RESULT 1317
ID ADV74262 standard; protein; 406 AA.
DE Human factor VII variant polypeptide #205.
PN WO2005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 281.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.4e-07;
RESULT 1318
ID ADV74293 standard; protein; 406 AA.
DE Human factor VII variant polypeptide #236.
PN WO2005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 281.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.4e-07;
RESULT 1319
ID ADV74189 standard; protein; 406 AA.
DE Human factor VII variant polypeptide #132.
PN WO2005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 281.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.4e-07;
RESULT 1320
ID ADV74308 standard; protein; 406 AA.
DE Human factor VII variant polypeptide #251.
PN WO2005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 281.5; DB 9; Length 406;
Best Local Similarity 22.8%; Pred. No. 2.4e-07;
RESULT 1321
ID ADV74201 standard; protein; 406 AA.
DE Human factor VII variant polypeptide #144.
PN WO2005024006-A2.

PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 281.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.4e-07;
RESULT 1322
ID ADV74157 standard; protein; 406 AA.
DE Human Factor VII variant polypeptide #100.
PN W02005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 281.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.4e-07;
RESULT 1323
ID ADV74199 standard; protein; 406 AA.
DE Human Factor VII variant polypeptide #142.
PN W02005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 281.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.4e-07;
RESULT 1324
ID AEF1516 standard; protein; 406 AA.
DE Variant human coagulation Factor VII protein #85.
PN W02005123916-A2.
PD 29-DEC-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 281.5; DB 10; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.4e-07;
RESULT 1325
ID AEF15122 standard; protein; 406 AA.
DE Variant human coagulation Factor VII protein #91.
PN W02005123916-A2.
PD 29-DEC-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 281.5; DB 10; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.4e-07;
RESULT 1326
ID AEF15072 standard; protein; 406 AA.
DE Variant human coagulation Factor VII protein #41.
PN W02005123916-A2.
PD 29-DEC-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 281.5; DB 10; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.4e-07;
RESULT 1327
ID AEF15160 standard; protein; 406 AA.
DE Variant human coagulation Factor VII protein #129.
PN W02005123916-A2.
PD 29-DEC-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 281.5; DB 10; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.4e-07;
RESULT 1328
ID AEF15083 standard; protein; 406 AA.
DE Variant human coagulation Factor VII protein #52.
PN W02005123916-A2.
PD 29-DEC-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 281.5; DB 10; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.4e-07;
RESULT 1329
ID AEF15124 standard; protein; 406 AA.
DE Variant human coagulation Factor VII protein #93.
PN W02005123916-A2.
PD 29-DEC-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 281.5; DB 10; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.4e-07;
RESULT 1330
ID AEF15157 standard; protein; 406 AA.
DE Variant human coagulation Factor VII protein #126.
PN W02005123916-A2.
PD 29-DEC-2005.

PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 281.5; DB 10; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.4e-07;
RESULT 1331
ID AAR09233 standard; protein; 522 AA.
DE t-PA deletion variant d297-301.
PN W09002798-A.
PD 22-MAR-1990.
PA (GENETH) GENENTECH INC.
Query Match 7.1%; Score 281.5; DB 2; Length 522;
Best Local Similarity 23.4%; Pred. No. 3.1e-07;
RESULT 1332
ID AAR13919 standard; protein; 522 AA.
DE Delta (466-470) tPA variant with E426A, R427A, K429A and E430A substitutions.
PN W09113149-A.
PD 05-SEP-1991.
PA (GENETH) GENENTECH INC.
Query Match 7.1%; Score 281.5; DB 2; Length 522;
Best Local Similarity 22.7%; Pred. No. 3.1e-07;
RESULT 1333
ID AAR09239 standard; protein; 524 AA.
DE t-PA deletion variant d300-302.
PN W09002798-A.
PD 22-MAR-1990.
PA (GENETH) GENENTECH INC.
Query Match 7.1%; Score 281.5; DB 2; Length 524;
Best Local Similarity 23.2%; Pred. No. 3.1e-07;
RESULT 1334
ID AAR12366 standard; protein; 562 AA.
DE T-PA with -ve charged finger and/or kringle domain (5).
PN JP03061483-A.
PD 18-MAR-1991.
PA (FUJII) FUJISAWA PHARM CO LTD.
Query Match 7.1%; Score 281.5; DB 2; Length 562;
Best Local Similarity 21.9%; Pred. No. 3.3e-07;
RESULT 1335
ID ADM20189 standard; protein; 407 AA.
DE Human factor VII (FVII) protein variant sequence #27.
PN W02004111242-A1.
PD 23-DEC-2004.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.1%; Score 281; DB 9; Length 407;
Best Local Similarity 22.2%; Pred. No. 2.6e-07;
RESULT 1336
ID AAR09249 standard; protein; 483 AA.
DE t-PA variant dl-44, I210R, G211A, K212R, V213K, F305H.
PN W09002798-A.
PD 22-MAR-1990.
PA (GENETH) GENENTECH INC.
Query Match 7.1%; Score 281; DB 2; Length 483;
Best Local Similarity 23.3%; Pred. No. 3e-07;
RESULT 1337
ID AAR70855 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N67,K210,E275,I277).
PN US5385732-A.
PD 31-JAN-1995.
PA (GENETH) GENENTECH INC.
Query Match 7.1%; Score 281; DB 2; Length 483;
Best Local Similarity 23.2%; Pred. No. 3e-07;
RESULT 1338
ID AAR70845 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N67,S184,E275).
PN US5385732-A.
PD 31-JAN-1995.
PA (GENETH) GENENTECH INC.
Query Match 7.1%; Score 281; DB 2; Length 483;
Best Local Similarity 23.2%; Pred. No. 3e-07;
RESULT 1339
ID AAR70848 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N67,R252,E275).
PN US5385732-A.

PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 281; DB 2; Length 483;
Best Local Similarity 23.2%; Pred. No. 3e-07;
RESULT 1340
ID AAR70849 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N67,K210,E275) .
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 281; DB 2; Length 483;
Best Local Similarity 23.2%; Pred. No. 3e-07;
RESULT 1341
ID AAR70854 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N67,R252,E275,I277) .
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 281; DB 2; Length 483;
Best Local Similarity 23.2%; Pred. No. 3e-07;
RESULT 1342
ID AAR70843 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N67,E275) .
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 281; DB 2; Length 483;
Best Local Similarity 23.2%; Pred. No. 3e-07;
RESULT 1343
ID AAR70846 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N67,K213,E275) .
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 281; DB 2; Length 483;
Best Local Similarity 23.2%; Pred. No. 3e-07;
RESULT 1344
ID AAR79144 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N67,S184,E275,I277) .
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 281; DB 2; Length 483;
Best Local Similarity 23.2%; Pred. No. 3e-07;
RESULT 1345
ID AAR70850 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N67,E275,I277) .
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 281; DB 2; Length 483;
Best Local Similarity 23.2%; Pred. No. 3e-07;
RESULT 1346
ID AAR70852 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N67,K213,E275,I277) .
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 281; DB 2; Length 483;
Best Local Similarity 23.2%; Pred. No. 3e-07;
RESULT 1347
ID AAR70847 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N67,R210,A211,R212,R213,E275) .
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 281; DB 2; Length 483;
Best Local Similarity 23.0%; Pred. No. 3e-07;
RESULT 1348
ID AAR70853 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N67,R210,A211,R212,R213,E275,I277) .
PN US5385732-A.
PD 31-JAN-1995.

PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 281; DB 2; Length 483;
Best Local Similarity 23.0%; Pred. No. 3e-07;
RESULT 1349
ID AAR60518 standard; protein; 487 AA.
DE Cattle Factor-Xa.
PN WO9418227-A2.
PD 18-AUG-1994.
PA (DENZ-) DENZYME APS.
Query Match 7.1%; Score 281; DB 2; Length 487;
Best Local Similarity 22.5%; Pred. No. 3.1e-07;
RESULT 1350
ID AAW76216 standard; protein; 488 AA.
DE Human Factor X protein.
PN WO9838317-A1.
PD 03-SEP-1998.
PA (IMMO) IMMOONO AG.
Query Match 7.1%; Score 281; DB 2; Length 488;
Best Local Similarity 24.0%; Pred. No. 3.1e-07;
RESULT 1351
ID AAW76217 standard; protein; 488 AA.
DE Human Factor X protein analogue.
PN WO9838317-A1.
PD 03-SEP-1998.
PA (IMMO) IMMOONO AG.
Query Match 7.1%; Score 281; DB 2; Length 488;
Best Local Similarity 22.6%; Pred. No. 3.1e-07;
RESULT 1352
ID AAW76218 standard; protein; 488 AA.
DE Human Factor X protein.
PN WO9838318-A1.
PD 03-SEP-1998.
PA (IMMO) IMMOONO AG.
Query Match 7.1%; Score 281; DB 2; Length 488;
Best Local Similarity 24.0%; Pred. No. 3.1e-07;
RESULT 1353
ID AAB70411 standard; protein; 488 AA.
DE Human factor X protein sequence SEQ ID NO:2.
PN WO200110896-A2.
PD 15-FEB-2001.
PA (BAXT) BAXTER AG.
Query Match 7.1%; Score 281; DB 4; Length 488;
Best Local Similarity 24.0%; Pred. No. 3.1e-07;
RESULT 1354
ID AAR60502 standard; protein; 492 AA.
DE Serine protease for fusion protein cleavage.
PN WO9418227-A2.
PD 18-AUG-1994.
PA (DENZ-) DENZYME APS.
Query Match 7.1%; Score 281; DB 2; Length 492;
Best Local Similarity 22.5%; Pred. No. 3.1e-07;
RESULT 1355
ID AAR09238 standard; protein; 525 AA.
DE t-PA deletion variant d300-301.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 281; DB 2; Length 525;
Best Local Similarity 22.8%; Pred. No. 3.3e-07;
RESULT 1356
ID AAR09276 standard; protein; 527 AA.
DE t-PA variant K416A, H417A, E418A.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 281; DB 2; Length 527;
Best Local Similarity 23.2%; Pred. No. 3.3e-07;
RESULT 1357
ID AAR09279 standard; protein; 527 AA.
DE t-PA variant R440A.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.

Query Match 7.1%; Score 281; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 3.3e-07;
RESULT 1358
ID AAR70875 standard; protein; 527 AA.
DE Human t-PA variant (N60,N103).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 281; DB 2; Length 527;
Best Local Similarity 23.2%; Pred. No. 3.3e-07;
RESULT 1359
ID AAR70876 standard; protein; 527 AA.
DE Human t-PA variant (N60,N67,N103).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 281; DB 2; Length 527;
Best Local Similarity 23.2%; Pred. No. 3.3e-07;
RESULT 1360
ID AAR70857 standard; protein; 527 AA.
DE Human t-PA variant (N67,A283,A287).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 281; DB 2; Length 527;
Best Local Similarity 23.2%; Pred. No. 3.3e-07;
RESULT 1361
ID AAR70898 standard; protein; 527 AA.
DE Human t-PA variant (N103,A364,A365,A366).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 281; DB 2; Length 527;
Best Local Similarity 23.2%; Pred. No. 3.3e-07;
RESULT 1362
ID AAR70906 standard; protein; 527 AA.
DE Human t-PA variant (N103,A449,A453).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 281; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 3.3e-07;
RESULT 1363
ID AAR70872 standard; protein; 527 AA.
DE Human t-PA variant (N67,A460,A462).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 281; DB 2; Length 527;
Best Local Similarity 23.2%; Pred. No. 3.3e-07;
RESULT 1364
ID AAR70842 standard; protein; 527 AA.
DE Wild type tissue plasminogen activator protein.
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 281; DB 2; Length 527;
Best Local Similarity 23.2%; Pred. No. 3.3e-07;
RESULT 1365
ID AAR13150 standard; protein; 558 AA.
DE T-PA with -ve charged finger and/or kringle domain (3).
PN JF03061483-A.
PD 18-MAR-1991.
PA (FUJI) FUJISAWA PHARM CO LTD.
Query Match 7.1%; Score 281; DB 2; Length 558;
Best Local Similarity 23.0%; Pred. No. 3.5e-07;
RESULT 1366
ID AAR13152 standard; protein; 559 AA.
DE T-PA with -ve charged finger and/or kringle domain (6).
PN JF03061483-A.
PD 18-MAR-1991.
PA (FUJI) FUJISAWA PHARM CO LTD.
Query Match 7.1%; Score 281; DB 2; Length 559;
Best Local Similarity 23.1%; Score 281; DB 2; Length 559;

Best Local Similarity 23.0%; Pred. No. 3.5e-07;
RESULT 1367
ID AAP80691 standard; protein; 1087 AA.
DE Hybrid plasminogen/t-PA compound 1.
PN EP292326-A.
PD 23-NOV-1988.
PA (BEECH) BECHAM GROUP PLC.
Query Match 7.1%; Score 281; DB 1; Length 1087;
Best Local Similarity 22.3%; Pred. No. 6.5e-07;
RESULT 1368
ID ABM81778 standard; protein; 264 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO2719, SEQ:4580.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 280.5; DB 8; Length 264;
Best Local Similarity 27.2%; Pred. No. 1.8e-07;
RESULT 1369
ID ABM64054 standard; protein; 279 AA.
DE Human diagnostic and therapeutic protease SEQ ID NO:4303.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 7.1%; Score 280.5; DB 8; Length 279;
Best Local Similarity 27.2%; Pred. No. 1.9e-07;
RESULT 1370
ID AAO30575 standard; protein; 406 AA.
DE Human coagulation factor VII variant (S314E/L305V/V158T/M298Q).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1371
ID AAO30604 standard; protein; 406 AA.
DE Human coagulation factor VII variant (K316H/L305V/V158T/K337A/M298Q).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1372
ID AAO30577 standard; protein; 406 AA.
DE Human coagulation factor VII variant (S314E/L305V/V158T/M298Q).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1373
ID AAO30594 standard; protein; 406 AA.
DE Human coagulation factor VII variant (K316H/L305V/K337A/M298Q).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1374
ID AAO30569 standard; protein; 406 AA.
DE Human coagulation factor VII variant (S314E/L305V/M298Q).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1375
ID AAO30606 standard; protein; 406 AA.
DE Human coagulation factor VII variant (K316H/L305V/V158T/K337A/M298Q).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;

RESULT 1376
ID AAO30613 standard; protein; 406 AA.
DE Human coagulation factor VII variant (K316Q/L305V/M298Q).
PN W02004000366-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1377
ID AAO30621 standard; protein; 406 AA.
DE Human coagulation factor VII variant (K316Q/L305V/V158T/M298Q).
PN W02004000366-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1378
ID AAO30619 standard; protein; 406 AA.
DE Human coagulation factor VII variant (K316Q/L305V/V158D/M298Q).
PN W02004000366-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1379
ID ADJ55876 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant / M298Q/ L305V/ K337A.
PN W02004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1380
ID ADJ55937 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant M298Q/ L305V/ K316H/ K337A.
PN W02004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1381
ID ADJ56047 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant F374Y/ V158D/ M298Q/ L305V/ S314E.
PN W02004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1382
ID ADJ55949 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant V158D/ M298Q/ L305V/ K316H/ K337A.
PN W02004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1383
ID ADJ55965 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant V158T/ M298Q/ L305V/ K316Q.
PN W02004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1384
ID ADJ55948 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant V158T/ M298Q/ L305V/ K316H/ K337A.
PN W02004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1385

ID ADJ56057 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant F374Y V158T M298Q L305V S314E.
PN W02004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1386
ID ADJ55885 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant V158T/ M298Q/ L305V/ K337A.
PN W02004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1387
ID ADJ55921 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant V158T/ M298Q/ L305V/ S314E.
PN W02004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1388
ID ADJ55958 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant M298Q/ L305V/ K316Q.
PN W02004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1389
ID ADJ55963 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant V158D/ M298Q/ L305V/ K316Q.
PN W02004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1390
ID ADJ56016 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant F374Y/ L305V/ M298Q/ S314E.
PN W02004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1391
ID ADJ56046 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant F374Y/ V158D/ M298Q/ L305V/ K337A.
PN W02004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1392
ID ADJ55919 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant V158D/ M298Q/ L305V/ S314E.
PN W02004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1393
ID ADJ56056 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant F374Y/ V158T/ M298Q/ L305V/ K337A.
PN W02004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1394
ID ADJ55887 standard; protein; 406 AA.

DE Human factor VII polypeptide mutant V158D/M298Q/L305V/K337A.
PN W02004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1395
ID ADV55914 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant M298Q/L305V/S314E.
PN W02004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1396
ID ADV5604 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant F374Y/L305V/K337A/M298Q.
PN W02004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1397
ID ADO10616 standard; protein; 406 AA.
DE Human factor VII/VIIa protein mutant #52.
PN W02004029091-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.6%; Pred. No. 2.8e-07;
RESULT 1398
ID ADO10607 standard; protein; 406 AA.
DE Human factor VII/VIIa protein mutant #43.
PN W02004029091-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.6%; Pred. No. 2.8e-07;
RESULT 1399
ID ADV44553 standard; protein; 406 AA.
DE Human factor VII mutant S314E/L305V/M298Q.
PN W02004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1400
ID ADV44514 standard; protein; 406 AA.
DE Human factor VII mutant L305V/K337A/M298Q.
PN W02004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1401
ID ADV44526 standard; protein; 406 AA.
DE Human factor VII mutant L305V/M298Q/K337A/V158D.
PN W02004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1402
ID ADV44588 standard; protein; 406 AA.
DE Human factor VII mutant K316H/L305V/V158T/K337A/M298Q.
PN W02004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1403

ID ADV44597 standard; protein; 406 AA.
DE Human factor VII mutant K316Q/L305V/M298Q.
PN W02004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1404
ID ADV44605 standard; protein; 406 AA.
DE Human factor VII mutant K316Q/L305V/V158T/M298Q.
PN W02004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1405
ID ADV44655 standard; protein; 406 AA.
DE Human factor VII mutant F374Y/L305V/M298Q/S314E.
PN W02004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1406
ID ADV44645 standard; protein; 406 AA.
DE Human factor VII mutant F374Y/L305V/K337A/M298Q.
PN W02004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1407
ID ADV44686 standard; protein; 406 AA.
DE Human factor VII mutant F374Y/L305V/V158D/S314E/M298Q.
PN W02004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1408
ID ADV44524 standard; protein; 406 AA.
DE Human factor VII mutant S314E/L305V/V158D/M298Q.
PN W02004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1409
ID ADV44559 standard; protein; 406 AA.
DE Human factor VII mutant L305V/M298Q/K337A/V158T.
PN W02004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1410
ID ADV44694 standard; protein; 406 AA.
DE Human factor VII mutant F374Y/V158T/L305V/K337A/M298Q.
PN W02004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1411
ID ADV44684 standard; protein; 406 AA.
DE Human factor VII mutant F374Y/L305V/V158D/K337A/M298Q.
PN W02004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1412
ID ADV44561 standard; protein; 406 AA.

DE Human factor VII mutant S314E/L305V/V158T/M298Q.
PN W02004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1413
ID ADV44696 standard; protein; 406 AA.
DE Human factor VII mutant F374Y/V158T/L305V/S314E/M298Q.
PN W02004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1414
ID ADV44578 standard; protein; 406 AA.
DE Human factor VII mutant K316H/L305V/K337A/M298Q.
PN W02004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1415
ID ADV44590 standard; protein; 406 AA.
DE Human factor VII mutant K316H/L305V/V158D/K337A/M298Q.
PN W02004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1416
ID ADV44603 standard; protein; 406 AA.
DE Human factor VII mutant K316Q/L305V/V158D/M298Q.
PN W02004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1417
ID ADM20180 standard; protein; 406 AA.
DE Human factor VII (FVII) protein variant sequence #18.
PN W02004111242-A1.
PD 23-DEC-2004.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.6%; Pred. No. 2.8e-07;
RESULT 1418
ID ADM20183 standard; protein; 406 AA.
DE Human factor VII (FVII) protein variant sequence #21.
PN W02004111242-A1.
PD 23-DEC-2004.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.6%; Pred. No. 2.8e-07;
RESULT 1419
ID ADV74113 standard; protein; 406 AA.
DE Human factor VII variant polypeptide #56.
PN W02005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1420
ID ADV74285 standard; protein; 406 AA.
DE Human factor VII variant polypeptide #228.
PN W02005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1421
ID ADV74273 standard; protein; 406 AA.
DE Human factor VII variant polypeptide #85.
PN W02005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1422
ID ADV74150 standard; protein; 406 AA.
DE Human factor VII variant polypeptide #93.
PN W02005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1423
ID ADV74177 standard; protein; 406 AA.
DE Human factor VII variant polypeptide #120.
PN W02005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1424
ID ADV74073 standard; protein; 406 AA.
DE Human factor VII variant polypeptide #16.
PN W02005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.6%; Pred. No. 2.8e-07;
RESULT 1425
ID ADV74148 standard; protein; 406 AA.
DE Human factor VII variant polypeptide #91.
PN W02005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1426
ID ADV74179 standard; protein; 406 AA.
DE Human factor VII variant polypeptide #122.
PN W02005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1427
ID ADV74275 standard; protein; 406 AA.
DE Human factor VII variant polypeptide #218.
PN W02005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1428
ID ADV74283 standard; protein; 406 AA.
DE Human factor VII variant polypeptide #226.
PN W02005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1429
ID ADV74103 standard; protein; 406 AA.
DE Human factor VII variant polypeptide #46.
PN W02005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1430
ID ADV74273 standard; protein; 406 AA.

DE Human Factor VII variant polypeptide #216.
PN WO2005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1431
ID ADY74194 standard; protein; 406 AA.
DE Human Factor VII variant polypeptide #137.
PN WO2005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1432
ID ADY74186 standard; protein; 406 AA.
DE Human Factor VII variant polypeptide #129.
PN WO2005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1433
ID ADY74192 standard; protein; 406 AA.
DE Human Factor VII variant polypeptide #135.
PN WO2005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1434
ID ADY74234 standard; protein; 406 AA.
DE Human Factor VII variant polypeptide #177.
PN WO2005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1435
ID ADY74115 standard; protein; 406 AA.
DE Human Factor VII variant polypeptide #58.
PN WO2005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1436
ID ADY74244 standard; protein; 406 AA.
DE Human Factor VII variant polypeptide #187.
PN WO2005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1437
ID ADY74167 standard; protein; 406 AA.
DE Human Factor VII variant polypeptide #110.
PN WO2005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1438
ID AEF15119 standard; protein; 406 AA.
DE Variant human coagulation Factor VII protein #88.
PN WO2005123916-A2.
PD 29-DEC-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 10; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1439
ID AEF15089 standard; protein; 406 AA.
DE Variant human coagulation Factor VII protein #58.

PN WO2005123916-A2.
PD 29-DEC-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 10; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1440
ID AEF15073 standard; protein; 406 AA.
DE Variant human coagulation Factor VII protein #42.
PN WO2005123916-A2.
PD 29-DEC-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 10; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1441
ID AEF15099 standard; protein; 406 AA.
DE Variant human coagulation Factor VII protein #68.
PN WO2005123916-A2.
PD 29-DEC-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 10; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1442
ID AEF15146 standard; protein; 406 AA.
DE Variant human coagulation Factor VII protein #115.
PN WO2005123916-A2.
PD 29-DEC-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 10; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1443
ID AEF15136 standard; protein; 406 AA.
DE Variant human coagulation Factor VII protein #105.
PN WO2005123916-A2.
PD 29-DEC-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 10; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1444
ID AEF15134 standard; protein; 406 AA.
DE Variant human coagulation Factor VII protein #103.
PN WO2005123916-A2.
PD 29-DEC-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 10; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1445
ID AEF15077 standard; protein; 406 AA.
DE Variant human coagulation Factor VII protein #46.
PN WO2005123916-A2.
PD 29-DEC-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 10; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1446
ID AEF15086 standard; protein; 406 AA.
DE Variant human coagulation Factor VII protein #55.
PN WO2005123916-A2.
PD 29-DEC-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 10; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1447
ID AEF15144 standard; protein; 406 AA.
DE Variant human coagulation Factor VII protein #113.
PN WO2005123916-A2.
PD 29-DEC-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 10; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1448
ID ADM20193 standard; protein; 407 AA.
DE Human factor VII (FVII) protein variant sequence #31.

PD 23-DEC-2004.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.1%; Score 280.5; DB 9; Length 407;
Best Local Similarity 22.6%; Pred. No. 2.8e-07;
RESULT 1449
ID AWM20196 standard; protein; 407 AA.
DE Human factor VII (FVII) protein variant sequence #34.
PN W0200411242-A1.
PD 23-DEC-2004.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.1%; Score 280.5; DB 9; Length 407;
Best Local Similarity 22.6%; Pred. No. 2.8e-07;
RESULT 1450
ID AAR09221 standard; protein; 526 AA.
DE t-PA deletion variant d297.
PN W09002798-A.
PD 22-MAR-1990.
PA (GENETH) GENENTECH INC.
Query Match 7.1%; Score 280.5; DB 2; Length 526;
Best Local Similarity 23.1%; Pred. No. 3.5e-07;
RESULT 1451
ID AAP70020 standard; protein; 561 AA.
DE Sequence of tissue plasminogen activator (tPA).
PN EP242836-A.
PD 28-OCT-1987.
PA (BOEF) BOEHRINGER MANNHEIM GMBH.
Query Match 7.1%; Score 280.5; DB 1; Length 561;
Best Local Similarity 21.7%; Pred. No. 3.7e-07;
RESULT 1452
ID AAR6249 standard; protein; 583 AA.
DE Bovine recombinant prothrombin, expressed in Escherichia coli.
PN W02003052059-A2.
PD 26-JUN-2003.
PA (ELIL) LILLY & CO ELI.
Query Match 7.1%; Score 280.5; DB 7; Length 583;
Best Local Similarity 21.9%; Pred. No. 3.9e-07;
RESULT 1453
ID AAR62451 standard; protein; 635 AA.
DE Bovine recombinant prothrombin, expressed in CHO cells.
PN W02003052059-A2.
PD 26-JUN-2003.
PA (ELIL) LILLY & CO ELI.
Query Match 7.1%; Score 280.5; DB 7; Length 635;
Best Local Similarity 21.9%; Pred. No. 4.2e-07;
RESULT 1454
ID ADM20176 standard; protein; 406 AA.
DE Human factor VII (FVII) protein variant sequence #14.
PN W0200411242-A1.
PD 23-DEC-2004.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.1%; Score 280; DB 9; Length 406;
Best Local Similarity 22.1%; Pred. No. 2.9e-07;
RESULT 1455
ID AWM20188 standard; protein; 407 AA.
DE Human factor VII (FVII) protein variant sequence #26.
PN W0200411242-A1.
PD 23-DEC-2004.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.1%; Score 280; DB 9; Length 407;
Best Local Similarity 22.2%; Pred. No. 2.9e-07;
RESULT 1456
ID AAR37402 standard; protein; 448 AA.
DE Factor X.
PN W09309803-A1.
PD 27-MAY-1993.
PA (SCHAF) SCHAFER S C.
Query Match 7.1%; Score 280; DB 2; Length 448;
Best Local Similarity 24.0%; Pred. No. 3.2e-07;

RESULT 1457
ID AAW6092 standard; peptide; 448 AA.
DE Human factor X variant.
PN W09839456-A1.
PD 11-SEP-1998.
PA (UNIW) UNIV WASHINGTON.
Query Match 7.1%; Score 280; DB 2; Length 448;
Best Local Similarity 24.0%; Pred. No. 3.2e-07;
RESULT 1458
ID AEC01740 standard; protein; 490 AA.
DE Modified FVII-UNA-GPI cassette.
PN W02005073375-A1.
PD 11-AUG-2005.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.1%; Score 280; DB 9; Length 490;
Best Local Similarity 22.1%; Pred. No. 3.5e-07;
RESULT 1459
ID AAR09245 standard; protein; 525 AA.
DE t-PA deletion variant d297, d305.
PN W09002798-A.
PD 22-MAR-1990.
PA (GENETH) GENENTECH INC.
Query Match 7.1%; Score 280; DB 2; Length 525;
Best Local Similarity 23.1%; Pred. No. 3.7e-07;
RESULT 1460
ID AAR05488 standard; protein; 527 AA.
DE tPA024 precursor protein.
PN EP373896-A.
PD 20-JUN-1990.
PA (YAMA) YAMANOUCHI PHARM CO LTD.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1461
ID AAR09267 standard; protein; 527 AA.
DE t-PA variant D283A, H287A.
PN W09002798-A.
PD 22-MAR-1990.
PA (GENETH) GENENTECH INC.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1462
ID AAR09282 standard; protein; 527 AA.
DE t-PA variant D460A, R462A.
PN W09002798-A.
PD 22-MAR-1990.
PA (GENETH) GENENTECH INC.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1463
ID AAR13911 standard; protein; 527 AA.
DE t-PA deriv. (II).
PN EP445464-A.
PD 11-SEP-1991.
PA (KANF) KANEGAFUCHI KAGAKU KOGYO KK.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1464
ID AAR13914 standard; protein; 527 AA.
DE t-PA deriv. (V).
PN EP445464-A.
PD 11-SEP-1991.
PA (KANF) KANEGAFUCHI KAGAKU KOGYO KK.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1465
ID AAR13912 standard; protein; 527 AA.
DE t-PA deriv. (III).
PN EP445464-A.
PD 11-SEP-1991.
PA (KANF) KANEGAFUCHI KAGAKU KOGYO KK.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;

Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1466
ID AAR13910 standard; protein; 527 AA.
DE t-PA deriv. (I).
PN EP445464-A.
PD 11-SEP-1991.
PA (KANF) KANEGAFUCHI KAGAKU KOGYO KK.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1467
ID AAR21594 standard; protein; 527 AA.
DE t-PA variant - D95A.
PN MO9202612-A.
PD 20-FEB-1992.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1468
ID AAR21593 standard; protein; 527 AA.
DE t-PA variant - E94A.
PN MO9202612-A.
PD 20-FEB-1992.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1469
ID AAR20221 standard; protein; 527 AA.
DE t-PA analogue expressed by pCDM6-013.
PN JP03285680-A.
PD 16-DEC-1991.
PA (SUMU) SUMITOMO SEIYAKU KK.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1470
ID AAR20215 standard; protein; 527 AA.
DE R462G t-PA analogue.
PN JP03285680-A.
PD 16-DEC-1991.
PA (SUMU) SUMITOMO SEIYAKU KK.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1471
ID AAR20216 standard; protein; 527 AA.
DE R462G t-PA analogue.
PN JP03285680-A.
PD 16-DEC-1991.
PA (SUMU) SUMITOMO SEIYAKU KK.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1472
ID AAR20222 standard; protein; 527 AA.
DE t-PA analogue expressed by pCDM6-014.
PN JP03285680-A.
PD 16-DEC-1991.
PA (SUMU) SUMITOMO SEIYAKU KK.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1473
ID AAR20223 standard; protein; 527 AA.
DE t-PA analogue expressed by pCDM6-018.
PN JP03285680-A.
PD 16-DEC-1991.
PA (SUMU) SUMITOMO SEIYAKU KK.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1474
ID AAR44811 standard; protein; 527 AA.
DE Human tPA variant N67.
PN US5270198-A.
PD 14-DEC-1993.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;

RESULT 1475
ID AAR70865 standard; protein; 527 AA.
DE Human t-PA variant (N67,A410).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 22.9%; Pred. No. 3.7e-07;
RESULT 1476
ID AAM57778 standard; protein; 527 AA.
DE R275E,H417D human tissue-type plasminogen activator protein mutant.
PN MO9821320-A2.
PD 22-MAY-1998.
PA (SCRI) SCRIPPS RES INST.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1477
ID AAM45907 standard; peptide; 527 AA.
DE Single chain form of the intact t-PA molecule.
PN MO9802454-A2.
PD 22-JAN-1998.
PA (ADPR-) ADPROTECH PLC.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1478
ID AAE24190 standard; protein; 527 AA.
DE Human tissue plasminogen activator (tPA) protein.
PN MO200240696-A2.
PD 23-MAY-2002.
PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
Query Match 7.1%; Score 280; DB 5; Length 527;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1479
ID AAG79362 standard; protein; 527 AA.
DE Human tissue plasminogen activator.
PN MO200243747-A2.
PD 06-JUN-2002.
PA (ISIS-) ISIS INNOVATION LTD.
Query Match 7.1%; Score 280; DB 5; Length 527;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1480
ID AAE25044 standard; protein; 527 AA.
DE Human tissue plasminogen activator (tPA) protein.
PN MO200240650-A2.
PD 23-MAY-2002.
PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
Query Match 7.1%; Score 280; DB 5; Length 527;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1481
ID ADL92126 standard; protein; 527 AA.
DE Alteplase protein sequence.
PN MO2003099862-A1.
PD 04-DEC-2003.
PA (NANO-) APPLIED NANOSYSTEMS BV.
Query Match 7.1%; Score 280; DB 8; Length 527;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1482
ID AED66381 standard; protein; 528 AA.
DE Recombinant human tissue type plasminogen activator (tPA) protein.
PN KR2005018231-A.
PD 23-FEB-2005.
PA (BIOB-) BIOBUD CO LTD.
Query Match 7.1%; Score 280; DB 9; Length 528;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1483
ID ABM82630 standard; protein; 534 AA.
DE Human diagnostic and therapeutic proprotein SEQ ID NO:2879.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 7.1%; Score 280; DB 8; Length 534;
Best Local Similarity 22.7%; Pred. No. 3.8e-07;
RESULT 1484

ID ABM2821 standard; protein; 534 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:3070.
PN MO2004023973-A2.
PD 25-MAR-2004.
PA (INCYTE-) INCYTE CORP.
Query Match 7.1%; Score 280; DB 8; Length 534;
Best Local Similarity 22.7%; Pred. No. 3.8e-07;
RESULT 1485
ID AAR13020 standard; protein; 557 AA.
DE T-PA variant contg. fibrinectin for thrombosis lysis (4).
PN JP03061482-A.
PD 18-MAR-1991.
PA (FUJII) FUJISAWA PHARM CO LTD.
Query Match 7.1%; Score 280; DB 2; Length 557;
Best Local Similarity 23.0%; Pred. No. 3.9e-07;
RESULT 1486
ID AAR13149 standard; protein; 557 AA.
DE T-PA variant contg. fibrinectin for thrombosis lysis (4).
PN JP03061482-A.
PD 18-MAR-1991.
PA (FUJII) FUJISAWA PHARM CO LTD.
Query Match 7.1%; Score 280; DB 2; Length 557;
Best Local Similarity 23.0%; Pred. No. 3.9e-07;
RESULT 1487
ID AAP50219 standard; protein; 561 AA.
DE Tissue plasminogen activator encoded by cDNA clone.
PN EP143081-A.
PD 29-MAY-1985.
PA (CIBA) CIBA GEIGY AG.
Query Match 7.1%; Score 280; DB 1; Length 561;
Best Local Similarity 23.0%; Pred. No. 4e-07;
RESULT 1488
ID AAP60790 standard; protein; 562 AA.
DE Sequence of human pre-tissue plasminogen activator (pre-t-PA).
PN GB2133804-A.
PD 22-OCT-1986.
PA (GENTECH) GENENTECH INC.
Query Match 7.1%; Score 280; DB 1; Length 562;
Best Local Similarity 23.0%; Pred. No. 4e-07;
RESULT 1489
ID AAP60810 standard; protein; 562 AA.
DE Sequence of modified human tissue plasminogen activator (t-PA).
PN FR2581652-A.
PD 14-NOV-1986.
PA (GENTECH) GENENTECH INC.
Query Match 7.1%; Score 280; DB 1; Length 562;
Best Local Similarity 23.0%; Pred. No. 4e-07;
RESULT 1490
ID AAP60214 standard; protein; 562 AA.
DE Sequence of active human uterine tissue plasminogen activator (UTPA).
PN EP178105-A.
PD 16-APR-1986.
PA (INTEG-) INTEG GENETICS INC.
Query Match 7.1%; Score 280; DB 1; Length 562;
Best Local Similarity 23.0%; Pred. No. 4e-07;
RESULT 1491
ID AAP81913 standard; protein; 562 AA.
DE Tissue plasminogen activator encoded by pEM1-CPA.
PN WO8800242-A.
PD 14-JAN-1988.
PA (DAMO-) DAMO BIOTECH INC.
Query Match 7.1%; Score 280; DB 1; Length 562;
Best Local Similarity 23.0%; Pred. No. 4e-07;
RESULT 1492
ID AAP80655 standard; protein; 562 AA.
DE Tissue plasminogen activator analogue.
PN EP293934-A.
PD 07-DEC-1988.
PA (ZYMO) ZYMOGENETICS INC.
PA (NOVO) NOVO IND AS.
PA (EISA) EISA CO LTD.
Query Match 7.1%; Score 280; DB 1; Length 562;
Best Local Similarity 23.0%; Pred. No. 4e-07;
RESULT 1493
ID AAP94406 standard; protein; 562 AA.
DE Sequence encoded by native tPA of plasmid pST112.
PN EP102456-A.
PD 08-FEB-1989.
PA (FUJII) FUJISAWA PHARM CO LTD.
Query Match 7.1%; Score 280; DB 1; Length 562;
Best Local Similarity 23.0%; Pred. No. 4e-07;
RESULT 1494
ID AAP93716 standard; protein; 562 AA.
DE Human melanoma t-PA encoded by plasmid pKG12.
PN EP297066-A.
PD 28-DEC-1988.
PA (KABI) KABI GEN AB.
Query Match 7.1%; Score 280; DB 1; Length 562;
Best Local Similarity 23.0%; Pred. No. 4e-07;
RESULT 1495
ID AAP90916 standard; protein; 562 AA.
DE Human tissue plasminogen activator.
PN JP01174388-A.
PD 10-JUL-1989.
PA (FUJII) FUJISAWA PHARM CO LTD.
Query Match 7.1%; Score 280; DB 1; Length 562;
Best Local Similarity 23.0%; Pred. No. 4e-07;
RESULT 1496
ID AAR09288 standard; protein; 562 AA.
DE Sequence of tissue plasminogen activator analogue BBNT11 (Ser 67, Leu 68).
PN WO8912681-A.
PD 28-DEC-1989.
PA (BRIT) BRIT BIO-TECHN LTD.
Query Match 7.1%; Score 280; DB 2; Length 562;
Best Local Similarity 23.0%; Pred. No. 4e-07;
RESULT 1497
ID AAR06237 standard; protein; 562 AA.
DE Novel tissue plasminogen activator (tPA) encoded by plasmid pST112.
PN EP379890-A.
PD 01-AUG-1990.
PA (FUJII) FUJISAWA PHARM CO LTD.
Query Match 7.1%; Score 280; DB 2; Length 562;
Best Local Similarity 23.0%; Pred. No. 4e-07;
RESULT 1498
ID AAR04700 standard; protein; 562 AA.
DE Sequence of tissue plasminogen activator (t-PA) analogue t-PA K419S with DE with altered residues 419 and 420.
PN EP351246-A.
PD 17-JAN-1990.
PA (NOVO) NOVO-NORDISK AS.
PA (NOVO) NOVO-NORDISK AS.
Query Match 7.1%; Score 280; DB 2; Length 562;
Best Local Similarity 23.0%; Pred. No. 4e-07;
RESULT 1499
ID AAR04701 standard; protein; 562 AA.
DE Sequence of tissue plasminogen activator (t-PA) analogue t-PA K419S with DE altered residue 419.
PN EP351246-A.
PD 17-JAN-1990.
PA (NOVO) NOVO-NORDISK AS.
PA (NOVO) NOVO-NORDISK AS.
Query Match 7.1%; Score 280; DB 2; Length 562;
Best Local Similarity 23.0%; Pred. No. 4e-07;
RESULT 1500
ID AAR04699 standard; protein; 562 AA.
DE Native tissue plasminogen activator (t-PA).
PN EP351246-A.
PD 17-JAN-1990.
PA (NOVO) NOVO-NORDISK AS.
PA (NOVO) NOVO-NORDISK AS.
Query Match 7.1%; Score 280; DB 2; Length 562;
Best Local Similarity 23.0%; Pred. No. 4e-07;

GenCore version 6.2
Copyright (c) 1993 - 2007 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 4, 2007, 22:20:34 ; Search time 187 Seconds

(without alignments)
1785.501 Million cell updates/sec

Perfect score: 3945

Sequence: 1 MEIGCMTQLGTLFLQLLTLIS.....LSTAFKVLPEFKWIERNNK 720

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database :

1: /EMC_Celerra_SIDS3/ptodata/2/pubppaa/US07_PUBSCOMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubppaa/US08_PUBSCOMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubppaa/US09_PUBSCOMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubppaa/US10_PUBSCOMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubppaa/US10B_PUBSCOMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubppaa/US11_PUBSCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
27	3945	100.0	720	3	US-09-997-428-231
562	3945	100.0	720	4	US-10-174-587-170
626	3945	100.0	720	4	US-10-063-742-38
741	3945	100.0	720	5	US-10-972-317-38
743	3945	100.0	720	5	US-10-950-374-231
751	3945	100.0	720	6	US-11-102-240-38
752	3945	100.0	720	6	US-11-103-195-38
753	3939	99.8	720	4	US-10-004-551-4
754	3939	99.8	720	4	US-10-098-871-26
755	3939	99.8	720	6	US-11-045-029-4
756	3921.5	99.4	727	4	US-10-408-765A-1196
757	3500.5	88.7	649	4	US-10-574-639-17
758	3500.5	88.7	649	4	US-10-333-574-17
759	3089.5	78.3	567	4	US-10-004-551-2
760	3089.5	78.3	567	6	US-11-045-029-2
761	2946.5	74.7	570	4	US-10-067-422-9
762	2413	61.2	455	3	US-09-833-245-1401
763	2413	61.2	455	6	US-11-264-096-1401
764	1708.5	43.3	323	6	US-09-833-245-1402
765	1708.5	43.3	323	6	US-11-264-096-1402
766	949	24.1	181	5	US-10-756-149-4828
767	672	17.0	1019	4	US-10-183-992-4
768	672	17.0	1019	5	US-10-480-254-4
769	665	16.9	1019	4	US-10-183-992-8
770	665	16.9	1019	4	US-10-638-125-4
771	665	16.9	1019	5	US-10-480-254-8
772	665	16.9	1083	4	US-10-183-992-6
773	665	16.9	1083	4	US-10-638-125-2

774	665	16.9	1083	5	US-10-480-254-6	Sequence 6, Appl1
775	478	12.1	699	6	US-11-150-887-43	Sequence 43, Appl1
776	476	12.1	699	6	US-10-388-322-2	Sequence 2, Appl1
777	475	12.0	699	5	US-10-820-155-93	Sequence 93, Appl1
778	475	12.0	704	5	US-10-989-891-148	Sequence 148, Appl1
779	471	11.9	728	4	US-10-148-671-5	Sequence 5, Appl1
780	469.5	11.9	679	3	US-09-874-198-6	Sequence 6, Appl1
781	469.5	11.9	679	3	US-09-874-238-6	Sequence 6, Appl1
782	469.5	11.9	679	6	US-11-032-149-6	Sequence 6, Appl1
783	468	11.9	728	4	US-10-388-322-4	Sequence 4, Appl1
784	468	11.9	728	5	US-10-820-155-92	Sequence 92, Appl1
785	461	11.7	728	5	US-10-239-032-1	Sequence 1, Appl1
786	423	10.7	670	6	US-11-150-883-55	Sequence 55, Appl1
787	423	10.7	685	6	US-11-150-883-54	Sequence 54, Appl1
788	412	10.4	670	6	US-11-150-883-52	Sequence 52, Appl1
789	412	10.4	685	6	US-11-150-883-51	Sequence 51, Appl1
790	403.5	10.2	688	3	US-09-874-198-7	Sequence 7, Appl1
791	403.5	10.2	688	3	US-09-874-238-7	Sequence 7, Appl1
792	403.5	10.2	688	6	US-11-032-149-7	Sequence 7, Appl1
793	403.5	10.2	705	3	US-09-808-602-94	Sequence 94, Appl1
794	403.5	10.2	705	3	US-09-808-198-81	Sequence 81, Appl1
795	403.5	10.2	705	4	US-10-257-021-66	Sequence 66, Appl1
796	403.5	10.2	705	5	US-10-287-436A-452	Sequence 452, Appl1
797	403.5	10.2	705	5	US-10-287-436A-1152	Sequence 1152, Appl1
798	403.5	10.2	705	5	US-10-989-891-144	Sequence 144, Appl1
799	403.5	10.2	705	5	US-10-821-234-1532	Sequence 1532, Appl1
800	401.5	10.2	686	3	US-09-874-198-2	Sequence 2, Appl1
801	401.5	10.2	686	3	US-09-874-238-2	Sequence 2, Appl1
802	401.5	10.2	686	5	US-10-974-148-12	Sequence 12, Appl1
803	401.5	10.2	686	5	US-10-820-155-90	Sequence 90, Appl1
804	401.5	10.2	686	5	US-10-974-148-12	Sequence 12, Appl1
805	401.5	10.2	686	5	US-11-032-149-2	Sequence 4705, Appl1
806	401.5	10.2	686	6	US-11-150-883-5	Sequence 2, Appl1
807	401.5	10.2	686	6	US-11-150-887-5	Sequence 5, Appl1
808	400.5	10.2	686	4	US-10-388-322-3	Sequence 3, Appl1
809	400.5	10.2	686	4	US-10-332-713-2	Sequence 2, Appl1
810	400.5	10.2	686	5	US-10-989-891-152	Sequence 152, Appl1
811	399.5	10.1	671	6	US-11-150-883-6	Sequence 6, Appl1
812	399.5	10.1	671	6	US-11-150-887-6	Sequence 6, Appl1
813	398.5	10.1	671	4	US-10-332-713-3	Sequence 3, Appl1
814	336	8.5	760	3	US-09-925-301-1024	Sequence 1024, Appl1
815	334	8.5	673	3	US-09-874-198-8	Sequence 8, Appl1
816	334	8.5	673	3	US-09-874-238-8	Sequence 8, Appl1
817	334	8.5	673	6	US-11-032-149-8	Sequence 8, Appl1
818	334	8.5	673	6	US-10-820-155-81	Sequence 81, Appl1
819	334	8.5	673	5	US-10-287-436A-99	Sequence 99, Appl1
820	334	8.5	673	5	US-10-287-436A-1256	Sequence 1256, Appl1
821	334	8.5	673	5	US-10-631-467-644	Sequence 644, Appl1
822	334	8.5	673	5	US-10-989-891-143	Sequence 143, Appl1
823	334	8.5	673	5	US-10-821-234-1533	Sequence 1533, Appl1
824	334	8.5	673	6	US-11-169-041-149	Sequence 149, Appl1
825	332	8.4	855	4	US-10-072-012-354	Sequence 354, Appl1
826	332	8.4	855	4	US-10-072-012-420	Sequence 420, Appl1
827	332	8.4	855	4	US-10-037-417-132	Sequence 132, Appl1
828	332	8.4	855	6	US-11-019-711-132	Sequence 132, Appl1
829	331.5	8.4	855	6	US-09-776-197-64	Sequence 64, Appl1
830	331.5	8.4	855	3	US-10-157-031-267	Sequence 267, Appl1
831	331.5	8.4	855	4	US-10-156-214A-31	Sequence 31, Appl1
832	331.5	8.4	855	4	US-10-729-807-37	Sequence 37, Appl1
833	330.5	8.4	855	4	US-10-408-765A-2243	Sequence 2243, Appl1
834	329.5	8.4	855	4	US-10-016-248-47	Sequence 47, Appl1
835	329.5	8.4	855	4	US-10-408-765A-2286	Sequence 2286, Appl1
836	329.5	8.4	855	4	US-10-016-248-46	Sequence 46, Appl1
837	329.5	8.4	855	5	US-10-453-377-1112	Sequence 1112, Appl1
838	329	8.3	854	4	US-10-016-248-45	Sequence 45, Appl1
839	328.5	8.3	854	4	US-10-467-044-11	Sequence 11, Appl1
840	328.5	8.3	854	6	US-11-046-866-11	Sequence 11, Appl1
841	328.5	8.3	854	6	US-10-276-934-12	Sequence 12, Appl1
842	328.5	8.3	854	4	US-10-276-934-10	Sequence 10, Appl1
843	328.5	8.3	854	4	US-10-276-934-9	Sequence 9, Appl1
844	328.5	8.3	854	4	US-10-276-934-11	Sequence 11, Appl1
845	328.5	8.3	854	4	US-10-276-934-14	Sequence 14, Appl1
846	328.5	8.3	854	4	US-10-276-934-13	Sequence 13, Appl1

847	328	8.3	762	4	US-10-729-807-1	Sequence 1, Appl1	920	309.5	7.8	799	4	US-10-072-012-410	Sequence 410, App
848	328	8.3	851	4	US-10-276-774-1798	Sequence 1798, Ap	921	309.5	7.8	799	4	US-10-072-012-416	Sequence 416, App
849	328	8.3	851	4	US-10-296-115-1143	Sequence 1185, Ap	922	309	7.8	799	4	US-10-182-263-3	Sequence 3, Appl1
850	328	8.3	855	4	US-10-295-027-1185	Sequence 353, App	923	309	7.8	799	4	US-10-182-263-5	Sequence 5, Appl1
851	328	8.3	855	4	US-10-072-012-353	Sequence 412, App	924	308	7.8	799	4	US-10-182-263-4	Sequence 4, Appl1
852	328	8.3	855	4	US-10-072-012-412	Sequence 419, App	925	301.5	7.6	799	4	US-09-825-751A-72	Sequence 72, Appl1
853	328	8.3	855	4	US-10-072-012-419	Sequence 612, App	926	301.5	7.6	799	4	US-10-851-438-72	Sequence 72, Appl1
854	327.5	8.3	449	3	US-09-925-302-612	Sequence 612, App	927	299.5	7.6	799	4	US-10-406-031-2	Sequence 2, Appl1
855	327.5	8.3	449	3	US-09-925-302-612	Sequence 612, App	928	298	7.6	799	4	US-10-104-042-394	Sequence 3904, Ap
856	327	8.3	688	4	US-10-453-827-884	Sequence 884, App	929	298	7.6	799	4	US-10-072-512-394	Sequence 3904, Ap
857	327	8.3	777	4	US-10-072-012-44	Sequence 44, App	930	296	7.5	799	4	US-10-051-874-101	Sequence 101, App
858	327	8.3	855	3	US-09-776-191-2	Sequence 2, Appl1	931	296	7.5	799	4	US-09-981-151A-87	Sequence 87, Appl1
859	327	8.3	855	3	US-10-099-700A-2	Sequence 2, Appl1	932	296	7.5	799	4	US-09-981-151A-96	Sequence 96, Appl1
860	327	8.3	855	4	US-10-190-030A-2	Sequence 2, Appl1	933	296	7.5	799	4	US-10-032-189-66	Sequence 66, Appl1
861	327	8.3	855	4	US-10-302-840A-2	Sequence 2, Appl1	934	296	7.5	799	4	US-10-074-978A-221	Sequence 221, App
862	327	8.3	855	4	US-10-267-219-2	Sequence 2, Appl1	935	296	7.5	799	4	US-10-074-978A-222	Sequence 222, App
863	327	8.3	855	4	US-10-112-221A-2	Sequence 2, Appl1	936	296	7.5	799	4	US-10-055-569A-96	Sequence 96, Appl1
864	327	8.3	855	4	US-10-104-271-2	Sequence 2, Appl1	937	296	7.5	799	4	US-10-042-865-155	Sequence 155, App
865	327	8.3	855	4	US-10-147-211A-2	Sequence 2, Appl1	938	296	7.5	799	4	US-10-072-012-804	Sequence 804, App
866	327	8.3	855	4	US-10-156-214A-2	Sequence 2, Appl1	939	296	7.5	799	4	US-10-072-012-812	Sequence 812, App
867	327	8.3	855	4	US-10-072-012-352	Sequence 352, App	940	296	7.5	799	4	US-10-037-417-135	Sequence 135, App
868	327	8.3	855	4	US-10-072-012-411	Sequence 411, App	941	296	7.5	799	4	US-11-019-711-135	Sequence 135, App
869	327	8.3	855	4	US-10-072-012-418	Sequence 418, App	942	296	7.5	799	4	US-10-450-763-51801	Sequence 51801, A
870	327	8.3	855	4	US-10-600-187-2	Sequence 2, Appl1	943	293	7.4	799	4	US-10-114-153-50	Sequence 50, Appl1
871	327	8.3	855	4	US-10-612-466B-2	Sequence 2, Appl1	944	293	7.4	799	4	US-10-741-600-909	Sequence 909, App
872	327	8.3	855	5	US-11-104-110-1	Sequence 1, Appl1	945	291.5	7.4	799	4	US-10-995-561-559	Sequence 559, App
873	327	8.3	855	6	US-11-104-110-1	Sequence 2, Appl1	946	291.5	7.4	799	4	US-10-406-031-31	Sequence 31, Appl1
874	324	8.2	3095	6	US-11-225-732-4	Sequence 42, Appl1	947	289.5	7.3	799	4	US-09-776-191-10	Sequence 10, Appl1
875	324	8.2	3130	5	US-10-453-372-42	Sequence 42, Appl1	948	289.5	7.3	799	4	US-10-156-214A-10	Sequence 10, Appl1
876	321	8.1	3546	5	US-10-453-372-40	Sequence 40, Appl1	949	289.5	7.3	799	4	US-09-776-191-8	Sequence 8, Appl1
877	321	8.1	3546	5	US-10-453-372-32	Sequence 32, Appl1	950	288.5	7.3	799	4	US-10-156-214A-8	Sequence 8, Appl1
878	319.5	8.1	455	4	US-10-406-031-17	Sequence 17, Appl1	951	288.5	7.3	799	4	US-09-888-615-113	Sequence 113, App
879	318	8.1	2612	5	US-10-453-372-38	Sequence 38, Appl1	952	288.5	7.3	799	4	US-10-167-749-169	Sequence 169, App
880	318	8.1	2659	4	US-10-016-248-4	Sequence 4, Appl1	953	288.5	7.3	799	4	US-10-170-481A-169	Sequence 169, App
881	318	8.1	2659	5	US-10-453-372-36	Sequence 36, Appl1	954	288.5	7.3	799	4	US-10-210-028-169	Sequence 169, App
882	318	8.1	3104	4	US-10-016-248-2	Sequence 2, Appl1	955	288.5	7.3	799	4	US-10-162-521A-169	Sequence 169, App
883	318	8.1	3104	5	US-10-453-372-34	Sequence 34, Appl1	956	288.5	7.3	799	4	US-10-318-851-169	Sequence 169, App
884	318	8.1	3104	5	US-10-453-372-62	Sequence 62, Appl1	957	288.5	7.3	799	4	US-10-805-667-169	Sequence 169, App
885	318	8.1	3104	5	US-10-453-372-64	Sequence 64, Appl1	958	288.5	7.3	799	4	US-10-897-359-169	Sequence 169, App
886	317.5	8.0	3069	6	US-11-235-732-2	Sequence 2, Appl1	959	288.5	7.3	799	4	US-10-893-802-169	Sequence 169, App
887	317.5	8.0	3100	6	US-11-235-732-7	Sequence 7, Appl1	960	288.5	7.3	799	4	US-10-897-362-169	Sequence 169, App
888	317.5	8.0	454	4	US-10-406-031-11	Sequence 11, Appl1	961	288.5	7.3	799	4	US-11-129-762-169	Sequence 169, App
889	314	8.0	855	3	US-09-900-751-2	Sequence 2, Appl1	962	288.5	7.3	799	4	US-11-037-243-113	Sequence 113, App
890	314	8.0	855	4	US-10-072-012-355	Sequence 355, App	963	288.5	7.3	799	4	US-10-333-743-3	Sequence 3, Appl1
891	314	8.0	855	4	US-10-072-012-413	Sequence 413, App	964	288.5	7.3	799	4	US-10-600-187-10	Sequence 10, Appl1
892	313	7.9	855	4	US-10-072-012-356	Sequence 356, App	965	288.5	7.3	799	4	US-10-297-987B-11	Sequence 11, Appl1
893	313	7.9	855	4	US-10-072-012-414	Sequence 414, App	966	288.5	7.3	799	4	US-10-406-031-5	Sequence 5, Appl1
894	313	7.9	855	4	US-10-072-012-415	Sequence 415, App	967	288.5	7.3	799	4	US-10-865-978A-25	Sequence 25, Appl1
895	312	7.9	459	4	US-10-168-407-5	Sequence 5, Appl1	968	281	7.1	488	4	US-10-348-504-44	Sequence 44, Appl1
896	312	7.9	467	4	US-10-168-407-5	Sequence 8, Appl1	969	281	7.1	488	4	US-10-407-123-27	Sequence 27, Appl1
897	312	7.9	1031	5	US-10-451-168-80	Sequence 80, Appl1	970	280	7.1	488	4	US-09-987-457-18	Sequence 18, Appl1
898	312	7.9	1031	5	US-10-980-387-80	Sequence 80, Appl1	971	280	7.1	488	4	US-09-987-457-18	Sequence 18, Appl1
899	311	7.9	419	4	US-10-168-407-6	Sequence 6, Appl1	972	280	7.1	488	4	US-10-360-101-203	Sequence 203, App
900	311	7.9	419	4	US-10-168-407-6	Sequence 6, Appl1	973	280	7.1	488	4	US-10-360-101-203	Sequence 203, App
901	310.5	7.9	409	5	US-10-506-301-2	Sequence 2, Appl1	974	280	7.1	488	4	US-10-705-623-1	Sequence 1, Appl1
902	310.5	7.9	410	5	US-10-506-301-1	Sequence 1, Appl1	975	280	7.1	488	4	US-10-705-623-1	Sequence 1, Appl1
903	310.5	7.9	415	4	US-10-670-628-2	Sequence 2, Appl1	976	280	7.1	488	4	US-10-411-037-26	Sequence 26, Appl1
904	310.5	7.9	419	3	US-09-997-623-4	Sequence 4, Appl1	977	280	7.1	488	4	US-10-411-037-26	Sequence 26, Appl1
905	310.5	7.9	419	3	US-09-978-917A-4	Sequence 4, Appl1	978	280	7.1	488	4	US-09-969-271-7	Sequence 7, Appl1
906	310.5	7.9	419	4	US-10-182-263-1	Sequence 1, Appl1	979	280	7.1	488	4	US-09-974-298-145	Sequence 145, App
907	310.5	7.9	419	4	US-10-168-407-1	Sequence 1, Appl1	980	280	7.1	488	4	US-10-193-935-8	Sequence 8, Appl1
908	310.5	7.9	419	5	US-10-506-301-3	Sequence 3, Appl1	981	280	7.1	488	4	US-10-493-701-4	Sequence 4, Appl1
909	310.5	7.9	419	5	US-10-492-191-1	Sequence 1, Appl1	982	280	7.1	488	4	US-10-411-037-26	Sequence 26, Appl1
910	310.5	7.9	419	6	US-11-004-111-4	Sequence 4, Appl1	983	280	7.1	488	4	US-10-411-037-26	Sequence 26, Appl1
911	310.5	7.9	433	4	US-10-406-031-14	Sequence 14, Appl1	984	280	7.1	488	4	US-10-110-962-26	Sequence 26, Appl1
912	310.5	7.9	461	3	US-09-997-623-2	Sequence 2, Appl1	985	280	7.1	488	4	US-10-411-037-26	Sequence 26, Appl1
913	310.5	7.9	461	3	US-09-978-917A-2	Sequence 2, Appl1	986	280	7.1	488	4	US-10-411-037-26	Sequence 26, Appl1
914	310.5	7.9	461	4	US-10-182-263-2	Sequence 2, Appl1	987	280	7.1	488	4	US-10-411-037-26	Sequence 26, Appl1
915	310.5	7.9	461	5	US-10-182-263-2	Sequence 2, Appl1	988	280	7.1	488	4	US-10-287-994-26	Sequence 26, Appl1
916	310.5	7.9	461	5	US-10-168-407-2	Sequence 2, Appl1	989	280	7.1	488	4	US-10-410-913-26	Sequence 26, Appl1
917	310.5	7.9	461	6	US-11-004-111-2	Sequence 2, Appl1	990	280	7.1	488	4	US-10-712-124-108	Sequence 108, App
918	310	7.9	419	4	US-10-182-263-6	Sequence 6, Appl1	991	280	7.1	488	4	US-10-741-600-911	Sequence 911, App
919	310	7.9	419	4	US-10-168-407-4	Sequence 4, Appl1	992	280	7.1	488	4	US-10-410-980-26	Sequence 26, Appl1

1080	280	7.1	562	5	US-10-410-897-26	Sequence 26, Appl	1153	275.5	7.0	444	4	US-10-410-997-8	Sequence 8, Appl1
1081	280	7.1	562	5	US-10-492-261-26	Sequence 26, Appl	1154	275.5	7.0	444	4	US-10-411-012-8	Sequence 8, Appl1
1082	280	7.1	562	5	US-10-995-561-561	Sequence 561, App	1155	275.5	7.0	444	4	US-10-287-994-8	Sequence 8, Appl1
1083	280	7.1	562	6	US-11-169-041-153	Sequence 153, App	1156	275.5	7.0	444	4	US-10-410-913-8	Sequence 8, Appl1
1084	280	7.1	562	6	US-11-183-205-26	Sequence 26, Appl	1157	275.5	7.0	444	4	US-10-738-777-3	Sequence 8, Appl1
1085	279.5	7.1	782	4	US-10-097-340-312	Sequence 312, App	1158	275.5	7.0	444	5	US-10-410-980-8	Sequence 8, Appl1
1086	279.5	7.1	782	6	US-11-050-926-312	Sequence 312, App	1159	275.5	7.0	444	5	US-10-410-897-8	Sequence 8, Appl1
1087	279	7.1	527	4	US-10-705-633-2	Sequence 2, Appl1	1160	275.5	7.0	444	5	US-10-492-261-8	Sequence 8, Appl1
1088	279	7.1	932	6	US-10-363-937-6	Sequence 6, Appl1	1161	275.5	7.0	444	6	US-11-183-205-8	Sequence 8, Appl1
1089	279	7.1	932	6	US-11-167-040-6	Sequence 6, Appl1	1162	275.5	7.0	459	4	US-10-741-601-503	Sequence 503, App
1090	279	7.1	970	6	US-09-888-615-101	Sequence 101, App	1163	275.5	7.0	459	4	US-10-741-601-504	Sequence 504, App
1091	279	7.1	970	6	US-11-037-243-101	Sequence 101, App	1164	275.5	7.0	641	4	US-10-617-619-8	Sequence 8, Appl1
1092	278.5	7.1	264	3	US-09-978-418-34	Sequence 34, Appl	1165	275.5	7.0	641	6	US-11-227-340-8	Sequence 8, Appl1
1093	278.5	7.1	264	5	US-10-485-231-34	Sequence 34, Appl	1166	275.5	7.0	671	5	US-10-841-250-6	Sequence 6, Appl1
1094	278.5	7.1	466	4	US-10-017-122-2	Sequence 2, Appl1	1167	275.5	7.0	671	6	US-11-029-003-6	Sequence 6, Appl1
1095	278.5	7.1	466	4	US-10-375-741-14	Sequence 14, Appl1	1168	275.5	7.0	679	4	US-10-617-619-11	Sequence 11, Appl1
1096	278.5	7.1	481	4	US-10-741-601-501	Sequence 501, App	1169	275.5	7.0	679	6	US-11-227-340-11	Sequence 11, Appl1
1097	278.5	7.1	481	4	US-10-741-601-502	Sequence 502, App	1170	275.5	7.0	1113	5	US-10-926-083-4	Sequence 4, Appl1
1098	278.5	7.1	701	6	US-10-617-619-6	Sequence 6, Appl1	1171	273	6.9	560	3	US-09-912-559-3	Sequence 3, Appl1
1099	278.5	7.1	701	6	US-11-227-340-6	Sequence 6, Appl1	1172	273	6.9	560	3	US-09-912-559-4	Sequence 4, Appl1
1100	278	7.0	488	4	US-11-097-143-42048	Sequence 42048, A	1173	273	6.9	560	4	US-10-172-712-32	Sequence 32, Appl1
1101	278	7.0	488	4	US-10-406-031-27	Sequence 27, Appl1	1174	273	6.9	560	4	US-10-391-215-5	Sequence 5, Appl1
1102	278	7.0	488	5	US-10-723-860-261	Sequence 261, App	1175	273	6.9	560	4	US-10-391-215-6	Sequence 6, Appl1
1103	278	7.0	488	5	US-10-492-191-23	Sequence 23, Appl1	1176	273	6.9	560	4	US-10-391-215-7	Sequence 7, Appl1
1104	278	7.0	1113	4	US-10-464-368-78	Sequence 78, Appl1	1177	273	6.9	560	4	US-10-391-215-8	Sequence 8, Appl1
1105	278	7.0	1113	6	US-11-067-811-4	Sequence 4, Appl1	1178	273	6.9	560	5	US-10-719-993-854	Sequence 854, App
1106	277.5	7.0	476	5	US-10-494-004-1	Sequence 1, Appl1	1179	273	6.9	560	5	US-10-930-754-3	Sequence 3, Appl1
1107	276.5	7.0	426	3	US-09-951-121A-1	Sequence 1, Appl1	1180	273	6.9	560	5	US-10-930-754-4	Sequence 4, Appl1
1108	276.5	7.0	426	3	US-09-848-107-1	Sequence 1, Appl1	1181	273	6.9	560	5	US-10-756-149-5450	Sequence 5450, App
1109	276.5	7.0	426	3	US-10-295-682-1	Sequence 1, Appl1	1182	272.5	6.9	296	4	US-10-148-617-17	Sequence 17, Appl1
1110	276.5	7.0	655	4	US-10-172-712-28	Sequence 28, Appl1	1183	272	6.9	488	4	US-10-712-333-1	GENERAL INFO
1111	276	7.0	249	3	US-09-961-721-5	Sequence 5, Appl1	1184	271.5	6.9	244	4	US-10-097-340-169	Sequence 169, App
1112	276	7.0	249	3	US-10-170-789-46	Sequence 46, Appl1	1185	271.5	6.9	244	4	US-10-282-907-2	Sequence 2, Appl1
1113	276	7.0	251	3	US-11-151-601-28	Sequence 28, Appl1	1186	271.5	6.9	244	4	US-10-301-822-97	Sequence 97, Appl1
1114	276	7.0	251	3	US-09-961-721-4	Sequence 4, Appl1	1187	271.5	6.9	244	4	US-10-295-027-530	Sequence 530, App
1115	276	7.0	251	6	US-11-170-789-45	Sequence 45, Appl1	1188	271.5	6.9	244	4	US-10-343-999-131	Sequence 131, App
1116	276	7.0	259	4	US-11-151-601-27	Sequence 27, Appl1	1189	271.5	6.9	244	4	US-10-344-394-25	Sequence 25, Appl1
1117	276	7.0	259	4	US-10-107-782-214	Sequence 214, App	1190	271.5	6.9	244	4	US-10-757-262-28	Sequence 28, Appl1
1118	276	7.0	396	4	US-10-038-854-100	Sequence 100, App	1191	271.5	6.9	244	5	US-10-868-490A-9	Sequence 9, Appl1
1119	276	7.0	396	4	US-10-700-778-1	Sequence 1, Appl1	1192	271.5	6.9	244	5	US-10-868-490A-11	Sequence 11, Appl1
1120	276	7.0	527	4	US-10-705-633-3	Sequence 3, Appl1	1193	271.5	6.9	244	5	US-10-868-490A-13	Sequence 13, Appl1
1121	275.5	7.0	405	4	US-10-360-101-225	Sequence 225, App	1194	271.5	6.9	244	5	US-10-868-490A-15	Sequence 15, Appl1
1122	275.5	7.0	406	3	US-09-782-587B-1	Sequence 1, Appl1	1195	271.5	6.9	244	5	US-10-961-139-14	Sequence 14, Appl1
1123	275.5	7.0	406	3	US-09-782-587B-3	Sequence 3, Appl1	1196	271.5	6.9	244	5	US-10-756-143-463	Sequence 463, App
1124	275.5	7.0	406	4	US-10-109-498-1	Sequence 1, Appl1	1197	271.5	6.9	244	6	US-11-050-926-169	Sequence 169, App
1125	275.5	7.0	406	4	US-10-255-032-1	Sequence 1, Appl1	1198	271.5	6.9	244	6	US-11-186-284-97	Sequence 97, Appl1
1126	275.5	7.0	406	4	US-10-281-727-1	Sequence 1, Appl1	1199	271.5	6.9	244	6	US-11-050-857-670	Sequence 670, App
1127	275.5	7.0	406	4	US-10-383-898-7	Sequence 7, Appl1	1200	271.5	6.9	253	6	US-11-050-857-671	Sequence 671, App
1128	275.5	7.0	406	4	US-10-383-898-1	Sequence 1, Appl1	1201	271.5	6.9	1006	4	US-10-210-130-62	Sequence 62, Appl1
1129	275.5	7.0	406	4	US-10-617-500-1	Sequence 1, Appl1	1202	271	6.9	650	4	US-10-401-077-1	Sequence 1, Appl1
1130	275.5	7.0	406	4	US-10-263-205B-2	Sequence 2, Appl1	1203	269	6.8	462	4	US-10-416-952-2	Sequence 2, Appl1
1131	275.5	7.0	406	4	US-10-617-619-1	Sequence 1, Appl1	1204	269	6.8	643	3	US-09-808-602-103	Sequence 103, App
1132	275.5	7.0	406	4	US-10-701-294-1	Sequence 1, Appl1	1205	269	6.8	643	3	US-09-808-602-103	Sequence 103, App
1133	275.5	7.0	406	4	US-10-669-537-1	Sequence 1, Appl1	1206	269	6.8	643	4	US-10-099-139-86	Sequence 86, App
1134	275.5	7.0	406	4	US-10-738-777-2	Sequence 2, Appl1	1207	269	6.8	643	4	US-10-099-139-86	Sequence 86, App
1135	275.5	7.0	406	5	US-10-900-490-1	Sequence 1, Appl1	1208	269	6.8	643	4	US-10-044-564-113	Sequence 113, App
1136	275.5	7.0	406	5	US-10-723-843-3	Sequence 3, Appl1	1209	267	6.8	643	6	US-11-054-281-113	Sequence 113, App
1137	275.5	7.0	406	5	US-10-609-701A-1	Sequence 1, Appl1	1210	267	6.8	462	4	US-10-411-037-10	Sequence 10, Appl1
1138	275.5	7.0	406	5	US-10-950-747-1	Sequence 1, Appl1	1211	267	6.8	462	4	US-10-411-037-10	Sequence 10, Appl1
1139	275.5	7.0	406	5	US-10-950-747-3	Sequence 3, Appl1	1212	267	6.8	462	4	US-10-410-963-10	Sequence 10, Appl1
1140	275.5	7.0	406	5	US-10-822-943-1	Sequence 1, Appl1	1213	267	6.8	462	4	US-10-410-963-10	Sequence 10, Appl1
1141	275.5	7.0	406	6	US-11-021-239-1	Sequence 1, Appl1	1214	267	6.8	462	4	US-10-410-980-10	Sequence 10, Appl1
1142	275.5	7.0	406	6	US-11-111-072-1	Sequence 1, Appl1	1215	267	6.8	462	4	US-10-410-980-10	Sequence 10, Appl1
1143	275.5	7.0	406	6	US-11-111-072-1	Sequence 1, Appl1	1216	267	6.8	462	4	US-10-410-980-10	Sequence 10, Appl1
1144	275.5	7.0	406	6	US-11-186-669-1	Sequence 1, Appl1	1217	267	6.8	462	4	US-10-287-994-10	Sequence 10, Appl1
1145	275.5	7.0	406	6	US-11-186-669-1	Sequence 1, Appl1	1218	267	6.8	462	5	US-10-410-980-10	Sequence 10, Appl1
1146	275.5	7.0	444	4	US-10-411-037-8	Sequence 8, Appl1	1219	267	6.8	462	5	US-10-410-980-10	Sequence 10, Appl1
1147	275.5	7.0	444	4	US-10-382-248-34	Sequence 34, Appl1	1220	267	6.8	462	5	US-10-410-980-10	Sequence 10, Appl1
1148	275.5	7.0	444	4	US-10-411-026-8	Sequence 8, Appl1	1221	267	6.8	462	6	US-10-492-261-10	Sequence 10, Appl1
1149	275.5	7.0	444	4	US-10-410-962-8	Sequence 8, Appl1	1222	265.5	6.7	250	6	US-11-183-205-10	Sequence 10, Appl1
1150	275.5	7.0	444	4	US-10-411-049-8	Sequence 8, Appl1	1223	265	6.7	419	6	US-11-097-143-24561	Sequence 24561, A
1151	275.5	7.0	444	4	US-10-263-205B-3	Sequence 3, Appl1	1224	264.5	6.7	900	5	US-10-382-248-36	Sequence 36, Appl1
1152	275.5	7.0	444	4	US-10-410-930-8	Sequence 8, Appl1	1225	264	6.7	431	4	US-10-865-978-15	Sequence 15, Appl1
												US-10-247-671-149	Sequence 149, App

1226	263.5	6.7	411	4	US-10-744-927-1	Sequence 1, Appl1	1299	258.5	6.6	411	4	US-10-407-821-2	Sequence 2, Appl1
1227	263.5	6.7	494	6	US-11-094-519A-35	Sequence 35, Appl1	1300	258.5	6.6	411	5	US-10-828-531B-16	Sequence 16, Appl1
1228	263	6.7	431	4	US-10-076-421-2	Sequence 2, Appl1	1301	258.5	6.6	411	6	US-11-019-448-3	Sequence 3, Appl1
1229	263	6.7	431	4	US-10-171-311-184	Sequence 184, App	1302	258.5	6.6	412	5	US-10-825-911-2	Sequence 2, Appl1
1230	263	6.7	431	4	US-10-301-822-161	Sequence 161, App	1303	258.5	6.6	787	6	US-11-097-143-40698	Sequence 40698, A
1231	263	6.7	431	4	US-10-131-985-91	Sequence 21, Appl	1304	257.5	6.5	591	5	US-10-865-978-17	Sequence 17, Appl1
1232	263	6.7	431	4	US-10-295-027-114	Sequence 114, App	1305	257	6.5	215	4	US-10-051-874-102	Sequence 102, App
1233	263	6.7	431	4	US-10-235-027-1275	Sequence 1275, App	1306	257	6.5	217	3	US-09-981-151A-88	Sequence 88, Appl1
1234	263	6.7	431	4	US-10-411-037-34	Sequence 34, Appl	1307	257	6.5	217	3	US-09-981-151A-97	Sequence 97, Appl1
1235	263	6.7	431	4	US-10-411-026-34	Sequence 34, Appl	1308	257	6.5	217	4	US-10-032-189-67	Sequence 67, Appl1
1236	263	6.7	431	4	US-10-410-962-34	Sequence 34, Appl	1309	257	6.5	217	4	US-10-074-978A-223	Sequence 223, App
1237	263	6.7	431	4	US-10-411-049-34	Sequence 34, Appl	1310	257	6.5	217	4	US-10-055-569A-97	Sequence 97, Appl1
1238	263	6.7	431	4	US-10-410-930-34	Sequence 34, Appl	1311	257	6.5	217	4	US-10-042-865-156	Sequence 156, App
1239	263	6.7	431	4	US-10-410-997-34	Sequence 34, Appl	1312	257	6.5	217	4	US-10-072-012-805	Sequence 805, App
1240	263	6.7	431	4	US-10-411-012-34	Sequence 34, Appl	1313	257	6.5	217	4	US-10-072-012-805	Sequence 805, App
1241	263	6.7	431	4	US-10-287-994-34	Sequence 34, Appl	1314	257	6.5	217	4	US-10-037-417-136	Sequence 136, App
1242	263	6.7	431	4	US-10-410-913-34	Sequence 34, Appl	1315	257	6.5	217	6	US-11-019-711-136	Sequence 136, App
1243	263	6.7	431	5	US-10-741-600-1265	Sequence 1265, Ap	1316	257	6.5	529	4	US-10-398-037-2	Sequence 2, Appl1
1244	263	6.7	431	5	US-10-741-600-1266	Sequence 1266, Ap	1317	257	6.5	1039	5	US-10-865-978B-30	Sequence 30, Appl1
1245	263	6.7	431	5	US-10-901-417-31	Sequence 21, Appl	1318	256	6.5	207	4	US-10-004-378A-147	Sequence 147, App
1246	263	6.7	431	5	US-10-410-980-34	Sequence 34, Appl	1319	255.5	6.5	244	3	US-09-796-479A-11	Sequence 11, Appl1
1247	263	6.7	431	5	US-10-645-756-38	Sequence 38, Appl	1320	255.5	6.5	244	4	US-10-461-787A-11	Sequence 11, Appl1
1248	263	6.7	431	5	US-10-410-897-38	Sequence 38, Appl	1321	255.5	6.5	244	6	US-11-251-455-13	Sequence 13, Appl1
1249	263	6.7	431	5	US-10-492-261-34	Sequence 34, Appl	1322	255.5	6.5	441	5	US-10-741-600-829	Sequence 829, App
1250	263	6.7	431	5	US-10-995-561-807	Sequence 807, App	1323	255.5	6.5	457	5	US-10-455-772-52	Sequence 52, Appl1
1251	263	6.7	431	5	US-10-995-561-808	Sequence 808, App	1324	254.5	6.5	437	4	US-10-712-332-3	GENERAL INFO
1252	263	6.7	431	6	US-11-186-284-161	Sequence 161, App	1325	254.5	6.5	465	5	US-10-455-772-24	Sequence 24, Appl1
1253	263	6.7	431	6	US-11-183-205-34	Sequence 34, Appl	1326	254.5	6.5	465	5	US-10-455-772-48	Sequence 48, Appl1
1254	263	6.7	437	4	US-10-087-182-294	Sequence 594, App	1327	254	6.4	431	6	US-11-097-413-6243	Sequence 6243, Ap
1255	262.5	6.7	415	4	US-10-466-998A-2	Sequence 2, Appl1	1328	254	6.4	413	3	US-09-264-468B-1	Sequence 1, Appl1
1256	262.5	6.7	415	6	US-11-166-028-1	Sequence 1, Appl1	1329	253.5	6.4	465	5	US-10-455-772-22	Sequence 22, Appl1
1257	262.5	6.7	433	5	US-10-488-671-1	Sequence 95, Appl	1330	253.5	6.4	464	3	US-09-808-602-95	Sequence 95, Appl1
1258	262.5	6.7	456	4	US-10-038-854-85	Sequence 95, Appl	1331	253.5	6.4	487	3	US-09-808-602-93	Sequence 93, Appl1
1259	262.5	6.7	456	4	US-10-038-854-86	Sequence 96, Appl	1332	253.5	6.4	487	3	US-09-800-198-80	Sequence 80, Appl1
1260	262.5	6.7	461	3	US-08-894-901-3	Sequence 3, Appl1	1333	253.5	6.4	487	5	US-10-455-772-16	Sequence 16, Appl1
1261	262.5	6.7	461	4	US-10-132-829-5	Sequence 5, Appl1	1334	253.5	6.4	487	5	US-10-455-772-46	Sequence 46, Appl1
1262	262.5	6.7	461	4	US-10-234-406-6	Sequence 6, Appl1	1335	253.5	6.4	487	5	US-10-455-772-50	Sequence 50, Appl1
1263	262.5	6.7	461	4	US-10-234-406-8	Sequence 8, Appl1	1336	253.5	6.4	1043	4	US-10-016-248-48	Sequence 48, Appl1
1264	262.5	6.7	461	4	US-10-133-907-5	Sequence 5, Appl1	1337	253.5	6.4	1048	4	US-10-016-248-49	Sequence 49, Appl1
1265	262.5	6.7	461	4	US-10-038-854-92	Sequence 92, Appl	1338	253	6.4	273	4	US-10-148-671-25	Sequence 25, Appl1
1266	262.5	6.7	461	4	US-10-038-854-93	Sequence 93, Appl	1339	253	6.4	433	5	US-10-455-772-26	Sequence 26, Appl1
1267	262.5	6.7	461	4	US-10-038-854-94	Sequence 94, Appl	1340	252.5	6.4	432	3	US-09-808-602-21	Sequence 21, Appl1
1268	262.5	6.7	461	4	US-10-239-498A-5	Sequence 5, Appl1	1341	252.5	6.4	465	5	US-10-455-772-32	Sequence 32, Appl1
1269	262.5	6.7	461	5	US-10-741-600-832	Sequence 832, App	1342	252.5	6.4	465	5	US-10-455-772-18	Sequence 18, Appl1
1270	262.5	6.7	461	5	US-10-455-772-752	Sequence 752, App	1343	252.5	6.4	465	5	US-10-455-772-30	Sequence 30, Appl1
1271	262.5	6.7	461	5	US-10-455-772-754	Sequence 754, App	1344	252.5	6.4	487	5	US-10-865-978-16	Sequence 16, Appl1
1272	262.5	6.7	461	6	US-11-172-459-1	Sequence 1, Appl1	1345	252	6.4	719	5	US-10-865-978-16	Sequence 16, Appl1
1273	262.5	6.7	696	5	US-10-841-250-8	Sequence 8, Appl1	1346	251.5	6.4	889	5	US-10-865-978-22	Sequence 22, Appl1
1274	262.5	6.7	696	5	US-10-841-819B-23	Sequence 23, Appl	1347	251.5	6.4	465	5	US-10-455-772-32	Sequence 32, Appl1
1275	262.5	6.7	696	6	US-11-029-003-8	Sequence 8, Appl1	1348	251.5	6.4	487	3	US-09-808-602-17	Sequence 17, Appl1
1276	262.5	6.7	696	6	US-09-776-191-62	Sequence 29, Appl	1349	251.5	6.4	487	3	US-09-808-602-19	Sequence 19, Appl1
1277	262.5	6.7	1042	4	US-10-156-214A-29	Sequence 2, Appl1	1350	251.5	6.4	487	3	US-09-800-198-17	Sequence 17, Appl1
1278	262.5	6.7	1042	5	US-10-865-978-2	Sequence 2, Appl1	1351	251.5	6.4	433	4	US-10-723-860-4046	Sequence 4046, Ap
1279	262.5	6.7	1042	5	US-10-926-083-2	Sequence 9, Appl1	1352	250	6.3	1379	6	US-11-097-143-3372	Sequence 3372, Ap
1280	262.5	6.7	1044	6	US-11-067-811-1	Sequence 1, Appl1	1353	249.5	6.3	403	3	US-09-880-503-6	Sequence 6, Appl1
1281	262.5	6.7	1044	5	US-10-865-978-9	Sequence 2245, Ap	1354	249.5	6.3	403	3	US-11-019-448-6	Sequence 6, Appl1
1282	262.5	6.7	1076	4	US-10-276-774-2345	Sequence 26, Appl	1355	249.5	6.3	822	3	US-09-147-947-6	Sequence 47, Appl1
1283	262	6.6	280	4	US-10-148-671-26	Sequence 26, Appl	1356	249.5	6.3	822	4	US-10-757-862-34	Sequence 34, Appl1
1284	261.5	6.6	415	3	US-09-118-748-2	Sequence 830, App	1357	249.5	6.3	875	5	US-10-723-860-4046	Sequence 4046, Ap
1285	261.5	6.6	443	4	US-10-741-600-830	Sequence 4, App	1358	249.5	6.3	875	5	US-10-843-299-2	Sequence 2, Appl1
1286	261	6.6	431	4	US-10-193-656-4	Sequence 870, App	1359	249.5	6.3	966	3	US-09-285-985C-19	Sequence 19, Appl1
1287	261	6.6	431	5	US-10-723-860-870	Sequence 4928, Ap	1360	249	6.3	225	3	US-09-786-191-6	Sequence 6, Appl1
1288	261	6.6	431	5	US-10-756-149-4928	Sequence 2, Appl1	1361	249	6.3	225	4	US-10-456-214A-6	Sequence 47, Appl1
1289	261	6.6	431	5	US-10-504-287-2	Sequence 814, App	1362	249	6.3	251	3	US-09-789-210-47	Sequence 96, Appl1
1290	260.5	6.6	437	4	US-10-712-332-2	Sequence 562, App	1363	249	6.3	263	3	US-09-888-615-96	Sequence 45, Appl1
1291	260.5	6.6	1032	5	US-10-719-993-814	Sequence 562, App	1364	249	6.3	260	3	US-11-037-443-95	Sequence 45, Appl1
1292	260	6.6	431	5	US-10-283-174-562	Sequence 34, Appl	1365	248.5	6.3	220	3	US-09-898-337A-45	Sequence 41, Appl1
1293	260	6.6	431	5	US-10-600-009-562	Sequence 34, Appl	1366	248.5	6.3	220	3	US-09-789-210-51	Sequence 62, Appl1
1294	259.5	6.6	227	4	US-10-865-978-34	Sequence 54, Appl	1367	248	6.3	230	6	US-09-789-210-62	Sequence 24, Appl1
1295	259	6.6	227	4	US-10-045-367A-4	Sequence 36, Appl	1368	248	6.3	230	6	US-11-104-110-3	Sequence 24, Appl1
1296	259	6.6	227	4	US-10-170-789-54	Sequence 3, Appl1	1369	248	6.3	230	6	US-11-104-111-24	Sequence 24, Appl1
1297	259	6.6	227	6	US-11-151-601-36		1370	248	6.3				
1298	258.5	6.6	411	3	US-09-880-503-3		1371	248	6.3				

1372	248	6.3	231	4	US-10-600-187-6	Sequence 6, Appl1	1445	244	6.2	638	6	US-11-054-283-114	Sequence 114, App
1373	248	6.3	263	5	US-10-733-969A-74	Sequence 74, Appl	1446	243.5	6.2	435	6	US-11-097-143-41688	Sequence 41688, A
1374	248	6.3	638	3	US-09-808-602-102	Sequence 102, App	1447	243	6.2	273	4	US-10-028-248A-63	Sequence 63, Appl
1375	248	6.3	638	3	US-09-800-198-85	Sequence 85, Appl	1448	243	6.2	273	4	US-10-107-782-63	Sequence 63, Appl
1376	248	6.3	638	4	US-10-099-322-111	Sequence 111, App	1449	243	6.2	282	4	US-10-051-874-97	Sequence 97, Appl
1377	248	6.3	638	4	US-10-044-564-111	Sequence 111, App	1450	242.5	6.1	232	4	US-10-156-214A-276	Sequence 276, App
1378	248	6.3	638	4	US-10-403-161-50	Sequence 50, Appl	1451	242.5	6.1	326	5	US-10-865-978-37	Sequence 37, Appl
1379	248	6.3	638	4	US-10-287-226-400	Sequence 400, App	1452	242.5	6.1	326	5	US-10-865-978-37	Sequence 37, Appl
1380	248	6.3	638	4	US-10-287-226-658	Sequence 658, App	1453	242.5	6.1	610	5	US-10-921-198-4	Sequence 4, Appl1
1381	248	6.3	638	4	US-10-741-601-303	Sequence 303, App	1454	242.5	6.1	610	5	US-10-931-198-4	Sequence 4, Appl1
1382	248	6.3	638	5	US-10-741-601-854	Sequence 854, App	1455	242.5	6.1	730	5	US-10-942-042-4	Sequence 461, App
1383	248	6.3	638	6	US-10-995-561-536	Sequence 536, App	1456	242.5	6.1	730	5	US-10-287-436A-461	Sequence 461, App
1384	247.5	6.3	635	4	US-11-054-281-111	Sequence 111, App	1457	242.5	6.1	730	5	US-10-287-436A-1158	Sequence 1158, App
1385	247.5	6.3	635	4	US-10-741-601-304	Sequence 304, App	1458	242.5	6.1	730	5	US-10-921-198-2	Sequence 2, Appl1
1386	247.5	6.3	635	5	US-10-741-600-855	Sequence 855, App	1459	242.5	6.1	730	5	US-10-931-198-2	Sequence 2, Appl1
1387	247	6.3	364	6	US-11-097-143-28392	Sequence 28392, A	1460	242.5	6.1	730	5	US-10-942-042-2	Sequence 2, Appl1
1388	247	6.3	455	5	US-10-865-978-18	Sequence 18, Appl	1461	242.5	6.1	1019	4	US-10-016-248-99	Sequence 99, Appl
1389	247	6.3	619	4	US-10-403-161-52	Sequence 52, Appl	1462	242.5	6.1	3371	4	US-10-603-283-2	Sequence 2, Appl1
1390	247	6.3	619	4	US-10-287-226-404	Sequence 404, App	1463	242	6.1	332	4	US-10-114-270-134	Sequence 134, App
1391	247	6.3	638	4	US-10-403-161-48	Sequence 48, App	1464	242	6.1	597	5	US-10-453-375-54	Sequence 54, Appl
1392	247	6.3	638	4	US-10-099-322-30	Sequence 30, Appl	1465	241.5	6.1	730	3	US-09-850-048A-2	Sequence 2, Appl1
1393	247	6.3	638	4	US-10-044-564-30	Sequence 30, Appl	1466	241.5	6.1	416	5	US-09-815-876-2	Sequence 2, Appl1
1394	247	6.3	638	4	US-10-403-161-46	Sequence 46, Appl	1467	241.5	6.1	823	4	US-10-239-032-8	Sequence 8, Appl1
1395	247	6.3	638	4	US-10-287-226-402	Sequence 402, App	1468	241	6.1	346	3	US-09-977-577-8	Sequence 8, Appl1
1396	247	6.3	638	6	US-11-054-281-30	Sequence 30, Appl	1469	241	6.1	346	5	US-10-885-784-8	Sequence 8, Appl1
1397	247	6.3	739	6	US-11-057-047-2	Sequence 2, Appl1	1470	241	6.1	986	3	US-09-850-048A-4	Sequence 4, Appl1
1398	247	6.3	764	4	US-10-177-293-27	Sequence 27, Appl	1471	240.5	6.1	278	3	US-09-813-432-12	Sequence 12, Appl
1399	247	6.3	764	4	US-10-236-031B-44	Sequence 44, Appl	1472	240.5	6.1	278	3	US-09-813-432-43	Sequence 43, Appl
1400	247	6.3	764	5	US-10-733-969A-4	Sequence 4, Appl1	1473	240.5	6.1	278	4	US-10-174-364-12	Sequence 12, Appl
1401	247	6.3	764	5	US-10-287-436A-423	Sequence 423, App	1474	240.5	6.1	278	4	US-10-174-364-43	Sequence 43, Appl
1402	247	6.3	764	5	US-10-287-436A-423	Sequence 423, App	1475	240.5	6.1	278	4	US-10-246-583-12	Sequence 12, Appl
1403	247	6.3	764	5	US-10-287-436A-516	Sequence 516, App	1476	240.5	6.1	278	4	US-10-246-583-43	Sequence 43, Appl
1404	247	6.3	764	5	US-10-287-436A-1120	Sequence 1120, App	1477	240.5	6.1	278	4	US-10-689-833-12	Sequence 12, Appl
1405	247	6.3	764	6	US-10-287-436A-1207	Sequence 1207, App	1478	240.5	6.1	278	4	US-10-689-833-43	Sequence 43, Appl
1406	247	6.3	798	4	US-11-057-047-1	Sequence 1, Appl1	1479	240.5	6.1	430	4	US-10-372-966-4	Sequence 4, Appl1
1407	247	6.3	986	3	US-10-821-234-1034	Sequence 1034, App	1480	240.5	6.1	970	5	US-10-016-248-42	Sequence 42, Appl
1408	247	6.3	986	4	US-09-918-715-242	Sequence 33, Appl	1481	240.5	6.1	970	5	US-10-455-772-92	Sequence 92, Appl
1409	247	6.3	986	4	US-10-366-345-33	Sequence 242, App	1482	240.5	6.1	3571	3	US-09-911-842-2	Sequence 2, Appl1
1410	247	6.3	986	5	US-10-474-794-242	Sequence 1377, App	1483	240.5	6.1	3571	4	US-10-150-881-2	Sequence 34, Appl
1411	247	6.3	986	5	US-10-723-860-1377	Sequence 242, App	1484	240	6.1	1128	4	US-10-926-083-34	Sequence 97, Appl
1412	247	6.3	986	5	US-10-979-159-242	Sequence 1377, App	1485	240	6.1	1128	4	US-09-888-615-97	Sequence 8, Appl1
1413	246.5	6.2	254	5	US-10-821-234-1310	Sequence 1310, App	1486	240	6.1	1128	4	US-10-399-645-8	Sequence 8, Appl1
1414	246.5	6.2	259	5	US-10-887-104-11	Sequence 11, Appl	1487	240	6.1	1128	6	US-11-037-243-97	Sequence 97, Appl
1415	246.5	6.2	259	5	US-10-872-198-5	Sequence 52, App	1488	239.5	6.1	406	3	US-09-977-577-2	Sequence 2, Appl1
1416	246.5	6.2	259	5	US-10-872-198-5	Sequence 5, Appl1	1489	239.5	6.1	406	3	US-10-764-649-6	Sequence 6, Appl1
1417	246.5	6.2	259	6	US-11-021-951-5	Sequence 5, Appl1	1490	239.5	6.1	406	5	US-10-764-649-6	Sequence 2, Appl1
1418	246.5	6.2	259	6	US-11-021-951-5	Sequence 2, Appl1	1491	239.5	6.1	406	5	US-10-885-784-2	Sequence 811, App
1419	246.5	6.2	347	3	US-09-977-577-3	Sequence 3, Appl1	1492	239.5	6.1	406	6	US-11-043-788-131	Sequence 131, App
1420	246.5	6.2	347	3	US-10-885-784-3	Sequence 3, Appl1	1493	239.5	6.1	406	6	US-11-043-788-132	Sequence 132, App
1421	246.5	6.2	632	4	US-10-020-141-8	Sequence 8, Appl1	1494	239.5	6.1	406	6	US-11-189-120-6	Sequence 6, Appl1
1422	246.5	6.2	632	4	US-10-017-631-2	Sequence 2, Appl1	1495	239.5	6.1	406	6	US-11-177-506-39	Sequence 39, App
1423	246.5	6.2	632	4	US-10-214-932-116	Sequence 116, App	1496	239.5	6.1	416	3	US-09-804-156-13	Sequence 13, App
1424	246.5	6.2	632	4	US-10-172-712-29	Sequence 29, App	1497	239.5	6.1	416	4	US-10-067-761-13	Sequence 13, App
1425	246.5	6.2	632	5	US-10-733-969A-67	Sequence 67, App	1498	239.5	6.1	416	4	US-10-319-518-13	Sequence 13, App
1426	246.5	6.2	632	5	US-10-872-198-149	Sequence 149, App	1499	239.5	6.1	1015	3	US-09-285-385C-2	Sequence 2, Appl1
1427	246.5	6.2	632	6	US-11-021-951-149	Sequence 149, App	1500	239.5	6.1	1015	4	US-10-016-248-97	Sequence 97, Appl
1428	246.5	6.2	639	5	US-10-792-498-16	Sequence 16, App							
1429	246.5	6.2	639	5	US-10-792-498-16	Sequence 16, App							
1430	246	6.2	812	3	US-09-825-751A-71	Sequence 71, Appl							
1431	246	6.2	812	5	US-10-851-438-71	Sequence 71, Appl							
1432	245.5	6.2	638	4	US-10-099-322-112	Sequence 112, App							
1433	245.5	6.2	638	4	US-10-044-564-112	Sequence 112, App							
1434	245.5	6.2	638	6	US-11-054-281-112	Sequence 112, App							
1435	245.5	6.2	823	4	US-10-112-944-309	Sequence 309, App							
1436	245	6.2	445	4	US-10-360-101-266	Sequence 266, App							
1437	244.5	6.2	259	3	US-09-981-123-2	Sequence 2, Appl1							
1438	244.5	6.2	280	4	US-10-148-671-23	Sequence 23, Appl							
1439	244.5	6.2	280	4	US-10-029-386-31995	Sequence 31995, A							
1440	244	6.2	322	4	US-10-051-874-96	Sequence 96, Appl							
1441	244	6.2	477	5	US-10-494-004-2	Sequence 56, Appl							
1442	244	6.2	638	4	US-10-099-322-114	Sequence 2, Appl1							
1443	244	6.2	638	4	US-10-044-564-114	Sequence 114, App							
1444	244	6.2	638	4	US-10-287-226-672	Sequence 672, App							

Search completed: April 4, 2007, 22:26:18
Job time : 217 secs

THIS PAGE BLANK (USPTO)

GenCore version 6.2
Copyright (c) 1993 - 2007 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 4, 2007, 22:23:11 ; Search time 97 Seconds
(without alignments)
1522.925 Million cell updates/sec

Perfect score: 3945

Sequence: 1 MELGCMTQLGLFTLLQLLIS.....ISTATPKVLPEFMDIERMNX 720

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched:

944695 seqs, 205171828 residues

944695

Total number of hits satisfying chosen parameters:
Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 1500 summaries

Database :

Published Applications AA.New:*
1: /EMC_Celerra_SIDS3/Ptodata/2/pubpaa/US08_NEW_PUB pep.*
2: /EMC_Celerra_SIDS3/Ptodata/2/pubpaa/US06_NEW_PUB pep.*
3: /EMC_Celerra_SIDS3/Ptodata/2/pubpaa/PCT_NEW_PUB pep.*
4: /EMC_Celerra_SIDS3/Ptodata/2/pubpaa/US09_NEW_PUB pep.*
5: /EMC_Celerra_SIDS3/Ptodata/2/pubpaa/US10_NEW_PUB pep.*
6: /EMC_Celerra_SIDS3/Ptodata/2/pubpaa/US11_NEW_PUB pep.*
7: /EMC_Celerra_SIDS3/Ptodata/2/pubpaa/US11_NEW_PUB pep.*
8: /EMC_Celerra_SIDS3/Ptodata/2/pubpaa/US60_NEW_PUB pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
4	3945	100.0	720	US-11-101-316-38	Sequence 38, Appl
5	3945	100.0	720	US-11-376-673-38	Sequence 38, Appl
6	3945	100.0	720	US-11-102-284-38	Sequence 38, Appl
7	3936	99.8	720	US-11-354-653-32	Sequence 32, Appl
8	3923	99.4	720	US-11-001-793-8647	Sequence 8647, Ap
9	3921.5	99.4	720	US-10-529-348-1034	Sequence 1034, Ap
10	3828	97.0	699	US-11-354-653-86	Sequence 86, Appl
11	3617	91.7	720	US-11-354-653-118	Sequence 118, Appl
12	2413	61.2	455	US-11-001-793-10886	Sequence 10886, A
13	1708.5	43.3	323	US-11-001-793-10884	Sequence 10884, A
14	580	14.7	103	US-10-631-441-2419	Sequence 2419, Ap
15	475	12.0	699	US-10-527-191-14	Sequence 14, Appl
16	469.5	11.9	679	US-11-476-754-6	Sequence 6, Appl
17	468	11.9	728	US-10-527-191-13	Sequence 13, Appl
18	403.5	10.2	688	US-11-476-754-7	Sequence 7, Appl
19	403.5	10.2	705	US-10-553-520-154	Sequence 154, App
20	403.5	10.2	705	US-11-371-354-65133	Sequence 65133, A
21	403.5	10.2	705	US-11-471-740-19	Sequence 19, Appl
22	401.5	10.2	686	US-10-527-191-11	Sequence 11, Appl
23	401.5	10.2	686	US-11-476-754-2	Sequence 2, Appl
24	400.5	10.2	686	US-10-556-509-1	Sequence 1, Appl
25	399.5	10.1	671	US-10-537-507A-1	Sequence 1, Appl
26	340.5	8.6	694	US-10-219-051B-2275	Sequence 2275, Ap
27	340.5	8.6	694	US-10-219-051B-1123	Sequence 1123, A
28	340.5	8.6	695	US-10-219-051B-2271	Sequence 2271, Ap
29	340.5	8.6	695	US-10-219-051B-10771	Sequence 10771, A

30	334	8.5	673	US-11-476-754-8	Sequence 8, Appl
31	334	8.5	688	US-10-527-191-6	Sequence 6, Appl
32	334	8.5	688	US-10-219-051B-2273	Sequence 2273, Ap
33	334	8.5	688	US-10-219-051B-10773	Sequence 10773, A
34	328	8.3	851	US-11-362-260A-339	Sequence 339, App
35	328	8.3	851	US-10-530-187-242	Sequence 242, App
36	328	8.3	855	US-10-533-519-428	Sequence 428, App
37	328	8.3	855	US-10-529-348-1148	Sequence 1148, Ap
38	328	8.3	855	US-11-254-185-2	Sequence 2, Appl
39	328	8.3	855	US-11-253-869-2	Sequence 2, Appl
40	328	8.3	855	US-11-303-608-1	Sequence 1, Appl
41	328	8.3	855	US-11-362-260A-338	Sequence 338, App
42	328	8.3	855	US-11-362-260A-594	Sequence 594, App
43	328	8.3	872	US-11-362-260A-340	Sequence 340, App
44	321	8.1	461	US-11-397-046-8	Sequence 8, Appl
45	318	8.1	3689	US-10-796-280-1056	Sequence 1056, Ap
46	315.5	8.0	461	US-11-397-046-5	Sequence 5, Appl
47	315	8.0	461	US-11-397-046-7	Sequence 7, Appl
48	314	8.0	461	US-11-397-046-6	Sequence 6, Appl
49	314	8.0	817	US-11-362-260A-341	Sequence 341, App
50	310.5	7.9	419	US-11-397-046-1	Sequence 1, Appl
51	310.5	7.9	461	US-11-397-046-2	Sequence 2, Appl
52	310.5	7.9	461	US-11-397-046-3	Sequence 3, Appl
53	310.5	7.9	461	US-11-397-046-4	Sequence 4, Appl
54	310.5	7.9	461	US-11-371-354-63147	Sequence 63147, A
55	297.5	7.5	543	US-11-090-997-2034	Sequence 2034, Ap
56	291.5	7.4	516	US-10-529-348-181	Sequence 181, App
57	291.5	7.4	516	US-11-090-997-2038	Sequence 2038, Ap
58	283.5	7.2	583	US-10-219-051B-11161	Sequence 11161, A
59	280.5	7.1	583	US-10-495-479-6	Sequence 2, Appl
60	280.5	7.1	525	US-10-495-479-6	Sequence 6, Appl
61	280	7.1	527	US-11-489-008A-1	Sequence 1, Appl
62	280	7.1	562	US-10-505-928-547	Sequence 547, App
63	280	7.1	562	US-10-530-972-26	Sequence 26, Appl
64	280	7.1	562	US-10-552-896-26	Sequence 26, Appl
65	280	7.1	562	US-10-410-946-26	Sequence 26, Appl
66	280	7.1	562	US-11-183-218-26	Sequence 26, Appl
67	280	7.1	562	US-11-090-997-2030	Sequence 2030, Ap
68	280	7.1	562	US-11-404-266-26	Sequence 26, Appl
69	278.5	7.1	481	US-10-796-307-761	Sequence 761, App
70	278.5	7.1	481	US-10-796-307-762	Sequence 762, App
71	278	7.0	1113	US-10-543-003-3	Sequence 3, Appl
72	277.5	7.0	260	US-11-403-988-4	Sequence 4, Appl
73	277.5	7.0	476	US-11-264-088-1	Sequence 1, Appl
74	277.5	7.0	476	US-11-311-475-1	Sequence 1, Appl
75	277	7.0	810	US-11-362-260A-344	Sequence 344, App
76	276.5	7.0	655	US-11-242-617-1	Sequence 1, Appl
77	276	7.0	559	US-11-090-997-1866	Sequence 1866, Ap
78	275.5	7.0	406	US-10-512-754-2	Sequence 2, Appl
79	275.5	7.0	406	US-10-529-624-1	Sequence 1, Appl
80	275.5	7.0	406	US-10-383-898-1	Sequence 1, Appl
81	275.5	7.0	406	US-10-549-506-2	Sequence 2, Appl
82	275.5	7.0	406	US-11-286-211A-1	Sequence 1, Appl
83	275.5	7.0	406	US-11-390-512-7	Sequence 7, Appl
84	275.5	7.0	406	US-11-088-477-1	Sequence 1, Appl
85	275.5	7.0	406	US-11-339-755-1	Sequence 1, Appl
86	275.5	7.0	406	US-11-367-189-1	Sequence 1, Appl
87	275.5	7.0	406	US-11-423-622-1	Sequence 1, Appl
88	275.5	7.0	406	US-11-423-622-3	Sequence 3, Appl
89	275.5	7.0	406	US-11-423-662-1	Sequence 1, Appl
90	275.5	7.0	406	US-11-423-662-3	Sequence 3, Appl
91	275.5	7.0	406	US-11-423-665-1	Sequence 1, Appl
92	275.5	7.0	406	US-11-423-665-3	Sequence 3, Appl
93	275.5	7.0	406	US-11-424-030-1	Sequence 1, Appl
94	275.5	7.0	406	US-11-424-035-1	Sequence 1, Appl
95	275.5	7.0	406	US-11-379-189-1	Sequence 1, Appl
96	275.5	7.0	406	US-11-379-189-3	Sequence 3, Appl
97	275.5	7.0	406	US-11-379-664-1	Sequence 1, Appl
98	275.5	7.0	406	US-11-426-394-1	Sequence 1, Appl
99	275.5	7.0	406	US-11-426-394-3	Sequence 3, Appl
100	275.5	7.0	406	US-11-426-401-1	Sequence 1, Appl
101	275.5	7.0	406	US-11-426-401-3	Sequence 3, Appl
102	275.5	7.0	406	US-11-486-586-1	Sequence 1, Appl

103	275.5	7.0	406	7	US-11-393-327-1	Sequence 1, Appl1	176	246	6.2	812	7	US-11-318-939-7	Sequence 7, Appl1
104	275.5	7.0	406	7	US-11-396-314-1	Sequence 1, Appl1	177	244	6.2	477	7	US-11-264-088-2	Sequence 2, Appl1
105	275.5	7.0	406	7	US-11-396-314-3	Sequence 3, Appl1	178	244	6.2	477	7	US-11-311-475-2	Sequence 2, Appl1
106	275.5	7.0	406	7	US-11-381-705-2	Sequence 2, Appl1	179	242.5	6.1	3574	7	US-11-508-301-15	Sequence 15, Appl1
107	275.5	7.0	406	7	US-11-381-713-2	Sequence 2, Appl1	180	241.5	6.1	219	7	US-11-327-490-42	Sequence 42, Appl1
108	275.5	7.0	406	7	US-11-381-717-2	Sequence 2, Appl1	181	241	6.1	1167	6	US-10-777-288A-2987	Sequence 2987, Ap
109	275.5	7.0	406	7	US-11-381-718-2	Sequence 2, Appl1	182	240.5	6.1	3571	7	US-11-429-673-2	Sequence 2, Appl1
110	275.5	7.0	444	6	US-10-511-937-2962	Sequence 2962, Ap	183	239.5	6.1	406	7	US-11-183-251-2	Sequence 2, Appl1
111	275.5	7.0	444	6	US-10-511-937-3014	Sequence 3014, Ap	184	239.5	6.1	416	7	US-11-375-359-128	Sequence 128, App
112	275.5	7.0	444	6	US-10-530-972-8	Sequence 8, Appl1	185	239.5	6.0	3594	7	US-11-429-673-4	Sequence 4, Appl1
113	275.5	7.0	444	6	US-10-552-896-8	Sequence 8, Appl1	186	236.5	6.0	396	6	US-10-219-051B-2018	Sequence 2018, Ap
114	275.5	7.0	444	6	US-10-410-945-8	Sequence 8, Appl1	187	236.5	6.0	416	7	US-11-090-997-2032	Sequence 2032, Ap
115	275.5	7.0	444	7	US-11-183-218-8	Sequence 8, Appl1	188	236.5	6.0	416	7	US-11-208-257-8	Sequence 8, Appl1
116	275.5	7.0	444	7	US-11-371-354-68475	Sequence 68475, A	189	236	6.0	783	6	US-11-327-490-27	Sequence 27, Appl
117	275.5	7.0	444	7	US-11-404-266-8	Sequence 8, Appl1	190	236	6.0	783	6	US-10-777-288A-2296	Sequence 2296, Ap
118	275.5	7.0	459	6	US-10-796-307-763	Sequence 763, App	191	230	5.8	347	6	US-10-514-476-2	Sequence 2, Appl1
119	275.5	7.0	459	6	US-10-796-307-764	Sequence 764, App	192	228.5	5.8	1953	7	US-11-264-423-16	Sequence 16, Appl
120	274.5	7.0	800	7	US-11-362-260A-349	Sequence 349, App	193	228	5.8	809	7	US-11-318-939-9	Sequence 9, Appl1
121	273	6.9	560	7	US-11-371-354-63145	Sequence 63145, A	194	228	5.8	812	7	US-11-318-939-12	Sequence 12, Appl
122	271.5	6.9	244	6	US-10-544-944-6	Sequence 6, Appl1	195	227.5	5.8	237	7	US-11-319-952-66	Sequence 66, Appl
123	271.5	6.9	244	6	US-10-546-435-4	Sequence 4, Appl1	196	227.5	5.8	251	6	US-10-529-163-5	Sequence 5, Appl1
124	271.5	6.9	244	6	US-10-405-027-5265	Sequence 5265, Ap	197	227.5	5.8	251	6	US-11-319-952-67	Sequence 67, Appl
125	271.5	6.9	244	6	US-10-529-348-468	Sequence 468, App	198	227.5	5.8	2505	6	US-10-669-920-15	Sequence 15, Appl
126	271.5	6.9	244	7	US-11-319-952-84	Sequence 84, Appl	199	227	5.8	241	7	US-11-254-185-3	Sequence 3, Appl1
127	271.5	6.9	244	7	US-11-371-354-55523	Sequence 55523, A	200	227	5.8	241	7	US-11-254-185-35	Sequence 35, Appl1
128	271.5	6.9	244	7	US-11-371-354-77543	Sequence 77543, A	201	227	5.8	241	7	US-11-253-869-3	Sequence 3, Appl1
129	271.5	6.9	244	7	US-11-436-059-4	Sequence 4, Appl1	202	227	5.8	241	7	US-11-253-869-35	Sequence 35, Appl
130	269.5	6.8	239	7	US-11-319-952-71	Sequence 71, Appl	203	227	5.8	387	7	US-11-303-608-2	Sequence 2, Appl1
131	267	6.8	462	6	US-10-530-972-10	Sequence 10, Appl	204	227	5.8	387	6	US-10-669-920-448	Sequence 448, App
132	267	6.8	462	6	US-10-552-896-10	Sequence 10, Appl	205	226.5	5.7	308	7	US-11-476-636-20	Sequence 20, Appl
133	267	6.8	462	6	US-10-410-945-10	Sequence 10, Appl	206	226.5	5.7	454	7	US-11-400-825-2	Sequence 2, Appl1
134	267	6.8	462	7	US-11-183-218-10	Sequence 10, Appl	207	226.5	5.7	1272	7	US-11-090-997-926	Sequence 926, App
135	267	6.8	462	7	US-11-404-266-10	Sequence 10, Appl	208	226.5	5.7	1429	7	US-11-090-997-928	Sequence 928, App
136	264	6.7	653	7	US-11-242-617-2	Sequence 2, Appl1	209	226	5.7	423	6	US-10-548-460-8	Sequence 8, Appl1
137	263	6.7	431	6	US-10-505-928-465	Sequence 465, App	210	226	5.7	433	6	US-10-530-951-42	Sequence 42, Appl
138	263	6.7	431	6	US-10-669-920-457	Sequence 457, App	211	226	5.7	432	7	US-11-101-316-112	Sequence 112, App
139	263	6.7	431	6	US-10-669-920-459	Sequence 459, App	215	226	5.7	432	7	US-11-376-673-112	Sequence 112, App
140	263	6.7	431	6	US-10-533-519-1049	Sequence 1049, Ap	216	226	5.7	432	7	US-11-102-284-112	Sequence 112, App
141	263	6.7	431	6	US-10-530-972-34	Sequence 34, Appl	217	226	5.7	437	6	US-10-529-348-1258	Sequence 1258, Ap
142	263	6.7	431	6	US-10-552-896-34	Sequence 34, Appl	218	226	5.7	437	7	US-11-371-354-13613	Sequence 13613, A
143	263	6.7	431	6	US-10-410-945-34	Sequence 34, Appl	219	226	5.7	437	7	US-11-371-354-60609	Sequence 60609, A
144	263	6.7	431	7	US-11-183-218-4	Sequence 34, Appl	220	226	5.7	437	7	US-11-371-354-78251	Sequence 78251, A
145	263	6.7	431	7	US-11-371-354-13081	Sequence 13081, A	221	225	5.7	220	7	US-11-327-490-4	Sequence 4, Appl1
146	263	6.7	431	7	US-11-371-354-75459	Sequence 75459, A	222	225	5.7	635	6	US-10-529-348-574	Sequence 574, Appl
147	263	6.7	431	7	US-11-371-354-77523	Sequence 77523, A	223	224.5	5.7	235	7	US-11-354-185-5	Sequence 5, Appl1
148	263	6.7	431	7	US-11-404-266-34	Sequence 34, Appl	224	224.5	5.7	235	7	US-11-254-185-37	Sequence 37, Appl
149	263	6.7	431	7	US-11-510-530-184	Sequence 184, App	225	224.5	5.7	235	7	US-11-253-869-5	Sequence 5, Appl1
150	262.5	6.7	461	6	US-10-219-051B-3545	Sequence 3545, Ap	226	224.5	5.7	235	7	US-11-253-869-37	Sequence 37, Appl
151	262.5	6.7	461	6	US-11-435-001-3	Sequence 3, Appl1	227	224.5	5.7	235	7	US-11-253-869-3	Sequence 3, Appl1
152	262.5	6.7	1042	6	US-10-543-003-4	Sequence 4, Appl1	228	224	5.7	272	7	US-11-327-490-40	Sequence 40, Appl
153	261	6.6	431	6	US-10-219-051B-12109	Sequence 12109, A	229	224	5.7	275	6	US-10-511-937-2457	Sequence 2457, Ap
154	258.5	6.6	412	7	US-11-444-594-2	Sequence 2, Appl1	230	224	5.7	275	6	US-10-530-798-22	Sequence 22, Appl
155	255.5	6.5	244	6	US-10-652-846-11	Sequence 11, Appl	231	223.5	5.7	388	7	US-11-327-490-36	Sequence 36, Appl
156	255	6.5	263	6	US-10-294-433-4117	Sequence 417, App	232	223.5	5.7	413	6	US-10-743-643-2421	Sequence 2421, Ap
157	253.5	6.4	314	6	US-10-533-520-3586	Sequence 3586, Ap	233	223.5	5.7	413	7	US-11-001-793-6341	Sequence 6341, Ap
158	252.5	6.4	314	6	US-10-495-479-4	Sequence 4, Appl1	234	223.5	5.7	413	7	US-11-001-793-9519	Sequence 9519, Ap
159	252.5	6.4	362	6	US-10-495-479-8	Sequence 8, Appl1	235	223.5	5.7	531	6	US-11-371-354-70079	Sequence 70079, A
160	251.5	6.4	787	7	US-11-363-260A-342	Sequence 342, App	236	223.5	5.7	1203	7	US-10-522-668-2	Sequence 2, Appl1
161	250.5	6.3	757	7	US-11-362-260A-345	Sequence 345, App	237	223	5.7	305	7	US-11-293-697-930	Sequence 930, App
162	249.5	6.3	875	6	US-10-570-909-19	Sequence 19, Appl	238	223	5.7	424	7	US-11-403-988-13	Sequence 13, Appl
163	249.5	6.3	875	6	US-10-570-909-92	Sequence 92, Appl	239	222.5	5.6	790	7	US-11-318-939-13	Sequence 13, Appl
164	248	6.3	230	7	US-11-254-185-8	Sequence 8, Appl1	240	222	5.6	275	6	US-10-530-798-23	Sequence 23, Appl
165	248	6.3	230	7	US-11-254-185-70	Sequence 40, Appl	241	222	5.6	275	6	US-10-530-798-25	Sequence 25, Appl
166	248	6.3	230	7	US-11-253-869-8	Sequence 8, Appl1	242	222	5.6	275	6	US-10-219-051B-8826	Sequence 8826, Ap
167	248	6.3	230	7	US-11-253-869-40	Sequence 40, Appl	243	222	5.6	275	6	US-11-371-354-63815	Sequence 63815, A
168	248	6.3	263	7	US-11-371-354-47719	Sequence 74719, A	244	222	5.6	422	7	US-11-355-120-472	Sequence 472, App
169	247	6.3	739	7	US-11-441-828-2	Sequence 2, Appl1	248	222	5.6	423	7	US-11-101-316-106	Sequence 106, App
170	247	6.3	764	6	US-10-529-348-2191	Sequence 2191, App	249	222	5.6	423	7	US-11-376-673-106	Sequence 106, App
171	247	6.3	764	7	US-11-371-354-37321	Sequence 73721, A	250	222	5.6	423	7	US-11-365-762-146	Sequence 146, App
172	247	6.3	764	7	US-11-441-828-1	Sequence 1, Appl1	251	222	5.6	423	7	US-11-102-284-106	Sequence 106, App
173	246.5	6.2	615	6	US-10-796-280-914	Sequence 914, App	252	222	5.6	428	7	US-11-510-530-218	Sequence 218, App
174	246.5	6.2	622	6	US-10-796-280-513	Sequence 913, App	255	221.5	5.6	428	7	US-10-245-882-206	Sequence 206, App
175	246.5	6.2	622	7	US-11-371-354-68137	Sequence 68137, A	256	221.5	5.6	453	7	US-11-403-988-2	Sequence 2, Appl1

257	221.5	5.6	2531	6	US-10-219-051B-9645	Sequence 9645, Ap	331	211	5.3	262	7	US-11-359-554-2	Sequence 2, Appli
258	221.5	5.6	2531	6	US-10-219-051B-9649	Sequence 9649, Ap	332	211	5.3	276	7	US-11-327-449-35	Sequence 35, Appli
259	221.5	5.6	2531	6	US-10-219-051B-9653	Sequence 9653, Ap	333	211	5.3	1067	7	US-11-054-369A-3	Sequence 3, Appli
260	221.5	5.6	2531	6	US-10-219-051B-9657	Sequence 9657, Ap	334	211	5.3	1218	6	US-10-833-833-134	Sequence 124, App
261	221	5.6	273	6	US-10-219-051B-8824	Sequence 8824, Ap	335	211	5.3	1218	6	US-10-219-051B-9286	Sequence 6286, Ap
262	221	5.6	273	6	US-10-219-051B-13255	Sequence 13255, A	336	211	5.3	1218	6	US-10-567-630-23	Sequence 23, Appl
263	221	5.6	273	6	US-10-219-051B-13259	Sequence 13259, A	337	211	5.3	1218	6	US-11-178-724-21	Sequence 21, Appl
264	221	5.6	1198	6	US-10-219-051B-4572	Sequence 4572, Ap	338	211	5.3	1218	7	US-11-071-796A-20	Sequence 20, Appl
265	220	5.6	275	6	US-10-530-798-24	Sequence 24, Appl	339	211	5.3	1218	7	US-11-188-417A-21	Sequence 21, Appl
266	220	5.6	275	6	US-10-530-798-26	Sequence 26, Appl	340	211	5.3	1218	7	US-11-231-494-21	Sequence 21, Appl
267	219.5	5.6	245	7	US-11-354-185-36	Sequence 36, Appl	341	210.5	5.3	339	7	US-11-404-745-2	Sequence 2, Appli
268	219.5	5.6	271	7	US-11-353-869-36	Sequence 36, Appl	342	210.5	5.3	505	7	US-11-293-697-3257	Sequence 2, Appli
269	219.5	5.6	243	7	US-11-327-490-39	Sequence 39, Appl	343	210.5	5.3	572	6	US-10-760-320A-4829	Sequence 3257, Ap
270	219.5	5.6	761	7	US-11-441-828-6	Sequence 6, Appli	344	210.5	5.3	1068	7	US-11-054-369A-1	Sequence 4829, Ap
271	219	5.6	343	6	US-10-219-051B-13257	Sequence 13257, A	345	210.5	5.3	1219	6	US-10-219-051B-3232	Sequence 1, Appli
272	219	5.6	343	6	US-10-219-051B-13261	Sequence 13261, A	346	210.5	5.3	1219	6	US-10-219-051B-6284	Sequence 3232, Ap
273	219	5.6	343	6	US-10-529-348-265	Sequence 265, App	347	209	5.3	307	6	US-11-066-316A-636	Sequence 6284, App
274	219	5.6	343	7	US-11-359-554-3	Sequence 3, Appli	348	209	5.3	433	6	US-10-760-320A-4755	Sequence 4755, Ap
275	219	5.6	343	7	US-11-359-865-1	Sequence 1, Appli	349	209	5.3	433	6	US-10-669-920-454	Sequence 454, App
276	218.5	5.5	1201	7	US-11-090-997-932	Sequence 932, App	350	208.5	5.3	492	5	US-09-976-885-173	Sequence 173, App
277	218.5	5.5	1379	6	US-10-502-394-46	Sequence 46, Appl	351	208.5	5.3	492	7	US-11-344-933-895	Sequence 895, App
278	218.5	5.5	1379	6	US-11-327-490-3	Sequence 3, Appli	352	208.5	5.3	492	7	US-11-200-973-4	Sequence 9, Appli
279	218	5.5	268	6	US-10-405-027-3748	Sequence 3748, Ap	353	208.5	5.3	492	7	US-11-538-764-94	Sequence 94, Appl
280	217	5.5	268	6	US-11-371-354-57523	Sequence 57523, A	354	208.5	5.3	492	7	US-11-212-799-173	Sequence 173, Appl
281	217	5.5	284	6	US-10-405-027-4680	Sequence 4680, Ap	355	208	5.3	271	7	US-11-292-215-10	Sequence 10, Appl
282	217	5.5	2703	6	US-10-781-059A-4	Sequence 4, Appli	356	207.5	5.3	269	7	US-11-371-354-74659	Sequence 74659, A
283	217	5.5	2703	6	US-11-359-554-6	Sequence 6, Appli	357	207.5	5.3	1047	7	US-11-288-992-12	Sequence 74659, A
284	216	5.5	272	7	US-11-359-554-6	Sequence 6, Appli	358	207.5	5.3	1463	7	US-11-288-992-48	Sequence 48, Appl
285	216	5.5	810	7	US-11-371-354-68191	Sequence 68191, A	359	207	5.2	550	6	US-10-796-280-1057	Sequence 1057, Ap
286	216	5.5	810	7	US-11-253-972-1	Sequence 1, Appli	360	206.5	5.2	250	7	US-11-478-144-657	Sequence 657, App
287	216	5.5	1218	6	US-10-833-833-121	Sequence 121, App	361	206.5	5.2	272	7	US-11-327-490-37	Sequence 37, Appl
288	215.5	5.5	306	7	US-11-476-636-6	Sequence 263, App	362	206	5.2	275	7	US-11-319-952-72	Sequence 72, Appl
289	215.5	5.5	317	6	US-10-970-823-263	Sequence 823, Ap	363	206	5.2	426	6	US-10-760-320A-9218	Sequence 3218, Ap
290	215.5	5.5	317	6	US-10-529-348-584	Sequence 584, App	364	206	5.2	1169	6	US-10-796-280-841	Sequence 841, App
291	215.5	5.5	317	6	US-11-476-636-2	Sequence 2, Appli	365	206	5.2	1169	6	US-11-073-360-156	Sequence 156, App
292	215.5	5.5	319	7	US-11-476-636-4	Sequence 4, Appli	366	205.5	5.2	269	7	US-11-371-354-70753	Sequence 70753 A
293	215	5.4	268	6	US-10-405-027-5294	Sequence 5294, Ap	367	205.5	5.2	492	7	US-11-344-933-932	Sequence 932, App
294	215	5.4	729	6	US-10-777-288A-2471	Sequence 2471, Ap	368	205.5	5.2	492	7	US-11-200-973-2	Sequence 2, Appli
295	215	5.4	790	7	US-11-350-703-1	Sequence 1, Appli	369	205.5	5.2	492	7	US-11-371-354-65497	Sequence 65497, A
296	215	5.4	791	7	US-11-318-939-6	Sequence 6, Appli	370	205	5.2	393	7	US-11-344-933-934	Sequence 934, App
297	215	5.4	810	7	US-11-371-354-68531	Sequence 68531, A	371	204.5	5.2	305	6	US-10-652-846-75	Sequence 75, Appl
298	214.5	5.4	1472	6	US-10-219-051B-4570	Sequence 4570, Ap	372	204.5	5.2	305	6	US-10-652-846-75	Sequence 841, App
299	214.5	5.4	1473	6	US-11-090-997-60	Sequence 60, Appl	373	204.5	5.2	305	6	US-10-405-027-4907	Sequence 4907, Ap
300	214	5.4	275	6	US-10-219-051B-2020	Sequence 2020, Ap	374	204.5	5.2	305	6	US-10-405-027-4910	Sequence 4910, Ap
301	214	5.4	810	7	US-11-431-526-2	Sequence 2, Appli	375	204.5	5.2	305	7	US-11-001-793-11184	Sequence 11184, A
302	214	5.4	810	7	US-11-431-526-2	Sequence 2, Appli	376	204	5.2	260	6	US-10-219-051B-12716	Sequence 12716, A
303	213.5	5.4	255	7	US-11-254-185-6	Sequence 6, Appli	377	204	5.2	260	6	US-10-544-944-13	Sequence 13, Appl
304	213.5	5.4	255	7	US-11-254-185-6	Sequence 6, Appli	378	204	5.2	260	6	US-10-652-846-7	Sequence 7, Appli
305	213.5	5.4	255	7	US-11-253-869-6	Sequence 38, Appli	379	204	5.2	260	6	US-10-964-241-396	Sequence 396, App
306	213.5	5.4	255	7	US-11-253-869-6	Sequence 38, Appli	380	204	5.2	260	6	US-10-529-348-608	Sequence 608, App
307	213	5.4	255	7	US-11-253-869-38	Sequence 38, Appl	381	204	5.2	260	6	US-11-319-952-83	Sequence 83, Appl
308	212.5	5.4	250	5	US-11-327-490-38	Sequence 38, Appl	382	204	5.2	260	7	US-11-295-040-7	Sequence 7, Appli
309	212.5	5.4	250	5	US-09-976-858-34	Sequence 34, Appl	383	203.5	5.2	224	7	US-11-254-185-7	Sequence 7, Appli
310	212.5	5.4	250	6	US-10-544-944-20	Sequence 20, Appl	384	203.5	5.2	224	7	US-11-254-185-39	Sequence 39, Appl
311	212.5	5.4	250	6	US-10-546-435-12	Sequence 12, Appl	385	203.5	5.2	224	7	US-11-253-869-7	Sequence 7, Appli
312	212.5	5.4	250	6	US-10-964-241-506	Sequence 506, App	386	203.5	5.2	224	7	US-11-253-869-39	Sequence 39, Appl
313	212.5	5.4	250	6	US-10-803-180-105	Sequence 106, App	387	203.5	5.2	224	7	US-11-441-635-6	Sequence 6, Appli
314	212.5	5.4	250	7	US-11-319-952-86	Sequence 86, Appl	388	203.5	5.2	224	7	US-10-529-348-534	Sequence 534, App
315	212.5	5.4	250	7	US-11-329-770-427	Sequence 427, App	389	203.5	5.2	239	7	US-11-387-443-4	Sequence 4092, Ap
316	212.5	5.4	250	7	US-11-371-354-57075	Sequence 57075, A	390	203.5	5.2	239	7	US-10-567-630-15	Sequence 15, Appl
317	212.5	5.4	250	7	US-11-371-354-77939	Sequence 77939, A	391	203.5	5.2	239	7	US-10-567-630-15	Sequence 15, Appl
318	212.5	5.4	250	7	US-11-001-793-7212	Sequence 7212, Ap	392	203.5	5.2	239	7	US-11-264-243-6	Sequence 6, Appli
319	212.5	5.4	250	7	US-11-212-799-34	Sequence 34, Appl	393	203	5.1	185	6	US-10-527-191-1	Sequence 1, Appli
320	212.5	5.4	282	6	US-10-544-944-19	Sequence 19, Appl	394	203	5.1	581	6	US-10-574-786-2	Sequence 2, Appli
321	212.5	5.4	282	6	US-10-546-435-11	Sequence 11, Appl	395	202.5	5.1	228	7	US-11-319-952-73	Sequence 73, Appl
322	212.5	5.4	282	6	US-10-553-436-234	Sequence 234, App	396	202.5	5.1	239	7	US-11-371-354-61593	Sequence 61593, A
323	212.5	5.4	282	6	US-10-529-088-1	Sequence 1, Appli	397	202.5	5.1	239	7	US-11-371-354-61593	Sequence 61593, A
324	212.5	5.4	282	6	US-10-803-180-107	Sequence 107, App	398	202	5.1	2000	6	US-10-533-519-674	Sequence 674, App
325	212	5.4	260	6	US-10-652-846-8	Sequence 8, Appli	399	202	5.1	2321	6	US-10-518-751-8	Sequence 8, Appli
326	212	5.4	260	7	US-11-393-040-10	Sequence 10, Appl	400	202	5.1	2321	6	US-10-567-630-19	Sequence 19, Appl
327	211.5	5.4	235	7	US-11-254-185-4	Sequence 4, Appli	401	201.5	5.1	256	6	US-10-529-163-7	Sequence 7, Appli
328	211.5	5.4	235	7	US-11-253-869-4	Sequence 4, Appli	402	201.5	5.1	256	6	US-11-066-316A-635	Sequence 635, App
329	211.5	5.4	418	6	US-10-529-348-693	Sequence 693, App	403	201.5	5.1	438	6	US-10-760-320A-2876	Sequence 2876, Ap
330	211.5	5.4	418	7	US-11-371-354-69437	Sequence 69437, A	404	201	5.1	1054	7	US-11-288-992-47	Sequence 47, Appl

405	200.5	5.1	185	6	US-10-527-191-12	Sequence 12, Appl	479	189	4.8	253	6	US-10-544-944-10	Sequence 10, Appl
406	200.5	5.1	185	7	US-11-371-354-68349	Sequence 68349, A	480	189	4.8	253	6	US-10-529-348-576	Sequence 576, App
407	200.5	5.1	415	6	US-10-970-823-104	Sequence 104, App	481	189	4.8	253	7	US-11-371-354-62399	Sequence 62399, A
408	200.5	5.1	752	7	US-11-371-354-64631	Sequence 64631, A	482	189	4.8	253	7	US-11-538-764-95	Sequence 95, Appl
409	200.5	5.1	810	7	US-11-318-939-11	Sequence 11, Appl	483	189	4.8	449	7	US-11-344-932-617	Sequence 617, App
410	200	5.1	385	7	US-11-371-354-62531	Sequence 62531, A	484	189	4.8	585	7	US-11-344-932-1020	Sequence 1020, Ap
411	199.5	5.1	348	7	US-11-371-354-65083	Sequence 65083, A	485	189	4.8	176	7	US-11-090-997-1018	Sequence 1018, Ap
412	199.5	5.1	2556	6	US-10-781-059A-2	Sequence 2, Appl	486	188.5	4.8	282	6	US-10-219-051B-3543	Sequence 3543, Ap
413	199.5	5.1	2556	7	US-11-071-796A-22	Sequence 22, Appl	488	188.5	4.8	290	6	US-10-964-241-222	Sequence 222, App
414	198.5	5.0	170	6	US-10-537-507A-2	Sequence 2, Appl	489	188.5	4.8	290	6	US-10-529-348-1862	Sequence 1862, Ap
415	198.5	5.0	223	7	US-11-359-858-2	Sequence 14, Appl	490	188.5	4.8	290	7	US-11-001-793-9088	Sequence 9088, Ap
416	198.5	5.0	311	7	US-11-359-858-2	Sequence 2, Appl	491	188.5	4.8	2451	6	US-10-669-920-908	Sequence 908, App
417	198.5	5.0	790	7	US-11-066-316A-1092	Sequence 1092, Ap	492	188.5	4.8	2503	6	US-10-539-228-723	Sequence 723, App
418	198.5	5.0	830	7	US-11-066-316A-1093	Sequence 1093, Ap	493	188	4.8	228	7	US-11-478-089-2	Sequence 2, Appl
419	198.5	5.0	830	7	US-11-066-316A-1094	Sequence 1094, Ap	494	188	4.8	249	7	US-11-478-089-2	Sequence 68, Appl
420	198	5.0	235	6	US-10-530-798-1	Sequence 1, Appl	495	188	4.8	253	6	US-10-219-051B-4094	Sequence 4094, Ap
421	198	5.0	235	7	US-11-430-214-72	Sequence 72, Appl	496	188	4.8	254	7	US-11-344-932-523	Sequence 523, Appl
422	198	5.0	1023	6	US-10-964-241-200	Sequence 200, App	497	188	4.8	288	6	US-10-530-643-22	Sequence 22, Appl
423	197.5	5.0	248	6	US-10-529-163-2	Sequence 2, Appl	498	188	4.8	311	7	US-11-327-490-41	Sequence 41, Appl
424	197.5	5.0	248	7	US-11-319-952-60	Sequence 60, Appl	499	188	4.8	333	7	US-11-319-952-60	Sequence 8, Appl
425	197.5	5.0	269	7	US-11-246-999-127	Sequence 127, App	500	187.5	4.8	224	7	US-11-441-635-8	Sequence 7, Appl
426	197.5	5.0	2494	6	US-10-669-920-22	Sequence 22, Appl	501	187.5	4.8	224	6	US-10-441-635-8	Sequence 691, App
427	197.5	5.0	235	6	US-10-530-798-2	Sequence 2, Appl	502	187.5	4.8	247	7	US-11-371-354-70767	Sequence 70767, A
428	197	5.0	338	7	US-11-318-939-10	Sequence 10, Appl	503	187.5	4.8	252	6	US-10-703-032-122453	Sequence 122453, A
429	196.5	5.0	1052	7	US-11-218-141-1000	Sequence 1000, Ap	504	187.5	4.8	932	7	US-11-090-997-1878	Sequence 1878, Ap
430	196.5	5.0	2523	6	US-10-781-059A-3	Sequence 3, Appl	505	187.5	4.8	932	7	US-11-090-997-1874	Sequence 1874, Ap
431	196.5	5.0	270	7	US-11-371-354-74827	Sequence 74827, A	506	187.5	4.8	1008	7	US-11-288-992-11	Sequence 11, Appl
432	196	5.0	257	7	US-11-371-354-57395	Sequence 57395, A	507	187.5	4.7	281	7	US-11-293-697-2976	Sequence 2976, Ap
433	195.5	5.0	257	7	US-11-127-581-8	Sequence 8, Appl	508	187	4.7	226	7	US-11-319-952-22	Sequence 22, Appl
434	195.5	5.0	2007	6	US-10-533-519-512	Sequence 512, App	509	186	4.7	1176	6	US-10-777-288A-29774	Sequence 2974, Appl
435	195.5	5.0	2471	6	US-10-781-059A-1	Sequence 1, Appl	510	185.5	4.7	711	7	US-11-478-193-1080	Sequence 1080, Ap
436	195.5	5.0	2471	6	US-10-219-051B-4116	Sequence 4116, Ap	511	185.5	4.7	713	7	US-11-175-714-5	Sequence 5, Appl
437	195.5	5.0	2471	6	US-10-219-051B-9647	Sequence 9647, Ap	512	185.5	4.7	621	6	US-10-990-328-10445	Sequence 10445, A
438	195.5	5.0	2471	6	US-10-219-051B-9651	Sequence 9651, Ap	513	184.5	4.7	705	6	US-11-090-997-1876	Sequence 1876, Ap
439	195.5	5.0	2471	6	US-10-219-051B-9655	Sequence 9655, Ap	514	184.5	4.7	917	7	US-11-090-997-1872	Sequence 1872, Ap
440	195.5	5.0	2471	6	US-10-219-051B-9659	Sequence 9659, Ap	515	184	4.7	144	6	US-10-652-846-1	Sequence 1, Appl
441	195.5	5.0	2471	6	US-10-219-051B-9659	Sequence 9659, Ap	516	184	4.7	144	6	US-11-295-040-1	Sequence 257, App
442	195.5	5.0	2471	6	US-10-567-630-17	Sequence 17, Appl	517	184	4.7	314	6	US-10-970-823-257	Sequence 257, App
443	195.5	5.0	2471	7	US-11-071-796A-23	Sequence 23, Appl	518	184	4.7	314	6	US-10-105-299-5979	Sequence 5979, App
444	195	4.9	258	7	US-11-319-952-85	Sequence 85, Appl	519	184	4.7	314	6	US-10-868-184-4975	Sequence 4975, Ap
445	195	4.9	432	6	US-10-254-185-26	Sequence 26, Appl	520	183.5	4.6	721	6	US-10-576-491-2	Sequence 2, Appl
446	194	4.9	113	7	US-11-253-869-56	Sequence 56, Appl	521	183.5	4.6	251	6	US-10-576-491-2	Sequence 5979, App
447	194	4.9	113	7	US-11-507-474-20	Sequence 20, Appl	522	183.5	4.6	758	7	US-11-066-316A-1991	Sequence 2, Appl
448	194	4.9	233	7	US-11-478-089-4	Sequence 4, Appl	523	182.5	4.6	157	6	US-10-760-320A-3310	Sequence 3310, Ap
449	194	4.9	233	6	US-10-990-920-451	Sequence 10446, A	524	182.5	4.6	260	7	US-11-429-599-21	Sequence 21, Appl
450	194	4.9	3609	6	US-10-669-920-451	Sequence 451, App	525	182.5	4.6	468	6	US-10-743-643-1064	Sequence 1064, Ap
451	194	4.9	347	6	US-10-743-643-2419	Sequence 2419, Ap	526	182.5	4.6	720	7	US-11-175-714-4	Sequence 4, Appl
452	193.5	4.9	2471	6	US-10-219-051B-4114	Sequence 4114, Ap	527	182	4.6	421	6	US-10-760-320A-4767	Sequence 4767, Appl
453	193.5	4.9	228	6	US-10-533-519-1031	Sequence 1031, Ap	528	182	4.6	721	7	US-11-175-714-7	Sequence 7, Appl
454	193	4.9	228	6	US-10-529-348-528	Sequence 528, App	529	182	4.6	1067	7	US-11-054-369A-5	Sequence 5, Appl
455	193	4.9	228	6	US-10-533-530-6140	Sequence 6140, Ap	530	182	4.6	1159	6	US-10-540-844-4	Sequence 4, Appl
456	193	4.9	228	6	US-10-533-530-6140	Sequence 69, Appl	531	182	4.6	1266	6	US-10-540-844-2	Sequence 2, Appl
457	193	4.9	253	7	US-11-319-952-59	Sequence 59, Appl	532	182	4.6	1266	6	US-10-540-844-2	Sequence 6747, Ap
458	192.5	4.9	194	6	US-10-530-798-31	Sequence 31, Appl	533	182	4.6	1238	6	US-10-219-051B-3334	Sequence 3334, Ap
459	192.5	4.9	226	6	US-10-530-798-31	Sequence 3, Appl	534	182	4.6	1238	6	US-10-567-630-35	Sequence 35, Appl
460	192.5	4.9	247	6	US-10-529-348-1120	Sequence 1120, Ap	535	182	4.6	1238	6	US-10-567-630-35	Sequence 25, Appl
461	192.5	4.9	281	7	US-11-292-215-7	Sequence 7, Appl	536	182	4.6	1238	6	US-10-529-348-10	Sequence 10, Appl
462	192	4.9	149	7	US-11-400-825-20	Sequence 20, Appl	537	182	4.6	1238	6	US-11-178-124-22	Sequence 22, Appl
463	191.5	4.9	224	7	US-11-441-635-5	Sequence 5, Appl	538	182	4.6	1238	7	US-11-071-796A-21	Sequence 21, Appl
464	191.5	4.9	246	6	US-10-547-510-54	Sequence 54, Appl	539	182	4.6	1238	7	US-11-188-4117A-22	Sequence 22, Appl
465	191.5	4.9	247	7	US-11-319-952-82	Sequence 82, Appl	540	182	4.6	1238	7	US-11-188-4117A-22	Sequence 22, Appl
466	191.5	4.9	579	7	US-11-166-372-1884	Sequence 1884, Ap	541	181.5	4.6	1238	7	US-11-231-894-22	Sequence 22, Appl
467	191.5	4.9	830	6	US-10-505-928-469	Sequence 469, App	542	181.5	4.6	829	7	US-11-292-315-8	Sequence 8, Appl
468	191	4.8	226	7	US-11-403-988-5	Sequence 5, Appl	543	181.5	4.6	873	7	US-11-090-997-1882	Sequence 1882, Ap
469	191	4.8	228	7	US-11-371-354-58221	Sequence 68221, A	544	181	4.6	876	7	US-11-090-997-1880	Sequence 1880, Ap
470	191	4.8	254	7	US-11-319-952-3	Sequence 3, Appl	545	181	4.6	257	7	US-11-319-952-87	Sequence 87, Appl
471	191	4.8	254	7	US-11-339-723-50	Sequence 50, Appl	546	181	4.6	831	7	US-11-218-141-3868	Sequence 3868, Ap
472	191	4.8	254	7	US-11-344-932-525	Sequence 525, App	547	181	4.6	832	7	US-11-218-141-1769	Sequence 1769, App
473	190.5	4.8	241	7	US-11-319-952-77	Sequence 77, Appl	548	181	4.6	832	7	US-11-218-141-3737	Sequence 3737, Ap
474	190	4.8	253	6	US-10-574-398-70	Sequence 70, Appl	549	181	4.6	910	6	US-11-218-141-3738	Sequence 3738, Ap
475	190	4.8	253	7	US-11-441-828-7	Sequence 7, Appl	550	181	4.6	254	6	US-10-964-241-112	Sequence 112, App
476	190	4.8	254	7	US-11-319-952-81	Sequence 81, Appl	551	180	4.6	254	6	US-10-529-163-1	Sequence 1, Appl
477	189	4.8	220	7	US-11-344-932-327	Sequence 327, App	552	180	4.6	254	7	US-11-319-952-59	Sequence 59, Appl
478	189	4.8	237	7	US-11-319-952-2	Sequence 2, Appl	553	180	4.6	2087	6	US-10-669-920-911	Sequence 911, App

554	180	4.6	2087	6	US-10-669-920-913	Sequence 913, App	627	171.5	4.3	2403	6	US-10-527-191-88	Sequence 88, App1
555	180	4.6	2203	7	US-10-539-228-726	Sequence 726, App	628	171.5	4.3	2413	6	US-10-511-937-2616	Sequence 2616, App
556	179.5	4.6	2205	7	US-11-349-541-176	Sequence 176, App	629	171.5	4.3	2413	6	US-10-527-191-89	Sequence 89, App1
557	179.5	4.6	205	7	US-11-944-932-176	Sequence 176, App	630	171.5	4.3	2413	6	US-10-527-191-106	Sequence 106, App
558	179.5	4.6	250	6	US-11-529-348-1910	Sequence 1910, App	631	171	4.3	256	7	US-11-319-952-44	Sequence 44, App1
559	179.5	4.6	250	7	US-11-319-952-23	Sequence 23, App1	632	171	4.3	258	7	US-11-158-252-63	Sequence 63, App1
560	178	4.5	556	6	US-10-796-280-915	Sequence 915, App	633	171	4.3	277	6	US-10-526-111-1	Sequence 1, App1
561	178	4.5	996	7	US-11-538-764-151	Sequence 151, App	634	171	4.3	277	6	US-10-529-348-578	Sequence 578, App
562	177.5	4.5	249	6	US-10-743-643-116	Sequence 116, App	635	171	4.3	277	6	US-11-319-952-45	Sequence 45, App1
563	177.5	4.5	121	7	US-11-429-599-23	Sequence 23, App1	636	171	4.3	277	7	US-11-371-354-70755	Sequence 70755, A
564	177	4.5	112	7	US-11-254-185-27	Sequence 27, App1	637	171	4.3	277	7	US-11-436-059-8	Sequence 8, App1
565	177	4.5	112	7	US-11-253-869-27	Sequence 27, App1	640	171	4.3	737	7	US-11-296-092-15	Sequence 15, App1
566	177	4.5	729	7	US-11-175-714-8	Sequence 8, App1	641	171	4.3	737	7	US-11-296-155-15	Sequence 15, App1
567	177	4.5	1088	6	US-10-669-920-1337	Sequence 1337, App	642	171	4.3	777	7	US-11-218-141-1900	Sequence 1900, App
568	177	4.5	1200	6	US-10-567-630-27	Sequence 27, App1	643	171	4.3	2412	6	US-10-527-191-70	Sequence 70, App1
569	176.5	4.5	1200	6	US-10-743-643-979	Sequence 979, App	644	171	4.3	2412	6	US-10-527-191-105	Sequence 105, App1
570	176.5	4.5	2002	6	US-10-567-630-21	Sequence 21, App1	645	171	4.3	2413	6	US-10-219-051B-8374	Sequence 8374, App
571	176.5	4.5	2003	6	US-10-767-471-911	Sequence 911, App	646	171	4.3	2413	6	US-10-219-051B-8378	Sequence 8378, App
572	176.5	4.5	2003	6	US-10-767-471-932	Sequence 932, App	647	171	4.3	2413	6	US-10-219-051B-11886	Sequence 11886, A
573	176.5	4.5	2003	6	US-10-990-328-10382	Sequence 10382, A	648	170	4.3	864	7	US-11-178-724-27	Sequence 27, App1
574	176.5	4.5	2003	6	US-10-990-328-10403	Sequence 10403, A	649	170	4.3	864	7	US-11-188-417A-98	Sequence 98, App1
575	176.5	4.5	2003	7	US-11-264-243-8	Sequence 8, App1	650	170	4.3	864	7	US-11-231-494-34	Sequence 34, App1
576	176.5	4.5	270	7	US-11-371-354-74657	Sequence 74657, A	651	169.5	4.3	542	7	US-11-054-369A-7	Sequence 7, App1
577	176	4.5	112	7	US-11-507-474-21	Sequence 21, App1	652	169.5	4.3	723	6	US-10-567-630-29	Sequence 29, App1
578	175	4.4	112	7	US-11-001-793-8731	Sequence 8731, App	653	169	4.3	2067	6	US-10-669-920-1343	Sequence 1343, App
579	175	4.4	467	6	US-10-105-299-6146	Sequence 6146, App	654	168	4.3	609	7	US-11-090-997-1904	Sequence 1904, App
580	175	4.4	487	6	US-10-105-299-6146	Sequence 6146, App	655	168	4.3	644	6	US-10-508-580-16	Sequence 16, App1
581	175	4.4	487	6	US-10-868-184-5142	Sequence 5142, App	656	168	4.3	644	6	US-10-405-027-4382	Sequence 4382, App
582	175	4.4	487	6	US-10-994-608-6146	Sequence 6146, App	657	168	4.3	698	6	US-10-405-027-3107	Sequence 3107, App
583	175	4.4	555	6	US-10-405-027-5382	Sequence 5382, App	658	168	4.3	923	6	US-10-533-519-1684	Sequence 1684, App
584	175	4.4	555	6	US-10-796-280-707	Sequence 707, App	659	168	4.3	923	7	US-11-090-997-1992	Sequence 1902, App
585	175	4.4	555	7	US-11-066-316A-586	Sequence 586, App	660	168	4.3	923	7	US-11-488-364-2	Sequence 2, App1
586	175	4.4	901	6	US-10-796-280-708	Sequence 708, App	661	167.5	4.2	255	7	US-11-319-952-74	Sequence 74, App1
587	175	4.4	901	6	US-11-066-316A-585	Sequence 585, App	662	167.5	4.2	256	7	US-11-319-952-76	Sequence 76, App1
588	175	4.4	909	6	US-10-796-280-704	Sequence 704, App	663	167.5	4.2	261	6	US-10-652-846-10	Sequence 10, App1
589	175	4.4	909	6	US-11-066-316A-588	Sequence 588, App	664	167.5	4.2	261	7	US-11-319-952-78	Sequence 78, App1
590	175	4.4	926	6	US-10-533-519-1635	Sequence 1635, App	665	167.5	4.2	261	7	US-11-323-964-10	Sequence 10, App1
591	175	4.4	926	6	US-10-796-280-706	Sequence 706, App	666	167.5	4.2	261	7	US-11-430-214-70	Sequence 70, App1
592	175	4.4	926	7	US-11-066-316A-583	Sequence 583, App	667	167.5	4.2	261	7	US-11-430-214-75	Sequence 75, App1
593	175	4.4	931	7	US-11-488-364-4	Sequence 4, App1	668	167.5	4.2	261	7	US-11-371-354-74655	Sequence 74655, A
594	175	4.4	969	6	US-10-796-280-710	Sequence 710, App	669	167.5	4.2	262	6	US-10-803-180-105	Sequence 105, App1
595	175	4.4	969	6	US-10-796-280-710	Sequence 710, App	670	167.5	4.2	262	7	US-11-319-952-80	Sequence 80, App1
596	175	4.4	1080	6	US-10-767-471-934	Sequence 934, App	671	167.5	4.2	262	7	US-11-066-316A-974	Sequence 974, App
597	175	4.4	1080	6	US-10-767-471-934	Sequence 934, App	672	167.5	4.2	262	7	US-10-570-909-118	Sequence 118, App
598	175	4.4	1080	6	US-10-990-328-10398	Sequence 10398, A	673	167	4.2	222	6	US-10-553-436-293	Sequence 293, App
599	175	4.4	1080	6	US-10-990-328-10405	Sequence 10405, A	674	166.5	4.2	262	7	US-11-371-354-74963	Sequence 74963, A
600	174.5	4.4	230	7	US-11-362-260A-346	Sequence 346, App	675	166.5	4.2	723	6	US-10-964-241-346	Sequence 346, App
601	174.5	4.4	544	6	US-10-538-197-26	Sequence 26, App1	676	166.5	4.2	723	7	US-11-178-724-18	Sequence 18, App1
602	174	4.4	258	7	US-10-449-902-31884	Sequence 31884, A	677	166.5	4.2	723	7	US-11-071-796A-17	Sequence 17, App1
603	174	4.4	286	7	US-11-292-215-9	Sequence 9, App1	678	166.5	4.2	723	7	US-11-188-417A-18	Sequence 18, App1
604	174	4.4	808	6	US-10-796-280-709	Sequence 709, App	679	166.5	4.2	723	7	US-11-231-494-18	Sequence 18, App1
605	174	4.4	808	6	US-11-066-316A-587	Sequence 587, App	680	166.5	4.2	723	7	US-11-231-494-18	Sequence 18, App1
606	174	4.4	931	7	US-11-343-271-40	Sequence 40, App1	681	166	4.2	241	6	US-10-553-436-292	Sequence 292, App
607	173.5	4.4	234	6	US-10-105-299-4807	Sequence 4807, App	682	166	4.2	300	7	US-11-371-354-57001	Sequence 57001, A
608	173.5	4.4	234	6	US-10-868-184-3803	Sequence 3803, App	683	166	4.2	923	6	US-10-533-519-1576	Sequence 1576, App
609	173.5	4.4	294	6	US-10-994-608-4807	Sequence 4807, App	684	165.5	4.2	383	7	US-11-371-354-73975	Sequence 73975, A
610	173.5	4.4	717	7	US-11-175-714-9	Sequence 9, App1	685	165.5	4.2	698	7	US-11-066-316A-594	Sequence 594, App
611	173.5	4.4	809	7	US-11-318-141-1770	Sequence 17581, A	687	164.5	4.2	241	6	US-10-964-241-248	Sequence 248, App
612	173.5	4.4	853	7	US-11-218-141-1770	Sequence 17581, A	688	164.5	4.2	241	7	US-11-371-354-65937	Sequence 65937, A
613	173	4.4	248	6	US-10-743-643-1289	Sequence 1289, App	689	164.5	4.2	249	6	US-10-219-051B-14650	Sequence 14650, A
614	173	4.4	270	7	US-11-371-354-75053	Sequence 75053, A	690	164.5	4.2	329	7	US-11-345-903-11	Sequence 11, App1
615	173	4.4	302	7	US-11-476-636-18	Sequence 18, App1	691	164.5	4.2	449	7	US-11-371-354-65587	Sequence 65587, A
616	173	4.4	701	7	US-11-362-260A-343	Sequence 343, App	692	164.5	4.2	449	7	US-11-354-559-4	Sequence 4, App1
617	173	4.4	768	6	US-10-219-051B-12714	Sequence 12714, A	693	164.5	4.2	1168	6	US-10-796-307-885	Sequence 885, App1
618	172.5	4.4	449	6	US-10-743-643-1066	Sequence 1066, App	694	164.5	4.2	1172	6	US-10-796-307-887	Sequence 887, App
619	172.5	4.4	449	6	US-11-371-354-71577	Sequence 71577, A	695	164.5	4.2	1172	6	US-10-796-307-888	Sequence 888, App
620	172.5	4.4	567	6	US-10-538-197-22	Sequence 22, App1	696	164.5	4.2	1231	6	US-10-796-307-884	Sequence 884, App
621	172.5	4.4	1208	6	US-10-219-051B-6745	Sequence 6745, App	697	164.5	4.2	1231	6	US-10-796-307-886	Sequence 886, App
622	172	4.4	1208	7	US-11-090-997-6	Sequence 6, App1	698	164.5	4.2	1231	6	US-11-354-559-2	Sequence 2, App1
623	171.5	4.3	262	6	US-10-652-846-9	Sequence 9, App1	699	164.5	4.2	1231	7	US-11-354-559-5	Sequence 5, App1
624	171.5	4.3	262	6	US-11-196-627-1021	Sequence 1021, App	700	164.5	4.2	1231	7	US-11-354-559-337	Sequence 337, App
625	171.5	4.3	1785	6	US-10-527-191-90	Sequence 90, App1	701	164	4.2	484	7	US-11-231-494-56	Sequence 56, App1
626	171.5	4.3	1785	7	US-11-510-493-5	Sequence 5, App1	702	164	4.2	859	6	US-10-533-519-1242	Sequence 1242, App

704	163.5	4.1	859	6	US-10-533-519-2355	Sequence 2355, Ap	781	156	4.0	866	6	US-10-669-920-1339	Sequence 1339, Ap
705	163.5	4.1	859	7	US-11-371-354-63565	Sequence 63565, A	782	155.5	3.9	830	7	US-11-175-714-11	Sequence 11, Appl
706	163	4.1	262	7	US-11-415-342-24	Sequence 24, Appl	783	155	3.9	243	6	US-10-553-869-1	Sequence 1, Appl
707	163	4.1	315	6	US-10-664-356-1774	Sequence 1774, Ap	784	155	3.9	2039	6	US-10-219-051B-3330	Sequence 3230, Ap
708	163	4.1	315	7	US-11-001-793-9386	Sequence 9386, Ap	785	155	3.9	2489	7	US-11-429-673-5	Sequence 5, Appl
709	163	4.1	600	6	US-10-664-356-1389	Sequence 1389, Ap	786	154.5	3.9	239	7	US-11-558-174-15	Sequence 15, Appl
710	163	4.1	600	7	US-11-001-793-6128	Sequence 6128, Ap	787	154.5	3.9	264	7	US-11-247-886-1	Sequence 1, Appl
711	163	4.1	607	6	US-10-970-823-190	Sequence 190, App	788	154	3.9	246	7	US-11-247-886-2	Sequence 2, Appl
712	163	4.1	607	6	US-10-964-241-344	Sequence 344, App	789	154	3.9	247	7	US-11-415-342-16	Sequence 16, Appl
713	163	4.1	261	7	US-11-430-214-89	Sequence 89, Appl	790	154	3.9	248	6	US-10-219-051B-1652	Sequence 14652, A
714	162.5	4.1	1291	6	US-10-219-051B-8372	Sequence 8372, Ap	791	154	3.9	339	6	US-10-527-191-31	Sequence 31, Appl
715	162.5	4.1	1291	6	US-10-219-051B-8376	Sequence 8376, Ap	792	154	3.9	1931	7	US-11-173-310-2	Sequence 3, Appl
716	162.5	4.1	1291	6	US-10-219-051B-11884	Sequence 11884, A	793	154	3.9	2039	6	US-10-219-051B-2028	Sequence 2, Appl
717	162.5	4.1	248	6	US-10-449-902-40162	Sequence 40162, A	794	154	3.9	2039	6	US-10-219-051B-2032	Sequence 2028, Ap
718	162	4.1	260	7	US-11-457-438-2	Sequence 2, Appl	795	154	3.9	2039	6	US-10-219-051B-8828	Sequence 2032, Ap
719	161.5	4.1	260	7	US-10-546-944-3	Sequence 3, Appl	796	153.5	3.9	260	6	US-10-219-051B-8828	Sequence 8828, Ap
720	161	4.1	293	6	US-10-546-435-1	Sequence 1, Appl	797	153.5	3.9	610	6	US-09-776-858-236	Sequence 236, App
721	161	4.1	293	6	US-10-664-356-1208	Sequence 1208, Ap	798	153.5	3.9	610	6	US-10-505-928-580	Sequence 580, App
722	161	4.1	293	6	US-10-664-356-1688	Sequence 1688, Ap	799	153.5	3.9	648	7	US-11-212-799-236	Sequence 236, App
723	161	4.1	293	6	US-10-664-356-1690	Sequence 1690, Ap	800	153.5	3.9	648	7	US-11-127-581-12	Sequence 12, Appl
724	161	4.1	293	6	US-10-664-356-1691	Sequence 1691, Ap	801	153	3.9	90	6	US-10-276-817B-15753	Sequence 15753, A
725	161	4.1	293	6	US-10-964-241-456	Sequence 456, App	802	153	3.9	156	6	US-10-528-260B-246	Sequence 246, App
726	161	4.1	293	6	US-11-319-952-14	Sequence 14, Appl	803	153	3.9	243	6	US-10-553-869-4	Sequence 4, Appl
727	161	4.1	293	7	US-11-371-354-73575	Sequence 73575, A	804	153	3.9	243	6	US-10-553-869-7	Sequence 7, Appl
728	161	4.1	293	7	US-11-436-059-2	Sequence 2, Appl	805	153	3.9	244	7	US-11-247-886-6	Sequence 6, Appl
729	161	4.1	293	7	US-11-001-793-5924	Sequence 5924, Ap	806	153	3.9	868	6	US-10-796-307-651	Sequence 1062, Ap
730	161	4.1	293	7	US-11-001-793-9286	Sequence 9286, Ap	807	153	3.9	868	6	US-10-796-307-651	Sequence 651, App
731	161	4.1	293	7	US-11-001-793-9288	Sequence 9288, Ap	808	152.5	3.9	227	7	US-11-415-342-15	Sequence 15, App
732	161	4.1	293	7	US-11-001-793-9289	Sequence 9289, Ap	809	152.5	3.9	264	6	US-10-245-882-266	Sequence 266, App
733	161	4.1	293	7	US-11-254-185-28	Sequence 28, Appl	810	152.5	3.9	264	6	US-10-533-520-1797	Sequence 1797, Ap
734	161	4.1	113	7	US-11-253-869-58	Sequence 58, Appl	811	152.5	3.9	264	6	US-10-533-520-6168	Sequence 6168, Ap
735	160	4.1	113	7	US-11-254-185-28	Sequence 28, Appl	812	152.5	3.9	264	7	US-11-255-634-1	Sequence 1, Appl
736	160	4.1	207	6	US-10-154-678-54	Sequence 54, Appl	813	152.5	3.9	264	7	US-11-486-321-26	Sequence 26, Appl
737	160	4.1	207	6	US-11-412-325-54	Sequence 54, Appl	814	152.5	3.9	264	7	US-11-371-354-64269	Sequence 64269, A
738	160	4.1	227	6	US-10-553-869-57	Sequence 57, Appl	815	152.5	3.9	264	7	US-11-478-193-404	Sequence 404, App
739	160	4.1	227	6	US-10-553-869-57	Sequence 57, Appl	816	152.5	3.9	400	6	US-10-796-280-1194	Sequence 1194, Ap
740	160	4.1	223	6	US-10-533-869-8	Sequence 8, Appl	817	152.5	3.9	422	6	US-11-371-354-68361	Sequence 68361, A
741	160	4.1	262	6	US-10-511-937-2431	Sequence 2431, Ap	818	152.5	3.9	513	7	US-10-796-280-1196	Sequence 1196, Ap
742	160	4.1	262	6	US-10-533-520-1629	Sequence 1629, Ap	819	152.5	3.9	662	7	US-11-175-714-10	Sequence 10, Appl
743	160	4.1	262	6	US-10-533-520-6470	Sequence 6470, Ap	820	152.5	3.9	243	6	US-10-553-869-2	Sequence 2, Appl
744	160	4.1	262	7	US-11-371-354-61057	Sequence 61057, A	821	152	3.9	243	6	US-10-553-869-3	Sequence 3, Appl
745	160	4.1	262	7	US-11-415-342-23	Sequence 23, Appl	822	152	3.9	243	6	US-10-553-869-5	Sequence 5, Appl
746	160	4.1	262	7	US-11-415-342-25	Sequence 25, Appl	823	152	3.9	243	6	US-10-553-869-6	Sequence 6, Appl
747	160	4.1	1042	6	US-10-796-280-1007	Sequence 1007, Ap	824	152	3.9	247	6	US-10-511-937-2290	Sequence 2290, Ap
748	160	4.1	2871	6	US-10-574-398-390	Sequence 390, App	825	152	3.9	247	6	US-10-511-937-2290	Sequence 2290, Ap
749	159.5	4.0	287	7	US-10-405-027-3719	Sequence 3719, Ap	826	152	3.9	247	6	US-10-511-937-2290	Sequence 2290, Ap
750	159.5	4.0	287	7	US-11-319-952-70	Sequence 70, Appl	827	152	3.9	247	6	US-10-743-643-118	Sequence 118, App
751	159	4.0	465	7	US-11-371-354-58635	Sequence 58635, A	828	152	3.9	247	6	US-10-325-899-9375	Sequence 9375, Ap
752	159	4.0	2608	6	US-10-669-920-1144	Sequence 1144, Ap	829	152	3.9	247	6	US-10-325-899-9375	Sequence 9375, Ap
753	159	4.0	2608	6	US-10-669-920-1144	Sequence 1144, Ap	830	152	3.9	247	6	US-10-533-520-2403	Sequence 2403, Ap
754	159	4.0	2614	6	US-10-796-307-589	Sequence 589, App	831	152	3.9	247	6	US-10-533-520-6338	Sequence 6338, Ap
755	159	4.0	2904	6	US-10-669-920-1146	Sequence 1146, Ap	832	152	3.9	247	7	US-11-415-342-11	Sequence 11, Appl
756	159	4.0	2904	6	US-10-669-920-1146	Sequence 1146, Ap	833	152	3.9	247	7	US-11-415-342-12	Sequence 12, Appl
757	159	4.0	2904	6	US-10-669-920-1146	Sequence 1146, Ap	834	152	3.9	247	7	US-11-415-342-14	Sequence 14, Appl
758	159	4.0	2904	6	US-10-669-920-1146	Sequence 1146, Ap	835	152	3.9	247	7	US-11-415-342-15	Sequence 15, Appl
759	159	4.0	2904	6	US-10-669-920-1146	Sequence 1146, Ap	836	152	3.9	247	7	US-11-389-543-155	Sequence 155, App
760	159	4.0	2912	6	US-10-796-307-588	Sequence 588, App	837	152	3.9	247	7	US-11-436-059-6	Sequence 6, Appl
761	159	4.0	2912	6	US-10-796-307-588	Sequence 588, App	838	152	3.9	247	7	US-11-436-059-6	Sequence 6, Appl
762	158.5	4.0	283	7	US-11-357-337-2	Sequence 2, Appl	839	152	3.9	247	7	US-11-415-342-13	Sequence 1336, Ap
763	158.5	4.0	385	7	US-11-090-997-144	Sequence 144, App	840	152	3.9	247	7	US-11-415-342-13	Sequence 13, App
764	158.5	4.0	211	6	US-10-760-320A-4851	Sequence 4851, Ap	841	152	3.9	247	7	US-11-415-342-13	Sequence 13, App
765	158	4.0	221	6	US-10-553-436-335	Sequence 235, App	842	152	3.9	247	7	US-11-415-342-13	Sequence 25, Appl
766	158	4.0	465	6	US-10-505-928-549	Sequence 549, App	843	152	3.9	247	7	US-11-175-714-4	Sequence 42, Appl
767	158	4.0	854	6	US-10-767-471-910	Sequence 910, App	844	152	3.9	247	7	US-11-175-714-4	Sequence 44, Appl
768	158	4.0	854	6	US-10-767-471-910	Sequence 910, App	845	152	3.9	247	7	US-11-175-714-4	Sequence 46, Appl
769	158	4.0	854	6	US-10-990-328-10381	Sequence 10381, A	846	152	3.9	247	7	US-11-175-714-4	Sequence 48, Appl
770	158	4.0	2902	6	US-10-669-920-1150	Sequence 1150, Ap	847	151.5	3.8	277	6	US-11-371-354-74699	Sequence 74699, A
771	158	4.0	2902	6	US-10-669-920-1150	Sequence 1150, Ap	848	151.5	3.8	277	6	US-10-245-882-213	Sequence 213, App
772	158	4.0	2910	6	US-10-669-920-1161	Sequence 1161, Ap	849	151.5	3.8	277	7	US-11-297-134-17	Sequence 17, App
773	158	4.0	383	7	US-10-796-307-587	Sequence 587, App	850	151.5	3.8	277	7	US-11-365-073-4	Sequence 4, Appl
774	157.5	4.0	686	7	US-11-090-997-1040	Sequence 1040, Ap	851	151.5	3.8	3690	6	US-10-796-280-1384	Sequence 1384, Ap
775	157	4.0	394	6	US-11-264-243-4	Sequence 4, Appl	852	151.5	3.8	3695	6	US-10-529-348-872	Sequence 872, App
776	156.5	4.0	184	7	US-11-484-421-2	Sequence 2, Appl	853	151	3.8	247	7	US-11-415-342-60	Sequence 60, Appl
777	156.5	4.0	255	7	US-10-527-571A-301	Sequence 301, App							
778	156	4.0	255	7	US-11-319-952-57	Sequence 57, Appl							
779	156	4.0	261	7	US-11-319-952-95	Sequence 79, Appl							
780	156	4.0			US-11-319-952-79	Sequence 79, Appl							

854	151	3.8	703	6	US-10-529-348-316	Sequence 316, App	928	145.5	3.7	334	7	US-11-090-997-146	Sequence 146, App
856	150.5	3.8	685	6	US-10-567-630-33	Sequence 33, Appl	929	145	3.7	372	7	US-10-669-920-208	Sequence 208, App
857	150.5	3.8	685	6	US-10-964-241-88	Sequence 88, Appl	930	145	3.7	372	7	US-11-327-164-4	Sequence 4, Appl1
858	150.5	3.8	685	7	US-11-175-714-2	Sequence 2, Appl1	931	145	3.7	566	6	US-10-574-398-10	Sequence 10, Appl
859	150.5	3.8	685	7	US-11-175-714-38	Sequence 38, Appl	932	145	3.7	566	6	US-10-529-348-173	Sequence 173, App
860	150.5	3.8	685	7	US-11-175-714-32	Sequence 32, Appl	933	145	3.7	566	6	US-11-066-316A-597	Sequence 597, App
861	150.5	3.8	685	7	US-11-175-714-34	Sequence 34, Appl	934	145	3.7	581	7	US-11-066-316A-595	Sequence 595, App
862	150.5	3.8	685	7	US-11-175-714-36	Sequence 36, Appl	935	144	3.7	234	7	US-11-476-636-14	Sequence 14, Appl
863	150.5	3.8	685	7	US-11-175-714-38	Sequence 38, Appl	936	144	3.7	244	7	US-11-247-886-10	Sequence 10, Appl
864	150.5	3.8	685	7	US-11-178-724-38	Sequence 20, Appl	937	144	3.7	683	7	US-11-371-354-55779	Sequence 55779, App
865	150.5	3.8	685	7	US-11-264-243-2	Sequence 2, Appl1	938	143.5	3.6	246	6	US-10-538-002-124	Sequence 124, App
866	150.5	3.8	685	7	US-11-071-796A-19	Sequence 19, Appl	939	143	3.6	119	7	US-11-486-448-100316	Sequence 100316, Sequence 7
867	150.5	3.8	685	7	US-11-188-417A-20	Sequence 20, Appl	940	143	3.6	244	7	US-11-247-886-7	Sequence 7, Appl1
868	150.5	3.8	685	7	US-11-231-494-20	Sequence 20, Appl	941	142.5	3.6	428	7	US-11-345-903-14	Sequence 14, Appl1
869	150.5	3.8	34	6	US-10-631-441-2439	Sequence 2439, Ap	942	142	3.6	611	7	US-11-302-782-3	Sequence 3, Appl1
870	150	3.8	113	7	US-11-507-474-22	Sequence 22, Appl	943	141.5	3.6	294	7	US-11-147-397-43	Sequence 43, Appl
871	150	3.8	267	6	US-10-524-434-589	Sequence 589, App	944	141.5	3.6	372	6	US-10-533-519-906	Sequence 906, App
872	150	3.8	267	6	US-10-405-027-2920	Sequence 2920, Ap	945	141.5	3.6	373	6	US-10-669-920-217	Sequence 217, App
873	150	3.8	267	6	US-10-405-027-2922	Sequence 2922, Ap	946	141.5	3.6	373	6	US-10-796-307-808	Sequence 808, App
874	150	3.8	267	6	US-10-405-027-4107	Sequence 4107, Ap	947	141.5	3.6	375	6	US-10-669-920-219	Sequence 219, App
875	150	3.8	267	6	US-10-570-186-4	Sequence 4, Appl1	948	141.5	3.6	375	6	US-10-796-307-806	Sequence 806, App
876	150	3.8	276	6	US-10-544-944-16	Sequence 16, Appl	949	141.5	3.6	385	6	US-10-669-920-215	Sequence 215, App
877	150	3.8	276	6	US-10-546-435-8	Sequence 8, Appl1	950	141.5	3.6	385	6	US-10-669-920-215	Sequence 215, App
878	150	3.8	276	6	US-10-529-348-840	Sequence 840, App	951	141.5	3.6	385	6	US-10-796-307-805	Sequence 805, App
879	150	3.8	276	6	US-11-292-215-1	Sequence 1, Appl1	952	141.5	3.6	385	6	US-10-796-307-809	Sequence 809, App
880	150	3.8	276	7	US-11-319-952-88	Sequence 88, Appl	953	141	3.6	244	7	US-11-247-886-9	Sequence 9, Appl1
881	150	3.8	276	7	US-11-043-842-177	Sequence 177, App	954	141	3.6	246	6	US-10-533-520-2430	Sequence 2430, Ap
882	150	3.8	276	7	US-11-571-354-73049	Sequence 73049, A	955	141	3.6	246	6	US-11-371-355-13796	Sequence 13796, A
883	150	3.8	276	7	US-11-545-891-52	Sequence 52, Appl	956	141	3.6	246	7	US-11-371-354-65041	Sequence 65041, A
884	150	3.8	703	6	US-11-066-316A-598	Sequence 598, App	957	141	3.6	246	7	US-11-371-354-78522	Sequence 78522, A
885	150	3.8	770	6	US-10-219-051B-156	Sequence 156, App	958	141	3.6	246	7	US-11-478-191-942	Sequence 942, App
886	150	3.8	770	6	US-10-219-051B-160	Sequence 160, App	959	141	3.6	246	7	US-11-545-891-48	Sequence 48, Appl
887	150	3.8	770	6	US-10-219-051B-160	Sequence 12192, A	960	140.5	3.6	656	6	US-10-219-051B-14301	Sequence 14301, A
888	150	3.8	770	6	US-10-219-051B-160	Sequence 12196, A	961	140	3.5	148	6	US-11-295-040-2	Sequence 2, Appl1
889	149.5	3.8	533	7	US-11-371-354-64691	Sequence 64691, A	962	140	3.5	148	6	US-11-652-846-2	Sequence 2, Appl1
890	149	3.8	601	7	US-10-777-288A-2134	Sequence 599, App	963	140	3.5	971	6	US-10-760-320A-2217	Sequence 3217, Ap
891	149	3.8	644	6	US-10-219-051B-158	Sequence 2134, Ap	964	140	3.5	4590	6	US-10-505-928-569	Sequence 569, App
892	149	3.8	770	6	US-10-219-051B-158	Sequence 158, App	965	139.5	3.5	207	7	US-11-357-337-4	Sequence 4, Appl1
893	149	3.8	770	6	US-10-219-051B-152	Sequence 162, App	966	139.5	3.5	804	6	US-10-760-320A-3258	Sequence 3258, Ap
894	149	3.8	770	6	US-10-219-051B-1194	Sequence 12194, A	967	139.5	3.5	1280	6	US-10-669-920-1139	Sequence 1139, Ap
895	149	3.8	770	6	US-10-219-051B-12198	Sequence 12198, A	968	139.5	3.5	2000	6	US-10-533-520-1992	Sequence 1992, Ap
896	148.5	3.8	202	6	US-10-276-817B-14446	Sequence 14446, A	969	139	3.5	464	6	US-10-505-928-757	Sequence 757, App
897	148.5	3.8	472	7	US-11-217-997-26	Sequence 26, Appl	970	139	3.5	464	6	US-10-533-519-969	Sequence 969, App
898	148.5	3.8	1063	7	US-11-214-063A-1296	Sequence 1296, Ap	971	139	3.5	464	6	US-10-405-021-3522	Sequence 3522, Ap
899	148.5	3.8	1403	7	US-11-217-997-12	Sequence 12, Appl	972	139	3.5	464	7	US-11-371-354-13350	Sequence 13350, A
900	148.5	3.8	1404	7	US-11-217-997-2	Sequence 22, Appl1	973	139	3.5	464	7	US-11-371-354-59423	Sequence 59423, A
901	148.5	3.8	1547	7	US-11-217-997-22	Sequence 16, Appl	974	139	3.5	464	7	US-11-371-354-77882	Sequence 77882, A
902	148.5	3.8	1577	7	US-11-217-997-16	Sequence 40, Appl	975	139	3.5	3588	7	US-11-526-1137-115	Sequence 115, App
903	148.5	3.8	1577	7	US-11-217-997-20	Sequence 42, Appl	976	138.5	3.5	158	7	US-11-400-825-22	Sequence 22, Appl
904	148.5	3.8	1620	7	US-11-217-997-42	Sequence 40, Appl	977	138.5	3.5	247	6	US-10-511-937-2422	Sequence 2422, Appl
905	148.5	3.8	1653	7	US-11-217-997-740	Sequence 70, App	978	138.5	3.5	247	6	US-10-219-051B-8830	Sequence 8830, Ap
906	148.5	3.8	1786	6	US-10-796-280-770	Sequence 366, App	979	138.5	3.5	247	6	US-10-796-280-11336	Sequence 11336, Ap
907	148.5	3.8	4393	6	US-10-525-573-366	Sequence 1, Appl1	980	138.5	3.5	247	6	US-10-796-280-11337	Sequence 11337, Ap
908	148.5	3.8	4393	7	US-11-450-360-1	Sequence 23, Appl	981	138.5	3.5	247	7	US-11-484-421-222	Sequence 22, Appl
909	148	3.8	113	7	US-11-507-474-23	Sequence 361, App	982	138	3.5	226	7	US-11-362-260A-348	Sequence 348, Appl
910	148	3.8	367	6	US-10-527-571A-361	Sequence 2292, Ap	983	138	3.5	291	7	US-11-292-215-11	Sequence 11, Appl
911	148	3.8	464	6	US-10-743-643-2292	Sequence 526, App	984	138	3.5	345	6	US-10-154-678-106	Sequence 106, App
912	147.5	3.7	683	7	US-11-066-316A-596	Sequence 523, App	985	138	3.5	345	7	US-11-412-321-106	Sequence 106, App
913	147.5	3.7	4346	7	US-11-478-193-523	Sequence 114, App	986	137	3.5	892	6	US-10-777-288A-2019	Sequence 2019, Ap
914	147.5	3.7	4346	7	US-11-526-137-114	Sequence 116, App	987	137	3.5	372	6	US-10-219-051B-7832	Sequence 7832, Ap
915	147.5	3.7	4347	7	US-11-526-137-116	Sequence 56, Appl	988	137	3.5	1117	6	US-10-767-471-1010	Sequence 1010, Ap
916	147.5	3.7	4391	7	US-11-183-325-56	Sequence 70, Appl	989	137	3.5	1106	6	US-10-669-920-1142	Sequence 1142, Ap
917	147.5	3.7	4391	7	US-11-183-325-56	Sequence 3, Appl1	990	137	3.5	1506	6	US-10-669-920-1153	Sequence 1153, App
918	147	3.7	244	7	US-11-592-451-70	Sequence 1317, Ap	991	137	3.5	137	6	US-10-796-307-590	Sequence 590, App
919	147	3.7	244	7	US-11-247-886-3	Sequence 4, Appl1	992	137	3.5	2000	6	US-11-533-519-666	Sequence 666, App
920	147	3.7	1029	6	US-10-669-920-1317	Sequence 214, App	993	136.5	3.5	439	7	US-11-001-793-9105	Sequence 9105, Ap
921	146.5	3.7	277	6	US-10-245-882-214	Sequence 6538, Ap	994	136.5	3.5	439	7	US-11-001-793-11193	Sequence 11193, A
922	146.5	3.7	277	6	US-10-533-820-658	Sequence 23, Appl	995	136.5	3.5	439	7	US-11-001-793-11194	Sequence 301, Appl
923	146	3.7	157	7	US-11-400-825-23	Sequence 3476, Ap	996	136.5	3.5	618	6	US-10-567-630-31	Sequence 301, Appl
924	146	3.7	207	6	US-10-405-027-3476	Sequence 4911, Ap	997	136.5	3.5	618	6	US-10-245-882-301	Sequence 19, Appl
925	146	3.7	207	6	US-10-405-027-4911	Sequence 5, Appl1	998	136.5	3.5	618	7	US-11-178-724-19	Sequence 18, Appl
926	146	3.7	244	7	US-11-247-886-5	Sequence 347, App	999	136.5	3.5	618	7	US-11-071-796A-18	
927	146	3.7	622	7	US-11-362-260A-347		1000	136.5	3.5				

1001	136.5	3.5	618	7	US-11-188-417A-19	Sequence 19, Appl	1075	131.5	3.3	810	6	US-10-219-051B-6576	Sequence 8576, Ap
1002	136.5	3.5	618	7	US-11-231-494-14	Sequence 19, Appl	1076	131.5	3.3	810	6	US-10-219-051B-6580	Sequence 8580, Ap
1003	136.5	3.5	1198	7	US-11-217-997-19	Sequence 14, Appl	1077	131.5	3.3	810	6	US-10-245-882-3541	Sequence 361, App
1004	136	3.4	335	6	US-10-796-280-950	Sequence 950, App	1078	131.5	3.3	838	6	US-10-777-288A-3063	Sequence 3063, App
1005	136	3.4	345	6	US-10-796-280-952	Sequence 952, App	1079	131.5	3.3	1334	6	US-10-219-051B-276	Sequence 276, App
1006	136	3.4	345	6	US-11-371-354-60253	Sequence 60253, A	1080	131	3.3	76	7	US-11-254-183-46	Sequence 46, Appl
1007	136	3.4	352	6	US-10-405-027-4739	Sequence 4739, App	1081	131	3.3	76	7	US-11-253-865-46	Sequence 46, Appl
1009	136	3.4	525	6	US-10-964-241-114	Sequence 114, App	1082	131	3.3	328	7	US-11-371-354-63081	Sequence 63081, A
1010	136	3.4	666	6	US-10-449-932-41608	Sequence 41608, A	1083	131	3.3	1511	6	US-10-376-817B-15026	Sequence 15026, A
1011	135.5	3.4	118	6	US-10-294-403-848	Sequence 848, Appl	1084	131	3.3	3714	6	US-10-796-280-1383	Sequence 1383, App
1012	135.5	3.4	372	7	US-11-327-164-2	Sequence 2, Appl1	1085	130.5	3.3	207	7	US-11-345-903-9	Sequence 9, Appl1
1013	135.5	3.4	636	7	US-11-265-762-120	Sequence 100, App	1086	130.5	3.3	265	7	US-11-345-903-10	Sequence 10, Appl
1014	135.5	3.4	666	7	US-11-265-762-124	Sequence 124, App	1087	130.5	3.3	320	7	US-11-166-372-1796	Sequence 1796, Ap
1015	135	3.4	324	6	US-10-669-920-906	Sequence 906, App	1088	130.5	3.3	1233	6	US-10-777-288A-2595	Sequence 2595, Ap
1016	135	3.4	326	7	US-11-339-192-22	Sequence 22, Appl	1089	130.5	3.3	1398	7	US-11-217-997-4	Sequence 4, Appl1
1017	135	3.4	469	6	US-10-664-356-1770	Sequence 1770, Ap	1090	130.5	3.3	1450	7	US-11-217-997-6	Sequence 6, Appl1
1018	135	3.4	469	7	US-11-246-999-41	Sequence 41, Appl	1091	130.5	3.3	1594	7	US-11-217-997-18	Sequence 18, Appl
1019	135	3.4	469	7	US-11-366-486-984	Sequence 984, App	1092	130	3.3	144	7	US-11-001-793-8901	Sequence 8901, App
1020	135	3.4	469	7	US-11-001-793-9379	Sequence 9379, App	1093	130	3.3	300	7	US-11-001-793-9098	Sequence 9098, App
1021	135	3.4	494	6	US-10-664-356-1381	Sequence 1381, App	1095	130	3.3	490	6	US-10-970-823-132	Sequence 132, App
1022	135	3.4	494	6	US-10-796-280-1214	Sequence 1214, Ap	1096	130	3.3	490	6	US-10-964-241-310	Sequence 310, App
1023	135	3.4	494	6	US-10-796-280-1215	Sequence 1215, Ap	1097	129.5	3.3	254	7	US-11-427-112-10	Sequence 10, Appl
1024	135	3.4	494	6	US-10-796-280-1216	Sequence 1216, Ap	1098	129.5	3.3	271	7	US-11-427-112-11	Sequence 11, Appl
1025	135	3.4	494	7	US-11-246-999-30	Sequence 30, Appl	1099	129.5	3.3	381	6	US-10-533-519-401	Sequence 401, App
1026	135	3.4	494	7	US-11-366-486-765	Sequence 765, App	1100	129.5	3.3	381	7	US-11-371-354-68837	Sequence 68837, A
1027	135	3.4	494	7	US-11-001-793-6117	Sequence 6117, Ap	1101	129.5	3.3	534	6	US-10-276-817B-10189	Sequence 10189, A
1028	135	3.4	557	7	US-11-339-192-23	Sequence 23, Appl	1102	129.5	3.3	652	6	US-10-527-191-4	Sequence 4, Appl1
1029	135	3.4	557	7	US-11-246-999-50	Sequence 50, Appl	1103	129.5	3.3	652	6	US-10-527-191-7	Sequence 7, Appl1
1030	135	3.4	868	6	US-10-760-320A-3374	Sequence 3374, Ap	1104	129.5	3.3	652	6	US-10-527-191-39	Sequence 39, Appl
1031	134.5	3.4	260	6	US-10-530-643-14	Sequence 14, Appl	1105	129.5	3.3	652	6	US-10-527-191-42	Sequence 42, Appl
1032	134.5	3.4	332	6	US-10-540-845-3	Sequence 3, Appl1	1106	129.5	3.3	652	6	US-10-533-519-622	Sequence 622, App
1033	134.5	3.4	332	6	US-10-540-845-2	Sequence 2, Appl1	1107	129	3.3	191	6	US-10-703-031-18738	Sequence 18738
1034	134.5	3.4	358	6	US-10-540-845-4	Sequence 4, Appl1	1108	128	3.3	244	7	US-11-247-886-8	Sequence 8, Appl1
1035	134.5	3.4	1329	6	US-10-529-348-2237	Sequence 2237, Ap	1109	129	3.3	490	7	US-11-293-657-3621	Sequence 3621, Ap
1036	134.5	3.4	1529	7	US-11-491-318-29	Sequence 29, Appl	1110	128.5	3.3	255	7	US-11-371-354-59461	Sequence 59461, A
1037	134.5	3.4	1529	7	US-11-499-833-67	Sequence 67, Appl	1111	128.5	3.3	833	7	US-11-090-997-496	Sequence 496, App
1038	134	3.4	535	6	US-10-553-436-355	Sequence 355, Appl	1112	128.5	3.3	2923	6	US-10-570-909-35	Sequence 35, Appl
1039	134	3.4	587	7	US-11-030-653-32	Sequence 32, Appl	1113	128.5	3.3	2923	6	US-10-570-909-39	Sequence 39, Appl
1040	134	3.4	1786	6	US-10-519-328-2	Sequence 2, Appl1	1114	128.5	3.3	2923	6	US-10-219-051B-210	Sequence 210, Appl
1041	134	3.4	1821	6	US-10-505-828-451	Sequence 451, App	1115	128.5	3.3	2923	6	US-10-219-051B-214	Sequence 214, App
1042	133.5	3.4	1821	6	US-10-519-328-1	Sequence 1, Appl1	1116	128.5	3.3	2923	6	US-10-743-643-1049	Sequence 1049, App
1043	133.5	3.4	381	6	US-10-219-051B-795	Sequence 795, App	1117	128.5	3.3	2923	7	US-11-214-063A-932	Sequence 932, App
1044	133.5	3.4	381	6	US-10-219-051B-799	Sequence 799, App	1118	128	3.2	342	7	US-11-038-783-9	Sequence 1, Appl1
1045	133	3.4	368	6	US-10-760-320A-3121	Sequence 3121, Ap	1119	128	3.2	357	6	US-10-540-845-9	Sequence 9, Appl1
1046	133	3.4	810	6	US-10-544-553-4	Sequence 4, Appl1	1120	128	3.2	353	6	US-10-540-845-17	Sequence 17, Appl
1047	133	3.4	810	6	US-10-219-051B-8574	Sequence 8574, Ap	1121	128	3.2	377	6	US-10-540-845-8	Sequence 8, Appl1
1048	133	3.4	810	6	US-10-219-051B-8578	Sequence 8578, Ap	1122	128	3.2	383	6	US-10-540-845-10	Sequence 10, Appl
1049	133	3.4	1356	7	US-11-214-063A-1338	Sequence 1338, Ap	1123	128	3.2	383	6	US-10-540-845-16	Sequence 16, Appl
1050	132.5	3.4	310	6	US-10-570-909-7	Sequence 7, Appl1	1124	128	3.2	383	7	US-11-166-372-2006	Sequence 2006, App
1051	132.5	3.4	310	7	US-11-090-997-1042	Sequence 1042, Ap	1125	128	3.2	383	7	US-11-001-793-7591	Sequence 7591, Ap
1052	132.5	3.4	682	6	US-10-777-288A-3971	Sequence 3971, App	1126	128	3.2	389	6	US-10-540-845-18	Sequence 18, Appl
1053	132.5	3.4	2136	7	US-11-218-141-1357	Sequence 1357, App	1127	128	3.2	689	6	US-10-669-920-1339	Sequence 1329, App
1054	132.5	3.4	2725	5	US-09-976-858-230	Sequence 230, App	1128	128	3.2	723	7	US-11-450-056-4	Sequence 4, Appl1
1055	132.5	3.4	2725	5	US-11-066-316A-918	Sequence 918, App	1129	128	3.2	872	6	US-10-760-320A-4791	Sequence 4791, Ap
1056	132.5	3.4	2725	7	US-11-212-799-230	Sequence 230, App	1130	128	3.2	1418	7	US-11-217-997-38	Sequence 38, Appl
1057	132.5	3.4	2727	6	US-10-276-817B-11200	Sequence 11200, A	1131	128	3.2	1654	6	US-10-767-471-1012	Sequence 1012, Ap
1058	132	3.3	119	7	US-11-507-474-24	Sequence 24, Appl	1132	127.5	3.2	207	7	US-11-241-607-61719	Sequence 61719, A
1059	132	3.3	159	7	US-11-349-541-172	Sequence 172, App	1133	127	3.2	1609	6	US-10-533-519-115	Sequence 115, App
1060	132	3.3	159	7	US-11-344-932-172	Sequence 172, App	1134	127	3.2	2107	6	US-10-796-280-1108	Sequence 1108, App
1061	132	3.3	236	7	US-11-344-932-838	Sequence 838, App	1135	127	3.2	2107	6	US-10-796-307-671	Sequence 671, App
1062	132	3.3	236	7	US-11-371-354-56873	Sequence 56873, A	1136	127	3.2	2480	6	US-10-796-280-1106	Sequence 1106, App
1063	132	3.3	290	7	US-11-371-354-12160	Sequence 12160, A	1137	127	3.2	2480	6	US-10-796-307-669	Sequence 669, App
1064	132	3.3	290	7	US-11-371-354-73355	Sequence 73355, A	1138	127	3.2	3004	6	US-10-562-469-6	Sequence 6, Appl1
1065	132	3.3	290	7	US-11-371-354-75890	Sequence 75890, A	1139	127	3.2	3106	6	US-10-519-051B-7719	Sequence 7719, App
1066	132	3.3	386	6	US-10-760-320A-4142	Sequence 4142, App	1140	127	3.2	3116	6	US-10-796-280-1107	Sequence 1107, App
1067	132	3.3	443	6	US-10-760-320A-3401	Sequence 3401, App	1141	127	3.2	3116	6	US-10-796-307-670	Sequence 670, App
1068	132	3.3	830	6	US-10-796-280-1209	Sequence 1209, App	1142	127	3.2	3122	6	US-10-219-051B-7721	Sequence 7721, App
1069	132	3.3	1421	6	US-10-767-471-1009	Sequence 1009, App	1143	126.5	3.2	448	6	US-10-219-051B-5202	Sequence 5198, App
1070	132	3.3	1557	6	US-10-767-471-1011	Sequence 1011, App	1144	126.5	3.2	448	6	US-10-219-051B-5202	Sequence 5202, App
1071	132	3.3	1557	6	US-10-767-471-1013	Sequence 1013, App	1145	126.5	3.2	567	7	US-11-371-354-59045	Sequence 59045, A
1072	132	3.3	1587	6	US-10-767-471-1013	Sequence 1013, App	1146	126.5	3.2	844	6	US-10-777-288A-3415	Sequence 3415, App
1073	131.5	3.3	810	6	US-10-781-841-34	Sequence 34, Appl	1147	126.5	3.2	1050	7	US-11-265-762-114	Sequence 114, App
1074	131.5	3.3	810	6	US-10-544-553-2	Sequence 2, Appl1	1148	126.5	3.2	1475	6	US-10-540-898-182	Sequence 182, App

1149	126	3.2	195	6	US-10-631-441-3019	Sequence 3019, Ap	1224	121	3.1	3396	6	US-10-219-051B-14303	Sequence 14303, A
1150	126	3.2	195	6	US-10-505-928-521	Sequence 521, App	1225	120.5	3.1	1431	7	US-11-352-664-2	Sequence 2, App11
1151	126	3.2	376	7	US-11-090-997-604	Sequence 604, App	1226	120.5	3.1	1601	6	US-10-219-051B-6292	Sequence 6292, Ap
1152	126	3.2	576	7	US-11-218-141-3820	Sequence 3820, Ap	1227	120	3.0	161	6	US-10-529-163-9	Sequence 9, App1
1153	126	3.2	576	7	US-11-218-141-3821	Sequence 3821, Ap	1228	120	3.0	161	7	US-11-066-316A-638	Sequence 638, App
1154	126	3.2	600	7	US-11-371-354-56941	Sequence 56941, A	1229	120	3.0	321	6	US-10-540-845-5	Sequence 5, App1
1155	126	3.2	600	7	US-11-218-141-1852	Sequence 1852, Ap	1230	120	3.0	493	6	US-10-219-051B-2303	Sequence 2303, Ap
1156	126	3.2	708	7	US-11-293-697-4329	Sequence 4329, Ap	1231	120	3.0	493	6	US-10-219-051B-2307	Sequence 2307, Ap
1157	126	3.2	999	5	US-09-576-858-189	Sequence 189, App	1232	120	3.0	493	6	US-10-219-051B-2311	Sequence 2311, Ap
1158	126	3.2	999	5	US-11-212-799-189	Sequence 189, App	1233	120	3.0	493	6	US-10-219-051B-2315	Sequence 2315, App
1159	126	3.2	1025	7	US-11-343-271-44	Sequence 44, App1	1234	120	3.0	493	6	US-11-267-942-3	Sequence 3, App1
1160	125.5	3.2	544	6	US-10-669-920-1321	Sequence 1321, Ap	1235	120	3.0	644	6	US-10-527-191-5	Sequence 58, App1
1161	125.5	3.2	544	6	US-11-166-372-2500	Sequence 2500, Ap	1236	120	3.0	747	7	US-11-240-891-58	Sequence 58, App1
1162	125.5	3.2	544	6	US-11-371-354-59629	Sequence 59629, A	1237	120	3.0	747	7	US-11-001-793-6933	Sequence 6933, Ap
1163	125.5	3.2	728	7	US-11-450-056-2	Sequence 2, App11	1238	119.5	3.0	315	6	US-10-540-845-6	Sequence 6, App11
1164	125.5	3.2	775	6	US-10-990-328-10859	Sequence 10859, A	1239	119.5	3.0	864	7	US-11-090-997-1584	Sequence 1584, Ap
1165	125.5	3.2	775	6	US-10-990-328-10860	Sequence 10860, A	1240	119	3.0	164	7	US-11-344-932-178	Sequence 178, App
1166	125	3.2	146	6	US-10-652-846-3	Sequence 3, App11	1241	119	3.0	164	7	US-11-449-541-178	Sequence 178, App
1167	125	3.2	146	6	US-11-295-040-3	Sequence 3, App11	1242	119	3.0	870	7	US-11-090-997-1582	Sequence 1582, Ap
1168	125	3.2	151	7	US-11-400-825-21	Sequence 21, App1	1243	118.5	3.0	178	6	US-10-405-027-5666	Sequence 5666, Ap
1169	125	3.2	1587	6	US-10-767-471-1015	Sequence 1015, Ap	1244	118.5	3.0	375	6	US-10-533-520-2822	Sequence 2822, Ap
1170	124.5	3.2	531	6	US-10-990-328-10443	Sequence 10443, A	1245	118.5	3.0	375	7	US-11-289-102-304	Sequence 304, App
1171	124	3.1	531	6	US-10-760-320A-3418	Sequence 3418, Ap	1246	118.5	3.0	601	7	US-11-441-587-20	Sequence 20, App1
1172	124	3.1	559	6	US-10-219-051B-2026	Sequence 2026, Ap	1247	118.5	3.0	648	6	US-10-669-920-807	Sequence 807, App
1173	124	3.1	559	6	US-10-219-051B-2030	Sequence 2030, Ap	1248	118.5	3.0	728	6	US-10-570-046-3	Sequence 3, App11
1174	124	3.1	559	6	US-10-219-051B-3228	Sequence 3228, Ap	1249	118.5	3.0	728	6	US-10-527-195-1	Sequence 1, App11
1175	124	3.1	883	6	US-10-219-051B-8512	Sequence 8512, Ap	1250	118.5	3.0	728	6	US-10-219-051B-13942	Sequence 13942, A
1176	124	3.1	883	6	US-11-036-255A-3	Sequence 3, App11	1251	118.5	3.0	728	6	US-10-555-925-1	Sequence 1, App11
1177	124	3.1	883	6	US-11-036-255A-6	Sequence 6, App11	1252	118.5	3.0	593	6	US-11-371-354-63803	Sequence 68503, A
1178	124	3.1	911	6	US-10-219-051B-8514	Sequence 8514, Ap	1253	118	3.0	593	6	US-10-294-433-267	Sequence 267, App
1179	124	3.1	911	7	US-11-226-554-89	Sequence 89, App1	1254	118	3.0	883	7	US-11-499-835-72	Sequence 72, App1
1180	124	3.1	911	7	US-11-248-718-89	Sequence 89, App1	1255	117.5	3.0	310	7	US-11-332-404-1	Sequence 1, App11
1181	124	3.1	911	7	US-11-248-718-89	Sequence 89, App1	1256	117.5	3.0	310	7	US-11-331-494-60	Sequence 1, App11
1182	124	3.1	911	7	US-11-371-354-55327	Sequence 55327, A	1257	117.5	3.0	332	7	US-11-231-494-46	Sequence 46, App1
1183	124	3.1	911	7	US-11-538-552-89	Sequence 89, App1	1258	117.5	3.0	332	7	US-11-188-417A-1	Sequence 1, App11
1184	123.5	3.1	239	7	US-11-043-842-178	Sequence 178, App	1259	117.5	3.0	332	7	US-11-188-417A-103	Sequence 103, App
1185	123.5	3.1	603	7	US-10-276-817B-8348	Sequence 8348, Ap	1260	117.5	3.0	332	7	US-11-331-494-60	Sequence 60, App1
1186	123.5	3.1	1533	6	US-10-533-365-236	Sequence 236, App	1261	117.5	3.0	955	7	US-11-166-317A-262	Sequence 262, App
1187	123.5	3.1	1533	6	US-10-405-027-4060	Sequence 4060, Ap	1262	117.5	3.0	2000	6	US-10-533-519-1101	Sequence 732, App
1188	123	3.1	330	6	US-10-669-920-211	Sequence 211, App	1263	117.5	3.0	2000	6	US-10-533-520-1101	Sequence 1101, App
1189	123	3.1	330	6	US-10-796-307-807	Sequence 807, App	1264	117.5	3.0	2214	6	US-10-570-909-52	Sequence 25, App1
1190	123	3.1	369	7	US-11-231-494-51	Sequence 51, App1	1265	117.5	3.0	2214	6	US-10-533-520-5266	Sequence 52, App1
1191	123	3.1	816	6	US-10-584-553-14	Sequence 14, App1	1266	117.5	3.0	2214	6	US-10-533-520-6253	Sequence 6253, Ap
1192	123	3.1	1573	6	US-10-796-280-1353	Sequence 1353, Ap	1267	117.5	3.0	2214	6	US-10-533-520-6253	Sequence 6253, Ap
1193	123	3.1	1573	6	US-10-796-280-1354	Sequence 1354, Ap	1268	117.5	3.0	2279	6	US-10-533-519-1728	Sequence 1728, Ap
1194	122.5	3.1	221	6	US-10-524-434-588	Sequence 588, App	1269	117.5	3.0	2279	6	US-10-533-520-2780	Sequence 2780, Ap
1195	122.5	3.1	330	7	US-11-371-354-58499	Sequence 58499, A	1270	117	3.0	76	7	US-11-253-869-47	Sequence 47, App1
1196	122.5	3.1	447	6	US-10-405-027-5488	Sequence 5488, Ap	1271	117	3.0	171	6	US-10-529-163-8	Sequence 8, App11
1197	122.5	3.1	650	6	US-10-219-051B-14611	Sequence 14611, A	1272	117	3.0	171	6	US-10-529-163-8	Sequence 8, App11
1198	122	3.1	676	6	US-10-533-519-1232	Sequence 1232, Ap	1273	117	3.0	858	7	US-11-066-316A-639	Sequence 639, App
1199	122	3.1	676	6	US-10-219-051B-7994	Sequence 7994, Ap	1274	117	3.0	858	7	US-11-090-997-434	Sequence 434, App
1200	122	3.1	676	6	US-10-219-051B-11815	Sequence 11815, A	1275	116.5	3.0	315	6	US-10-558-279-15	Sequence 15, App1
1201	122	3.1	676	6	US-11-371-354-54991	Sequence 54991, A	1276	116.5	3.0	329	6	US-10-558-279-17	Sequence 17, App1
1202	122	3.1	879	6	US-10-276-817B-8349	Sequence 8349, Ap	1277	116.5	3.0	329	6	US-10-558-279-17	Sequence 17, App1
1203	122	3.1	879	6	US-10-276-817B-8349	Sequence 8349, Ap	1278	116.5	3.0	377	6	US-10-558-279-2	Sequence 2, App11
1204	122	3.1	3313	6	US-10-219-051B-208	Sequence 208, App	1279	116.5	3.0	384	7	US-11-371-354-62547	Sequence 62547, A
1205	122	3.1	3313	6	US-10-219-051B-212	Sequence 212, App	1280	116.5	3.0	556	6	US-10-558-279-1	Sequence 19, App1
1206	122	3.1	448	6	US-10-405-027-5323	Sequence 5323, Ap	1281	116.5	3.0	581	6	US-10-558-279-21	Sequence 21, App1
1207	121.5	3.1	448	6	US-10-405-027-5324	Sequence 5324, Ap	1282	116.5	3.0	1799	6	US-10-562-469-8	Sequence 8, App11
1208	121.5	3.1	448	6	US-10-405-027-5325	Sequence 5325, Ap	1283	116	2.9	159	7	US-11-400-825-24	Sequence 24, App1
1209	121.5	3.1	491	7	US-11-217-997-503	Sequence 30, App1	1284	116	2.9	332	6	US-10-276-817B-12437	Sequence 12437, A
1210	121.5	3.1	553	6	US-10-405-027-5322	Sequence 5322, Ap	1285	116	2.9	916	6	US-10-669-920-1259	Sequence 1259, Ap
1211	121.5	3.1	553	6	US-11-265-762-14	Sequence 14, App1	1286	116	2.9	916	6	US-10-669-920-1257	Sequence 1257, Ap
1212	121.5	3.1	650	6	US-10-520-741-11	Sequence 11, App1	1287	116	2.9	916	6	US-10-669-920-1257	Sequence 1257, Ap
1213	121.5	3.1	650	6	US-10-527-469-88	Sequence 88, App1	1288	116	2.9	916	6	US-10-669-920-1257	Sequence 1257, Ap
1214	121.5	3.1	344	6	US-10-533-520-3800	Sequence 3800, Ap	1289	116	2.9	1099	6	US-10-529-348-1134	Sequence 1124, Ap
1215	121	3.1	344	6	US-11-371-354-69383	Sequence 69383, A	1290	116	2.9	1375	6	US-10-796-280-1101	Sequence 1101, Ap
1216	121	3.1	364	6	US-10-505-928-605	Sequence 605, App	1291	115.5	2.9	210	6	US-10-405-027-4909	Sequence 4909, App
1217	121	3.1	493	7	US-11-267-942-4	Sequence 4, App11	1292	115.5	2.9	256	7	US-11-336-707-1	Sequence 1, App11
1218	121	3.1	1028	6	US-10-516-803-14	Sequence 14, App1	1293	115.5	2.9	344	6	US-10-964-241-186	Sequence 186, App
1219	121	3.1	1028	6	US-10-505-928-449	Sequence 449, App	1294	115.5	2.9	344	6	US-11-371-354-62581	Sequence 62581, A
1220	121	3.1	3396	6	US-10-700-439-118	Sequence 118, App	1295	115.5	2.9	364	7	US-11-371-354-78515	Sequence 78515, A
1221	121	3.1	3396	6	US-10-574-398-233	Sequence 233, App	1296	115.5	2.9	448	7	US-11-267-942-5	Sequence 5, App11
1222	121	3.1	3396	6	US-10-574-398-233	Sequence 233, App	1297	115.5	2.9	448	7	US-11-267-942-5	Sequence 5, App11

1298	115.5	2.9	723	6	US-10-570-046-1	Sequence 1, Appl1	1373	112.5	2.9	370	7	US-11-552-378-37	Sequence 37, Appl1
1299	115.5	2.9	735	6	US-10-760-320A-4794	Sequence 4794, App	1374	112.5	2.9	643	6	US-10-527-191-10	Sequence 10, Appl1
1300	115.5	2.9	819	7	US-11-090-997-436	Sequence 436, App	1375	112.5	2.9	1247	6	US-10-505-928-371	Sequence 371, Appl1
1301	115.5	2.9	819	7	US-11-090-997-438	Sequence 438, App	1376	112	2.8	210	6	US-10-534-578-3	Sequence 3, Appl1
1302	115.5	2.9	911	6	US-10-526-326-12	Sequence 12, Appl1	1377	112	2.8	303	7	US-11-550-237-57	Sequence 57, Appl1
1303	115.5	2.9	911	6	US-10-760-320A-4840	Sequence 4840, Ap	1378	112	2.8	303	7	US-11-550-246-57	Sequence 57, Appl1
1304	115.5	2.9	1680	6	US-10-527-571A-189	Sequence 189, App	1379	112	2.8	488	6	US-10-574-398-372	Sequence 372, App
1305	115.5	2.9	547	6	US-10-405-027-5236	Sequence 5236, Ap	1380	112	2.8	488	6	US-10-505-928-676	Sequence 676, App
1306	115	2.9	555	6	US-10-405-027-5238	Sequence 5238, Ap	1381	112	2.8	493	6	US-10-219-051B-2305	Sequence 2305, Ap
1307	115	2.9	555	6	US-10-405-027-5239	Sequence 5239, Ap	1382	112	2.8	493	6	US-10-219-051B-2209	Sequence 2309, Ap
1308	115	2.9	775	7	US-11-293-697-4433	Sequence 4433, Ap	1383	112	2.8	493	6	US-10-219-051B-2213	Sequence 2313, Ap
1309	115	2.9	969	7	US-11-371-354-66101	Sequence 66101, A	1384	112	2.8	493	6	US-10-219-051B-2217	Sequence 2317, Ap
1310	115	2.9	1019	7	US-11-442-244-76	Sequence 76, Appl1	1385	112	2.8	493	7	US-11-267-942-2	Sequence 2, Appl1
1311	115	2.9	1032	6	US-11-442-244-75	Sequence 75, Appl1	1386	112	2.8	493	7	US-11-371-354-13181	Sequence 13181, A
1312	115	2.9	1036	6	US-10-516-803-42	Sequence 12, Appl1	1387	112	2.8	493	7	US-11-371-354-58031	Sequence 58031, A
1313	115	2.9	1036	6	US-10-533-519-536	Sequence 536, App	1388	112	2.8	493	7	US-11-371-354-77652	Sequence 77652, A
1314	115	2.9	1036	6	US-10-528-260B-201	Sequence 528, App	1389	112	2.8	2006	6	US-10-533-519-1676	Sequence 1676, A
1315	115	2.9	1036	6	US-10-528-260B-201	Sequence 528, App	1389	112	2.8	2006	6	US-10-505-928-831	Sequence 831, App
1316	115	2.9	1036	6	US-10-528-260B-201	Sequence 528, App	1390	112	2.8	2006	6	US-10-505-928-831	Sequence 831, App
1317	115	2.9	1207	6	US-10-537-102-26	Sequence 26, Appl1	1391	112	2.8	4349	7	US-11-526-137-64	Sequence 64, Appl1
1318	115	2.9	1207	6	US-11-218-141-1186	Sequence 186, Ap	1392	111.5	2.8	118	6	US-10-664-025-5522	Sequence 5522, App
1319	115	2.9	1207	7	US-11-442-244-35	Sequence 35, Appl1	1393	111.5	2.8	256	7	US-11-188-417B-28	Sequence 28, Appl1
1320	115	2.9	1222	7	US-11-218-141-1154	Sequence 354, Ap	1394	111.5	2.8	317	6	US-10-669-920-1319	Sequence 1319, Ap
1321	114.5	2.9	270	7	US-11-371-354-13304	Sequence 13304, A	1395	111.5	2.8	317	6	US-10-669-920-1315	Sequence 1315, Ap
1322	114.5	2.9	270	7	US-11-371-354-59513	Sequence 59513, A	1396	111.5	2.8	317	6	US-10-669-920-1335	Sequence 1325, Ap
1323	114.5	2.9	270	7	US-11-371-354-77819	Sequence 77819, A	1397	111.5	2.8	436	6	US-10-669-920-1312	Sequence 1312, Ap
1324	114.5	2.9	314	6	US-10-558-279-13	Sequence 13, Appl1	1398	111.5	2.8	488	7	US-11-274-634-21	Sequence 21, Appl1
1325	114.5	2.9	333	7	US-11-265-762-26	Sequence 26, Appl1	1399	111.5	2.8	682	7	US-11-274-634-31708	Sequence 3708, Ap
1326	114.5	2.9	381	7	US-11-109-181-12	Sequence 12, Appl1	1400	111.5	2.8	722	7	US-11-274-634-3	Sequence 3, Appl1
1328	114.5	2.9	443	6	US-10-964-241-118	Sequence 318, App	1401	111.5	2.8	722	7	US-11-274-634-14	Sequence 14, Appl1
1329	114.5	2.9	443	6	US-11-371-354-15247	Sequence 75247, A	1402	111.5	2.8	816	6	US-10-544-553-10	Sequence 10, Appl1
1330	114.5	2.9	443	7	US-11-371-354-76113	Sequence 76113, A	1403	111.5	2.8	816	6	US-10-743-634-673	Sequence 673, App
1331	114.5	2.9	819	6	US-10-544-553-12	Sequence 12, Appl1	1404	111.5	2.8	961	7	US-11-371-354-65039	Sequence 65039, A
1332	114.5	2.9	934	6	US-11-001-793-10694	Sequence 10694, A	1405	111.5	2.8	961	7	US-11-526-137-118	Sequence 118, App
1333	114.5	2.9	1798	6	US-10-219-051B-6294	Sequence 6294, Ap	1406	111	2.8	201	6	US-10-796-280-1135	Sequence 1135, App
1334	114.5	2.9	1798	6	US-10-796-307-899	Sequence 899, App	1407	111	2.8	317	6	US-11-550-237-56	Sequence 56, Appl1
1335	114.5	2.9	1798	6	US-10-796-307-900	Sequence 900, App	1408	111	2.8	317	7	US-11-550-246-56	Sequence 56, Appl1
1336	114	2.9	231	6	US-10-595-576-1	Sequence 1, Appl1	1409	111	2.8	322	7	US-11-507-474-6	Sequence 6, Appl1
1337	114	2.9	291	7	US-11-412-325-212	Sequence 212, App	1410	110.5	2.8	615	6	US-10-953-349-11116	Sequence 1116, A
1338	114	2.9	397	7	US-11-412-325-211	Sequence 211, App	1411	110.5	2.8	679	6	US-10-528-260B-433	Sequence 433, App
1339	114	2.9	413	7	US-11-001-793-7164	Sequence 7164, Ap	1412	110.5	2.8	776	6	US-11-218-141-1740	Sequence 1740, Ap
1340	114	2.9	466	7	US-11-511-685-6	Sequence 6, Appl1	1413	110.5	2.8	776	6	US-11-254-185-48	Sequence 48, Appl1
1341	114	2.9	542	7	US-11-511-685-35	Sequence 35, Appl1	1414	110.5	2.8	1217	6	US-10-537-102-28	Sequence 28, Appl1
1342	114	2.9	575	6	US-10-669-920-804	Sequence 804, App	1415	110	2.8	76	7	US-11-253-869-48	Sequence 48, Appl1
1343	114	2.9	598	6	US-10-669-920-802	Sequence 70, Appl1	1416	110	2.8	357	7	US-11-129-740-131	Sequence 131, App
1344	114	2.9	787	6	US-10-154-678-70	Sequence 70, Appl1	1417	110	2.8	448	7	US-11-240-891-15	Sequence 15, App
1345	114	2.9	787	6	US-11-412-325-70	Sequence 8322, Ap	1420	110	2.8	448	6	US-10-219-051B-801	Sequence 801, App
1346	114	2.9	794	7	US-11-001-793-9322	Sequence 185, App	1421	110	2.8	448	6	US-11-354-559-8	Sequence 8, Appl1
1347	114	2.9	807	5	US-09-976-858-185	Sequence 185, App	1422	110	2.8	624	6	US-10-760-320B-4368	Sequence 4368, Ap
1348	114	2.9	807	5	US-11-212-799-185	Sequence 8, Appl1	1424	110	2.8	704	7	US-11-538-764-141	Sequence 2, Appl1
1349	114	2.9	822	7	US-11-371-354-63937	Sequence 63937, A	1425	110	2.8	864	7	US-11-416-613-2	Sequence 105, App
1350	114	2.9	956	6	US-10-529-348-249	Sequence 249, App	1426	110	2.8	864	7	US-11-129-740-105	Sequence 105, App
1351	114	2.9	1394	7	US-11-352-664-35	Sequence 25, Appl1	1427	110	2.8	977	7	US-11-416-613-1	Sequence 1, Appl1
1352	114	2.9	100	6	US-10-276-817B-15239	Sequence 15239, A	1428	110	2.8	1101	7	US-11-371-354-67173	Sequence 67173, A
1353	113.5	2.9	373	6	US-10-669-920-1333	Sequence 1333, App	1429	110	2.8	1124	7	US-11-365-989-190	Sequence 190, App
1354	113.5	2.9	382	6	US-10-669-920-1341	Sequence 1341, Ap	1430	110	2.8	1124	7	US-11-401-340-42	Sequence 42, Appl1
1355	113.5	2.9	879	6	US-10-219-051B-9341	Sequence 9341, Ap	1431	110	2.8	1124	7	US-11-129-740-309	Sequence 278, App
1356	113.5	2.9	879	6	US-10-219-051B-9341	Sequence 12041, A	1432	110	2.8	1124	7	US-11-129-740-309	Sequence 309, App
1357	113.5	2.9	1712	6	US-10-219-051B-7254	Sequence 7254, App	1433	110	2.8	1124	7	US-11-389-543-189	Sequence 189, App
1358	113.5	2.9	3439	6	US-10-276-817B-11661	Sequence 11661, A	1434	109.5	2.8	867	6	US-10-777-888B-3380	Sequence 6, Appl1
1359	113	2.9	254	7	US-11-166-372-2110	Sequence 2110, Ap	1435	109.5	2.8	339	7	US-11-371-354-63505	Sequence 3980, Appl1
1360	112.5	2.9	370	7	US-11-001-793-7098	Sequence 7098, Ap	1436	109	2.8	108	6	US-10-544-553-6	Sequence 63505, A
1361	112.5	2.9	370	7	US-11-001-793-9997	Sequence 9997, Ap	1437	108.5	2.8	108	6	US-10-777-888B-3380	Sequence 10545, A
1362	112.5	2.9	370	7	US-11-001-793-9997	Sequence 9998, Ap	1438	108.5	2.8	273	6	US-10-405-027-4045	Sequence 4045, App
1363	112.5	2.9	370	7	US-11-507-474-8	Sequence 8, Appl1	1442	108.5	2.8	545	7	US-11-101-316-110	Sequence 110, App
1364	112.5	2.9	370	7	US-11-538-706-2	Sequence 2, Appl1	1443	108.5	2.8	545	7	US-11-293-697-3725	Sequence 3725, App
1365	112.5	2.9	370	7	US-11-539-271-2	Sequence 2, Appl1	1444	108.5	2.8	545	7	US-11-376-673-110	Sequence 110, App
1366	112.5	2.9	370	7	US-11-550-155-2	Sequence 2, Appl1	1445	108.5	2.8	545	7	US-11-102-984-110	Sequence 110, App
1367	112.5	2.9	370	7	US-11-550-237-2	Sequence 2, Appl1	1446	108.5	2.8	545	6	US-10-574-398-183	Sequence 183, App
1368	112.5	2.9	370	7	US-11-550-246-2	Sequence 2, Appl1	1447	108.5	2.8	713	6	US-10-664-556-1274	Sequence 1274, App
1369	112.5	2.9	370	7	US-11-552-848-5	Sequence 5, Appl1	1448	108.5	2.8	713	7	US-11-265-762-4	Sequence 4, Appl1
1370	112.5	2.9	370	7	US-11-552-848-5	Sequence 5, Appl1	1450	108.5	2.8	713	7	US-11-001-793-5998	Sequence 5998, App
1371	112.5	2.9	370	7	US-11-552-848-5	Sequence 5, Appl1	1451	108.5	2.8	21	7	US-11-354-653-74	Sequence 74, Appl1
1372	112.5	2.9	370	7	US-11-552-848-5	Sequence 5, Appl1	1452	108	2.7	21	7	US-11-354-653-74	Sequence 74, Appl1

1453	108	2.7	251	7	US-11-248-110-6	Sequence 6, Appl
1454	108	2.7	251	7	US-11-300-928-45	Sequence 45, Appl
1455	108	2.7	251	7	US-11-478-193-1102	Sequence 1102, Ap
1456	108	2.7	392	6	US-10-405-027-4803	Sequence 4803, Ap
1457	108	2.7	448	6	US-10-219-051B-5200	Sequence 5200, Ap
1458	108	2.7	448	6	US-10-219-051B-5204	Sequence 5204, Ap
1459	108	2.7	448	6	US-10-405-027-3398	Sequence 3398, Ap
1460	108	2.7	448	6	US-10-405-027-4802	Sequence 4802, Ap
1461	108	2.7	448	7	US-11-371-354-57595	Sequence 57595, A
1462	108	2.7	448	7	US-11-371-354-77886	Sequence 77886, A
1463	108	2.7	1321	7	US-11-538-566-82	Sequence 82, Appl
1464	107.5	2.7	769	7	US-11-343-271-26	Sequence 26, Appl
1465	107.5	2.7	2000	6	US-10-529-348-1019	Sequence 1019, Ap
1466	107.5	2.7	3014	7	US-11-538-566-107	Sequence 107, App
1467	107.5	2.7	4060	6	US-10-767-471-942	Sequence 942, App
1468	107.5	2.7	4060	6	US-10-990-328-10412	Sequence 10412, A
1469	107.5	2.7	4289	6	US-10-767-471-943	Sequence 943, App
1470	107.5	2.7	4289	6	US-10-990-328-10414	Sequence 10414, A
1471	107.5	2.7	4419	6	US-10-530-393-9	Sequence 9, Appl
1472	107.5	2.7	4419	6	US-10-530-393-11	Sequence 11, Appl
1473	107.5	2.7	4454	6	US-10-530-393-8	Sequence 8, Appl
1474	107.5	2.7	4464	6	US-10-530-393-10	Sequence 10, Appl
1475	107.5	2.7	4465	6	US-10-569-920-477	Sequence 477, Appl
1476	107.5	2.7	4544	6	US-10-530-393-5	Sequence 5, Appl
1477	107.5	2.7	4544	7	US-11-218-141-1753	Sequence 1753, Ap
1478	107	2.7	372	6	US-10-405-027-5237	Sequence 5237, Ap
1480	107	2.7	379	6	US-10-970-823-4	Sequence 4, Appl
1481	107	2.7	379	6	US-10-405-027-4643	Sequence 4643, Ap
1482	107	2.7	379	6	US-10-405-027-5532	Sequence 5532, Ap
1483	107	2.7	379	6	US-10-405-027-5534	Sequence 5534, Ap
1484	107	2.7	379	6	US-10-964-241-308	Sequence 308, App
1485	107	2.7	379	7	US-11-355-441-4	Sequence 4, Appl
1486	107	2.7	379	7	US-11-090-997-1694	Sequence 1694, Ap
1487	107	2.7	379	7	US-11-240-891-22	Sequence 22, Appl
1488	107	2.7	379	7	US-11-371-354-56509	Sequence 56509, A
1489	107	2.7	379	7	US-11-001-793-7725	Sequence 7725, Ap
1490	107	2.7	394	6	US-10-405-027-5240	Sequence 5240, Ap
1491	107	2.7	480	6	US-10-563-166-2	Sequence 2, Appl
1492	107	2.7	586	6	US-10-553-349-11117	Sequence 11117, A
1493	107	2.7	1322	6	US-10-276-817B-10945	Sequence 10945, A
1494	106.5	2.7	113	7	US-11-254-185-23	Sequence 23, Appl
1495	106.5	2.7	113	7	US-11-253-869-23	Sequence 23, Appl
1496	106.5	2.7	159	6	US-10-652-846-5	Sequence 5, Appl
1497	106.5	2.7	159	6	US-11-295-040-5	Sequence 5, Appl
1498	106.5	2.7	164	7	US-11-400-825-25	Sequence 25, Appl
1499	106.5	2.7	352	7	US-11-511-685-8	Sequence 8, Appl
1500	106.5	2.7	755	6	US-10-219-051B-13977	Sequence 13977, A

Search completed: April 4, 2007, 22:27:48
Job time : 114 secs

THIS PAGE BLANK (USPTO)